



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 110963

TO: James Schultz
Location: CM1-12E18/11E12
Art Unit: 1635
Wednesday, December 24, 2003
Case Serial Number: 10/001,844

From: Paul Schulwitz
Location: Biotech-Chem Library
CM1-6B06
Phone: 305-1954

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(703)305-1954



03P 12/18

Schulwitz, Paul

From: Schreiber, David
Sent: Wednesday, December 17, 2003 11:38 AM
To: Schulwitz, Paul
Subject: FW: Sequence search 10/001,844

Here is a new one.

David Schreiber, Ph.D.
Scientific and Technical Information Center
Biotech/Chem Library
CM1-6A03
703-308-4292

QM58

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Wednesday, December 17, 2003 10:49 AM
To: Schreiber, David
Subject: FW: Sequence search 10/001,844

-----Original Message-----

From: Schultz, James
Sent: Wednesday, December 17, 2003 10:00 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/001,844

Hi David,

I need to order a "length over score" nucleotide sequence search on nucleotides ~~1000-1000~~ of SEQ ID NO:3 (1576 nt long) in the above entitled case. I need the lower and upper limits to be 8 and 50, respectively, I need those hits complementary to the 70% level, and please transfer as many hits into the excel program as possible. I do not need the interference databases searched.

Thanks,

Doug Schultz

1248
entire sequence

James Douglas Schultz, PhD
AU 1635 (Biotechnology)
Patent Examiner
United States Patent and Trademark Office
CM1-12E18
703-308-9355 Office
703-746-3973 FAX
AFTER JAN. 13, 2003:
REM 2D18
(571) 272-0763

rge	940	✓
rng	70	✓
rni	605	✓
rnrb	145	✓
rst	137	

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:32:52 ; Search time 26 Seconds
(without alignments)
2.044 Million cell updates/sec

Title: us-10-001-844-3

Perfect score: 1576

Sequence: 1 gcggagcagccagcagagga.....gaggggcgcggagggggcc 1576

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 921 seqs, 16857 residues

Total number of hits satisfying chosen parameters: 1842

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 940 summaries

Database : rge.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	50	3.2	50	1	AX146582
C 2	48.4	3.1	50	1	AX146613
C 3	48.4	3.1	50	1	AX146614
C 4	45.2	2.9	50	1	AX146616
C 5	43.8	2.8	47	1	AX146608
C 6	43.8	2.8	47	1	AX146609
C 7	43.4	2.8	45	1	AX146612
C 8	42	2.7	50	1	AX146615
C 9	41.4	2.6	43	1	AX146617
C 10	40.6	2.6	47	1	AX146611
C 11	37.4	2.4	47	1	AX146610
C 12	36	2.3	49	1	AR226529
C 13	27	1.7	27	1	AX548365
C 14	27	1.7	27	1	HS2270316
C 15	25	1.6	33	1	HS2270316
C 16	24	1.5	24	1	AR063105
C 17	24	1.5	24	1	AR122632
C 18	24	1.5	24	1	AR164260
C 19	24	1.5	24	1	AR208932
C 20	23.6	1.5	30	1	184401
C 21	23.6	1.5	31	1	AR1419
C 22	22.6	1.4	30	1	AR242044
C 23	22.4	1.4	32	1	AR62993
C 24	22.4	1.4	32	1	AR179068
C 25	22	1.4	23	1	HS2270315
C 26	22	1.4	24	1	AX548364
C 27	22	1.4	29	1	AX146574
C 28	22	1.4	29	1	AX147112
C 29	19.2	1.2	24	1	AX327693
C 30	19	1.2	19	1	AR154250
C 31	19	1.2	19	1	AR154250
C 32	18.6	1.2	25	1	AR028113
C 33	18.6	1.2	25	1	AR030289

18.6	1.2	25	1	AX689173
18.6	1.2	25	1	I42108
18.2	1.2	24	1	AR063245
18.2	1.2	25	1	AX689174
18.2	1.2	25	1	AX689175
18.2	1.2	25	1	E16881
18	1.1	18	1	AR154251
17.8	1.1	21	1	AR177692
17.8	1.1	21	1	AX616896
17.6	1.1	25	1	AX548233
17.6	1.1	25	1	AX689172
17.2	1.1	24	1	AR028416
17.2	1.1	24	1	AR130926
17.2	1.1	24	1	AR161892
17.2	1.1	24	1	AR240225
16.8	1.1	24	1	AX548360
16.6	1.1	24	1	AR063245
16.4	1.0	18	1	AR137168
16.4	1.0	18	1	BD136502
16.4	1.0	20	1	AX537662
16.4	1.0	21	1	AS8260
16.4	1.0	21	1	AX244168
16.2	1.0	21	1	AR084563
16.2	1.0	21	1	AR084566
16.2	1.0	21	1	AR084567
16.2	1.0	21	1	AR084578
16.2	1.0	21	1	AR084579
16.2	1.0	21	1	AR084582
16.2	1.0	21	1	AR093142
16.2	1.0	22	1	A88669
16.2	1.0	22	1	AR0636
16.2	1.0	22	1	AR028417
16.2	1.0	22	1	AR028420
16.2	1.0	22	1	AR130927
16.2	1.0	20	1	AR130930
16.2	1.0	22	1	AR161893
16.2	1.0	22	1	AR161896
16.2	1.0	22	1	BD066182
16.2	1.0	23	1	E41382
15.8	1.0	20	1	AR099499
15.8	1.0	20	1	AR178780
15.8	1.0	20	1	AR182885
15.8	1.0	20	1	AR221407
15.8	1.0	20	1	AR271204
15.8	1.0	20	1	AX104051
15.8	1.0	20	1	AX355382
15.8	1.0	20	1	AX547104
15.8	1.0	20	1	BD069976
15.8	1.0	21	1	AR109586
15.8	1.0	21	1	AX094992
15.8	1.0	21	1	AX095827
15.8	1.0	21	1	AX146231
15.6	1.0	21	1	E08187
15.6	1.0	22	1	DOG2016P01
15.4	1.0	17	1	A88670
15.4	1.0	17	1	A90637
15.4	1.0	17	1	BD066183
15.4	1.0	17	1	BD141639
15.4	1.0	18	1	A67594
15.4	1.0	18	1	AR089732
15.4	1.0	20	1	AR315298
15.2	1.0	22	1	BD139686
15.2	1.0	20	1	AR137400
15.2	1.0	20	1	AR174482
15.2	1.0	20	1	AR212475
15.2	1.0	20	1	AR217890
15.2	1.0	20	1	AX027702
15.2	1.0	21	1	AR001196
15.2	1.0	21	1	AX154080
15.2	1.0	21	1	E11034
15	1.0	16	1	I07164
15	1.0	19	1	SSAJ793
15	1.0	21	1	AS1144

ACCESSION:AX689173
ACCESSION:I42108
ACCESSION:AR063245
ACCESSION:AX689174
ACCESSION:AX689175
ACCESSION:E16881
ACCESSION:AR154251
ACCESSION:AR177692
ACCESSION:AX616896
ACCESSION:AX548233
ACCESSION:AX689172
ACCESSION:AR028416
ACCESSION:AR130926
ACCESSION:AR161892
ACCESSION:AR240225
ACCESSION:AX548360
ACCESSION:AR063245
ACCESSION:AR137168
ACCESSION:BD136502
ACCESSION:AX537662
ACCESSION:AS8260
ACCESSION:AX244168
ACCESSION:AR084563
ACCESSION:AR084566
ACCESSION:AR084567
ACCESSION:AR084578
ACCESSION:AR084579
ACCESSION:AR084582
ACCESSION:AR093142
ACCESSION:A88669
ACCESSION:AR0636
ACCESSION:AR028417
ACCESSION:AR028420
ACCESSION:AR130927
ACCESSION:AR130930
ACCESSION:AR161893
ACCESSION:AR161896
ACCESSION:BD066182
ACCESSION:E41382
ACCESSION:AR099499
ACCESSION:AR178780
ACCESSION:AR182885
ACCESSION:AR221407
ACCESSION:AR271204
ACCESSION:AX104051
ACCESSION:AX355382
ACCESSION:AX547104
ACCESSION:BD069976
ACCESSION:AR109586
ACCESSION:AX094992
ACCESSION:AX095827
ACCESSION:AX146231
ACCESSION:E08187
ACCESSION:L78581
ACCESSION:A88670
ACCESSION:A90637
ACCESSION:BD066183
ACCESSION:BD141639
ACCESSION:A67594
ACCESSION:AR089732
ACCESSION:AR315298
ACCESSION:BD139686
ACCESSION:AR137400
ACCESSION:AR174482
ACCESSION:AR212475
ACCESSION:AR217890
ACCESSION:AX027702
ACCESSION:AR001196
ACCESSION:AX154080
ACCESSION:E11034
ACCESSION:T07164
ACCESSION:AJ000793
ACCESSION:AS1144

107	15	1.0	21	1	A76969	180	14.2	0.9	20	1	AR234546
108	14.8	0.9	18	1	A67588	C 181	14.2	0.9	20	1	AR262768
C 109	14.8	0.9	18	1	AR085574	C 182	14.2	0.9	20	1	AR271767
110	14.8	0.9	18	1	AR085577	C 183	14.2	0.9	20	1	AX008654
111	14.8	0.9	18	1	AR083726	C 184	14.2	0.9	20	1	AX009450
112	14.8	0.9	18	1	AR171053	C 185	14.2	0.9	20	1	AX037348
113	14.8	0.9	18	1	AX063650	C 186	14.2	0.9	20	1	AX048785
C 114	14.8	0.9	18	1	AX115187	C 187	14.2	0.9	20	1	AX224942
115	14.8	0.9	18	1	BD178357	C 188	14.2	0.9	20	1	AX224943
116	14.8	0.9	19	1	AR101713	C 189	14.2	0.9	20	1	AX293815
117	14.8	0.9	20	1	AR052628	C 190	14.2	0.9	20	1	AX299012
C 118	14.8	0.9	20	1	AR124135	C 191	14.2	0.9	20	1	AX671167
C 119	14.8	0.9	20	1	AR123752	C 192	14.2	0.9	20	1	BD006253
C 120	14.8	0.9	20	1	AX224938	C 193	14.2	0.9	20	1	BD073147
C 121	14.8	0.9	20	1	AX250649	C 194	14.2	0.9	20	1	BD138116
C 122	14.8	0.9	20	1	AX250651	C 195	14.2	0.9	20	1	BD162107
C 123	14.8	0.9	20	1	BD001973	C 196	14.2	0.9	20	1	E05616
C 124	14.8	0.9	20	1	BD178509	C 197	14.2	0.9	20	1	E34262
C 125	14.8	0.9	20	1	E31674	C 198	14.2	0.9	20	1	I12355
C 126	14.8	0.9	20	1	I12609	C 199	14.2	0.9	20	1	I19642
C 127	14.8	0.9	21	1	A56957	C 200	14.2	0.9	20	1	I27426
C 128	14.8	0.9	21	1	AR052917	C 201	14.2	0.9	20	1	I27459
C 129	14.8	0.9	21	1	AR054280	C 202	14.2	0.9	20	1	I33964
C 130	14.8	0.9	21	1	AR054482	C 203	14.2	0.9	20	1	I77271
131	14.8	0.9	21	1	AR148289	C 204	14	0.9	15	1	A86671
132	14.8	0.9	21	1	AX13267	C 205	14	0.9	15	1	A86671
C 133	14.4	0.9	17	1	A31925	C 206	14	0.9	15	1	A86671
C 134	14.4	0.9	17	1	AR053075	C 207	14	0.9	15	1	AR116349
C 135	14.4	0.9	17	1	AR065036	C 208	14	0.9	15	1	AR131625
C 136	14.4	0.9	17	1	AX423136	C 209	14	0.9	16	1	BD066184
C 137	14.4	0.9	17	1	I32581	C 210	14	0.9	17	1	AX007862
C 138	14.4	0.9	18	1	AR181637	C 211	14	0.9	17	1	AX216347
C 139	14.4	0.9	18	1	AR196700	C 212	14	0.9	17	1	AX216895
C 140	14.4	0.9	19	1	AR295385	C 213	14	0.9	19	1	AR029261
141	14.4	0.9	13	1	AX123738	C 214	14	0.9	19	1	AR141675
C 142	14.4	0.9	20	1	AR163839	C 215	14	0.9	20	1	AX052895
C 143	14.4	0.9	20	1	AR163929	C 216	14	0.9	20	1	AR086184
C 144	14.4	0.9	20	1	AR163930	C 217	14	0.9	20	1	AR116329
C 145	14.4	0.9	20	1	AR208802	C 218	14	0.9	20	1	AR172916
C 146	14.4	0.9	20	1	AX456510	C 219	14	0.9	20	1	AR176750
147	14.4	0.9	20	1	AX613784	C 220	14	0.9	20	1	AR296674
C 148	14.4	0.9	20	1	BD090479	C 221	14	0.9	20	1	AX360175
C 149	14.4	0.9	20	1	E31668	C 222	13.8	0.9	17	1	BD016571
C 150	14.4	0.9	20	1	E31668	C 223	13.8	0.9	17	1	AR190074
C 151	14.2	0.9	19	1	AR161796	C 224	13.8	0.9	17	1	AR285007
152	14.2	0.9	19	1	AX469761	C 225	13.8	0.9	17	1	AR300148
153	14.2	0.9	19	1	AX535777	C 226	13.8	0.9	17	1	AX012584
154	14.2	0.9	19	1	AX557192	C 227	13.8	0.9	17	1	AX13249
C 155	14.2	0.9	19	1	BD094590	C 228	13.8	0.9	17	1	AX215399
C 156	14.2	0.9	20	1	D0GP18802	C 229	13.8	0.9	17	1	AX216373
C 157	14.2	0.9	20	1	AR027799	C 230	13.8	0.9	17	1	AX216946
C 158	14.2	0.9	20	1	AR028728	C 231	13.8	0.9	17	1	AX273287
C 159	14.2	0.9	20	1	AR036620	C 232	13.8	0.9	17	1	AX326057
C 160	14.2	0.9	20	1	AR037348	C 233	13.8	0.9	17	1	AX326058
161	14.2	0.9	20	1	AR040531	C 234	13.8	0.9	17	1	AX422333
C 162	14.2	0.9	20	1	AR060544	C 235	13.8	0.9	17	1	AX422334
C 163	14.2	0.9	20	1	AR060544	C 236	13.8	0.9	17	1	AX422337
C 164	14.2	0.9	20	1	AR069073	C 237	13.8	0.9	17	1	AX499047
C 165	14.2	0.9	20	1	AR073640	C 238	13.8	0.9	17	1	AX530992
C 166	14.2	0.9	20	1	AR088462	C 239	13.8	0.9	17	1	AX531303
C 167	14.2	0.9	20	1	AR100185	C 240	13.8	0.9	17	1	AX531304
C 168	14.2	0.9	20	1	AR102403	C 241	13.8	0.9	17	1	AX531305
C 169	14.2	0.9	20	1	AR124487	C 242	13.8	0.9	17	1	AX531620
C 170	14.2	0.9	20	1	AR130116	C 243	13.8	0.9	17	1	AX531621
C 171	14.2	0.9	20	1	AR137875	C 244	13.8	0.9	17	1	AX531622
C 172	14.2	0.9	20	1	AR139321	C 245	13.8	0.9	17	1	AX531927
C 173	14.2	0.9	20	1	AR149869	C 246	13.8	0.9	17	1	AX532239
C 174	14.2	0.9	20	1	AR178908	C 247	13.8	0.9	17	1	AX587568
C 175	14.2	0.9	20	1	AR201438	C 248	13.8	0.9	17	1	BD013533
C 176	14.2	0.9	20	1	AR206614	C 249	13.8	0.9	17	1	BD104924
C 177	14.2	0.9	20	1	AR220167	C 250	13.8	0.9	17	1	BD105163
C 178	14.2	0.9	20	1	AR221462	C 251	13.8	0.9	17	1	I46478
179	14.2	0.9	20	1	AR224718	C 252	13.8	0.9	17	1	I46479

253	13.8	0.9	18	1	A88003	ACCESSION:A88003	326	13.4	0.9	17	1	AX422879	ACCESSION:AX422879
254	13.8	0.9	18	1	A89970	ACCESSION:A89970	327	13.4	0.9	17	1	AX422915	ACCESSION:AX422915
255	13.8	0.9	18	1	A94014	ACCESSION:A94014	328	13.4	0.9	17	1	AX423599	ACCESSION:AX423599
256	13.8	0.9	18	1	AR042339	ACCESSION:AR042339	329	13.4	0.9	17	1	AX498855	ACCESSION:AX498855
257	13.8	0.9	18	1	AR073408	ACCESSION:AR073408	330	13.4	0.9	17	1	AX498856	ACCESSION:AX498856
258	13.8	0.9	18	1	AR098790	ACCESSION:AR098790	331	13.4	0.9	17	1	AX498857	ACCESSION:AX498857
259	13.8	0.9	18	1	AR187553	ACCESSION:AR187553	332	13.4	0.9	17	1	AX687669	ACCESSION:AX687669
260	13.8	0.9	18	1	AR196702	ACCESSION:AR196702	333	13.4	0.9	17	1	AX687670	ACCESSION:AX687670
261	13.8	0.9	18	1	AR208235	ACCESSION:AR208235	334	13.4	0.9	17	1	AX687747	ACCESSION:AX687747
262	13.8	0.9	18	1	AR264376	ACCESSION:AR264376	335	13.4	0.9	17	1	AX687748	ACCESSION:AX687748
263	13.8	0.9	18	1	AR284966	ACCESSION:AR284966	336	13.4	0.9	17	1	AX687749	ACCESSION:AX687749
264	13.8	0.9	18	1	AX003659	ACCESSION:AX003659	337	13.4	0.9	17	1	AX723430	ACCESSION:AX723430
265	13.8	0.9	18	1	AX003663	ACCESSION:AX003663	338	13.4	0.9	17	1	AX728094	ACCESSION:AX728094
266	13.8	0.9	18	1	AX012542	ACCESSION:AX012542	339	13.4	0.9	17	1	AX729048	ACCESSION:AX729048
267	13.8	0.9	18	1	AX111434	ACCESSION:AX111434	340	13.4	0.9	17	1	BD058091	ACCESSION:BD058091
268	13.8	0.9	18	1	AX286197	ACCESSION:AX286197	341	13.4	0.9	17	1	BD058092	ACCESSION:BD058092
269	13.8	0.9	18	1	AX637770	ACCESSION:AX637770	342	13.4	0.9	17	1	E33640	ACCESSION:E33640
270	13.8	0.9	18	1	AX644831	ACCESSION:AX644831	343	13.4	0.9	17	1	I26645	ACCESSION:I26645
271	13.8	0.9	18	1	BD065516	ACCESSION:BD065516	344	13.4	0.9	17	1	AR7319	ACCESSION:AR7319
272	13.8	0.9	18	1	E06269	ACCESSION:E06269	345	13.4	0.9	18	1	AR096628	ACCESSION:AR096628
273	13.8	0.9	18	1	E06465	ACCESSION:E06465	346	13.4	0.9	18	1	AX003666	ACCESSION:AX003666
274	13.8	0.9	18	1	I21664	ACCESSION:I21664	347	13.4	0.9	18	1	AX353569	ACCESSION:AX353569
275	13.8	0.9	18	1	I21665	ACCESSION:I21665	348	13.4	0.9	18	1	AX412098	ACCESSION:AX412098
276	13.8	0.9	18	1	I76077	ACCESSION:I76077	349	13.4	0.9	18	1	AX598747	ACCESSION:AX598747
277	13.8	0.9	18	1	I76078	ACCESSION:I76078	350	13.4	0.9	18	1	BD057397	ACCESSION:BD057397
278	13.8	0.9	19	1	A33509	ACCESSION:A33509	351	13.4	0.9	19	1	AR222933	ACCESSION:AR222933
279	13.8	0.9	19	1	AR020487	ACCESSION:AR020487	352	13.4	0.9	19	1	AX007819	ACCESSION:AX007819
280	13.8	0.9	19	1	AR051219	ACCESSION:AR051219	353	13.4	0.9	19	1	AX300524	ACCESSION:AX300524
281	13.8	0.9	19	1	AR053210	ACCESSION:AR053210	354	13.4	0.9	19	1	AX421254	ACCESSION:AX421254
282	13.8	0.9	19	1	AR069473	ACCESSION:AR069473	355	13.4	0.9	19	1	AX643373	ACCESSION:AX643373
283	13.8	0.9	19	1	AR073794	ACCESSION:AR073794	356	13.4	0.9	19	1	AX643376	ACCESSION:AX643376
284	13.8	0.9	19	1	AR162790	ACCESSION:AR162790	357	13.4	0.9	19	1	E63275	ACCESSION:E63275
285	13.8	0.9	19	1	AR205717	ACCESSION:AR205717	358	13.4	0.9	19	1	I88039	ACCESSION:I88039
286	13.8	0.9	19	1	AX128970	ACCESSION:AX128970	359	13.2	0.8	18	1	A18145	ACCESSION:A18145
287	13.8	0.9	19	1	AX132668	ACCESSION:AX132668	360	13.2	0.8	18	1	A34806	ACCESSION:A34806
288	13.8	0.9	19	1	AX398139	ACCESSION:AX398139	361	13.2	0.8	18	1	A63132	ACCESSION:A63132
289	13.8	0.9	19	1	AX643372	ACCESSION:AX643372	362	13.2	0.8	18	1	AR007264	ACCESSION:AR007264
290	13.8	0.9	19	1	AX643375	ACCESSION:AX643375	363	13.2	0.8	18	1	AR007265	ACCESSION:AR007265
291	13.8	0.9	19	1	E21863	ACCESSION:E21863	364	13.2	0.8	18	1	AR034870	ACCESSION:AR034870
292	13.8	0.9	19	1	E30322	ACCESSION:E30322	365	13.2	0.8	18	1	AR034880	ACCESSION:AR034880
293	13.8	0.9	19	1	I88034	ACCESSION:I88034	366	13.2	0.8	18	1	AR034902	ACCESSION:AR034902
294	13.8	0.9	33	1	I84406	ACCESSION:I84406	367	13.2	0.8	18	1	AR049396	ACCESSION:AR049396
295	13.8	0.9	43	1	AX146617	ACCESSION:AX146617	368	13.2	0.8	18	1	AR067397	ACCESSION:AR067397
296	13.6	0.9	20	1	AR139321	ACCESSION:AR139321	369	13.2	0.8	18	1	AR067989	ACCESSION:AR067989
297	13.6	0.9	45	1	AX146612	ACCESSION:AX146612	370	13.2	0.8	18	1	AR067990	ACCESSION:AR067990
298	13.4	0.9	15	1	A88145	ACCESSION:A88145	371	13.2	0.8	18	1	AR069478	ACCESSION:AR069478
299	13.4	0.9	15	1	A90112	ACCESSION:A90112	372	13.2	0.8	18	1	AR071801	ACCESSION:AR071801
300	13.4	0.9	15	1	AR084532	ACCESSION:AR084532	373	13.2	0.8	18	1	AR084251	ACCESSION:AR084251
301	13.4	0.9	15	1	AR131624	ACCESSION:AR131624	374	13.2	0.8	18	1	AR084252	ACCESSION:AR084252
302	13.4	0.9	15	1	AR131626	ACCESSION:AR131626	375	13.2	0.8	18	1	AR085578	ACCESSION:AR085578
303	13.4	0.9	15	1	AR278935	ACCESSION:AR278935	376	13.2	0.8	18	1	AR096650	ACCESSION:AR096650
304	13.4	0.9	15	1	AX007909	ACCESSION:AX007909	377	13.2	0.8	18	1	AR097623	ACCESSION:AR097623
305	13.4	0.9	15	1	AX328777	ACCESSION:AX328777	378	13.2	0.8	18	1	AR097624	ACCESSION:AR097624
306	13.4	0.9	15	1	BD065658	ACCESSION:BD065658	379	13.2	0.8	18	1	AR098789	ACCESSION:AR098789
307	13.4	0.9	15	1	BD132342	ACCESSION:BD132342	380	13.2	0.8	18	1	AR153937	ACCESSION:AR153937
308	13.4	0.9	16	1	AR050989	ACCESSION:AR050989	381	13.2	0.8	18	1	AR162795	ACCESSION:AR162795
309	13.4	0.9	16	1	AR204607	ACCESSION:AR204607	382	13.2	0.8	18	1	AR165009	ACCESSION:AR165009
310	13.4	0.9	16	1	AR307317	ACCESSION:AR307317	383	13.2	0.8	18	1	AR168816	ACCESSION:AR168816
311	13.4	0.9	16	1	AX696120	ACCESSION:AX696120	384	13.2	0.8	18	1	AR168817	ACCESSION:AR168817
312	13.4	0.9	16	1	I51790	ACCESSION:I51790	385	13.2	0.8	18	1	AR178168	ACCESSION:AR178168
313	13.4	0.9	16	1	I84399	ACCESSION:I84399	386	13.2	0.8	18	1	AR200285	ACCESSION:AR200285
314	13.4	0.9	17	1	AR112330	ACCESSION:AR112330	387	13.2	0.8	18	1	AR200286	ACCESSION:AR200286
315	13.4	0.9	17	1	AR164080	ACCESSION:AR164080	388	13.2	0.8	18	1	AR205722	ACCESSION:AR205722
316	13.4	0.9	17	1	AR164081	ACCESSION:AR164081	389	13.2	0.8	18	1	AR211763	ACCESSION:AR211763
317	13.4	0.9	17	1	AR286066	ACCESSION:AR286066	390	13.2	0.8	18	1	AR211764	ACCESSION:AR211764
318	13.4	0.9	17	1	AX007921	ACCESSION:AX007921	391	13.2	0.8	18	1	AR262417	ACCESSION:AR262417
319	13.4	0.9	17	1	AX215376	ACCESSION:AX215376	392	13.2	0.8	18	1	AR262418	ACCESSION:AR262418
320	13.4	0.9	17	1	AX215397	ACCESSION:AX215397	393	13.2	0.8	18	1	AR267617	ACCESSION:AR267617
321	13.4	0.9	17	1	AX216951	ACCESSION:AX216951	394	13.2	0.8	18	1	AR267618	ACCESSION:AR267618
322	13.4	0.9	17	1	AX226812	ACCESSION:AX226812	395	13.2	0.8	18	1	AR293539	ACCESSION:AR293539
323	13.4	0.9	17	1	AX227179	ACCESSION:AX227179	396	13.2	0.8	18	1	AR298227	ACCESSION:AR298227
324	13.4	0.9	17	1	AX273063	ACCESSION:AX273063	397	13.2	0.8	18	1	AX015243	ACCESSION:AX015243
325	13.4	0.9	17	1	AX398152	ACCESSION:AX398152	398	13.2	0.8	18	1	AX047272	ACCESSION:AX047272

399	13.2	0.8	18	1	AX047274	ACCESSION:AX047274	C 472	12.8	0.8	17	1	AX215323	ACCESSION:AX215323
400	13.2	0.8	18	1	AX166763	ACCESSION:AX166763	C 473	12.8	0.8	17	1	AX215324	ACCESSION:AX215324
401	13.2	0.8	18	1	AX557236	ACCESSION:AX557236	C 474	12.8	0.8	17	1	AX215378	ACCESSION:AX215378
402	13.2	0.8	18	1	AX598360	ACCESSION:AX598360	C 475	12.8	0.8	17	1	AX215389	ACCESSION:AX215389
403	13.2	0.8	18	1	AX718621	ACCESSION:AX718621	476	12.8	0.8	17	1	AX215398	ACCESSION:AX215398
404	13.2	0.8	18	1	BD099302	ACCESSION:BD099302	477	12.8	0.8	17	1	AX215400	ACCESSION:AX215400
C 405	13.2	0.8	18	1	BD104066	ACCESSION:BD104066	C 478	12.8	0.8	17	1	AX215460	ACCESSION:AX215460
C 406	13.2	0.8	18	1	EC08945	ACCESSION:EC08945	C 479	12.8	0.8	17	1	AX215727	ACCESSION:AX215727
C 407	13.2	0.8	18	1	EC09072	ACCESSION:EC09072	C 480	12.8	0.8	17	1	AX216350	ACCESSION:AX216350
C 408	13.2	0.8	18	1	EC09194	ACCESSION:EC09194	C 481	12.8	0.8	17	1	AX216369	ACCESSION:AX216369
C 409	13.2	0.8	18	1	EC09963	ACCESSION:EC09963	C 482	12.8	0.8	17	1	AX216370	ACCESSION:AX216370
410	13.2	0.8	18	1	112014	ACCESSION:112014	C 483	12.8	0.8	17	1	AX216371	ACCESSION:AX216371
411	13.2	0.8	18	1	113566	ACCESSION:113566	484	12.8	0.8	17	1	AX216894	ACCESSION:AX216894
412	13.2	0.8	18	1	121930	ACCESSION:121930	485	12.8	0.8	17	1	AX216952	ACCESSION:AX216952
C 413	13.2	0.8	18	1	127810	ACCESSION:127810	486	12.8	0.8	17	1	AX216953	ACCESSION:AX216953
C 414	13.2	0.8	18	1	127811	ACCESSION:127811	487	12.8	0.8	17	1	AX218005	ACCESSION:AX218005
415	13.2	0.8	18	1	130029	ACCESSION:130029	488	12.8	0.8	17	1	AX218198	ACCESSION:AX218198
416	13.2	0.8	18	1	134952	ACCESSION:134952	489	12.8	0.8	17	1	AX239680	ACCESSION:AX239680
417	13.2	0.8	18	1	150676	ACCESSION:150676	C 490	12.8	0.8	17	1	AX272860	ACCESSION:AX272860
418	13	0.8	13	1	AR024073	ACCESSION:AR024073	C 491	12.8	0.8	17	1	AX273062	ACCESSION:AX273062
419	13	0.8	13	1	AR224292	ACCESSION:AR224292	C 492	12.8	0.8	17	1	AX325861	ACCESSION:AX325861
420	13	0.8	13	1	AX711059	ACCESSION:AX711059	C 493	12.8	0.8	17	1	AX325862	ACCESSION:AX325862
421	13	0.8	13	1	BD001177	ACCESSION:BD001177	C 494	12.8	0.8	17	1	AX325881	ACCESSION:AX325881
422	13	0.8	13	1	BD001606	ACCESSION:BD001606	495	12.8	0.8	17	1	AX325882	ACCESSION:AX325882
423	13	0.8	15	1	AX007863	ACCESSION:AX007863	496	12.8	0.8	17	1	AX421845	ACCESSION:AX421845
424	13	0.8	15	1	AX007920	ACCESSION:AX007920	497	12.8	0.8	17	1	AX422332	ACCESSION:AX422332
425	13	0.8	16	1	AX007923	ACCESSION:AX007923	C 498	12.8	0.8	17	1	AX422748	ACCESSION:AX422748
426	13	0.8	16	1	AX139231	ACCESSION:AX139231	C 499	12.8	0.8	17	1	AX422749	ACCESSION:AX422749
427	13	0.8	16	1	BD013515	ACCESSION:BD013515	500	12.8	0.8	17	1	AX422880	ACCESSION:AX422880
C 428	13	0.8	17	1	AR005305	ACCESSION:AR005305	501	12.8	0.8	17	1	AX422914	ACCESSION:AX422914
C 429	13	0.8	17	1	AX215364	ACCESSION:AX215364	502	12.8	0.8	17	1	AX423093	ACCESSION:AX423093
C 430	13	0.8	17	1	AX215365	ACCESSION:AX215365	503	12.8	0.8	17	1	AX499046	ACCESSION:AX499046
C 431	13	0.8	17	1	AX215111	ACCESSION:AX215111	504	12.8	0.8	17	1	AX499048	ACCESSION:AX499048
432	13	0.8	17	1	AX216346	ACCESSION:AX216346	505	12.8	0.8	17	1	AX530591	ACCESSION:AX530591
433	13	0.8	17	1	AX216896	ACCESSION:AX216896	506	12.8	0.8	17	1	AX530993	ACCESSION:AX530993
C 434	13	0.8	17	1	AX216909	ACCESSION:AX216909	C 507	12.8	0.8	17	1	AX531072	ACCESSION:AX531072
C 435	13	0.8	17	1	AX532240	ACCESSION:AX532240	C 508	12.8	0.8	17	1	AX531073	ACCESSION:AX531073
C 436	13	0.8	17	1	AX532241	ACCESSION:AX532241	C 509	12.8	0.8	17	1	AX531302	ACCESSION:AX531302
C 437	13	0.8	17	1	AX532242	ACCESSION:AX532242	C 510	12.8	0.8	17	1	AX531306	ACCESSION:AX531306
C 438	13	0.8	17	1	AX532243	ACCESSION:AX532243	C 511	12.8	0.8	17	1	AX531619	ACCESSION:AX531619
C 439	13	0.8	17	1	AX724723	ACCESSION:AX724723	C 512	12.8	0.8	17	1	AX531623	ACCESSION:AX531623
C 440	13	0.8	17	1	AX733595	ACCESSION:AX733595	C 513	12.8	0.8	17	1	AX531926	ACCESSION:AX531926
441	13	0.8	17	1	AX736617	ACCESSION:AX736617	C 514	12.8	0.8	17	1	AX531928	ACCESSION:AX531928
C 442	13	0.8	18	1	AR085575	ACCESSION:AR085575	C 515	12.8	0.8	17	1	AX532238	ACCESSION:AX532238
443	13	0.8	18	1	AR293763	ACCESSION:AR293763	516	12.8	0.8	17	1	AX578660	ACCESSION:AX578660
444	13	0.8	31	1	A01419	ACCESSION:A01419	517	12.8	0.8	17	1	AX579335	ACCESSION:AX579335
445	12.8	0.8	16	1	A98144	ACCESSION:A98144	C 518	12.8	0.8	17	1	AX648902	ACCESSION:AX648902
446	12.8	0.8	16	1	A90111	ACCESSION:A90111	C 519	12.8	0.8	17	1	AX648903	ACCESSION:AX648903
C 447	12.8	0.8	16	1	AX009040	ACCESSION:AX009040	C 520	12.8	0.8	17	1	AX672061	ACCESSION:AX672061
448	12.8	0.8	16	1	AX743950	ACCESSION:AX743950	521	12.8	0.8	17	1	AX687648	ACCESSION:AX687648
449	12.8	0.8	16	1	BD065657	ACCESSION:BD065657	522	12.8	0.8	17	1	AX687649	ACCESSION:AX687649
450	12.8	0.8	16	1	BD086650	ACCESSION:BD086650	523	12.8	0.8	17	1	AX687667	ACCESSION:AX687667
451	12.8	0.8	16	1	A9069179	ACCESSION:A9069179	C 524	12.8	0.8	17	1	AX688672	ACCESSION:AX688672
C 452	12.8	0.8	17	1	A26883	ACCESSION:A26883	C 525	12.8	0.8	17	1	AX688673	ACCESSION:AX688673
C 453	12.8	0.8	17	1	A27314	ACCESSION:A27314	526	12.8	0.8	17	1	AX690655	ACCESSION:AX690655
454	12.8	0.8	17	1	A96622	ACCESSION:A96622	527	12.8	0.8	17	1	AX690656	ACCESSION:AX690656
C 455	12.8	0.8	17	1	AR039947	ACCESSION:AR039947	C 528	12.8	0.8	17	1	AX724644	ACCESSION:AX724644
C 456	12.8	0.8	17	1	AR053045	ACCESSION:AR053045	529	12.8	0.8	17	1	AX725179	ACCESSION:AX725179
C 457	12.8	0.8	17	1	AR053062	ACCESSION:AR053062	C 530	12.8	0.8	17	1	AX725846	ACCESSION:AX725846
C 458	12.8	0.8	17	1	AR065006	ACCESSION:AR065006	C 531	12.8	0.8	17	1	AX729300	ACCESSION:AX729300
C 459	12.8	0.8	17	1	AR065023	ACCESSION:AR065023	C 532	12.8	0.8	17	1	AX738076	ACCESSION:AX738076
460	12.8	0.8	17	1	AR159843	ACCESSION:AR159843	C 533	12.8	0.8	17	1	BD013480	ACCESSION:BD013480
461	12.8	0.8	17	1	AR176117	ACCESSION:AR176117	534	12.8	0.8	17	1	BD056833	ACCESSION:BD056833
C 462	12.8	0.8	17	1	AR185974	ACCESSION:AR185974	535	12.8	0.8	17	1	BD103923	ACCESSION:BD103923
463	12.8	0.8	17	1	AR186641	ACCESSION:AR186641	536	12.8	0.8	17	1	BD105164	ACCESSION:BD105164
C 464	12.8	0.8	17	1	AR189483	ACCESSION:AR189483	C 537	12.8	0.8	17	1	BD105171	ACCESSION:BD105171
C 465	12.8	0.8	17	1	AR192381	ACCESSION:AR192381	538	12.8	0.8	17	1	I26684	ACCESSION:I26684
466	12.8	0.8	17	1	AR224417	ACCESSION:AR224417	C 539	12.8	0.8	17	1	I32551	ACCESSION:I32551
C 467	12.8	0.8	17	1	AR242714	ACCESSION:AR242714	C 540	12.8	0.8	17	1	I32568	ACCESSION:I32568
C 468	12.8	0.8	17	1	AR286220	ACCESSION:AR286220	C 541	12.8	0.8	17	1	I46480	ACCESSION:I46480
469	12.8	0.8	17	1	AR286443	ACCESSION:AR286443	C 542	12.8	0.8	17	1	I88026	ACCESSION:I88026
470	12.8	0.8	17	1	AX139196	ACCESSION:AX139196	543	12.8	0.8	18	1	A12313	ACCESSION:A12313
C 471	12.8	0.8	17	1	AX214605	ACCESSION:AX214605	544	12.8	0.8	18	1	A19460	ACCESSION:A19460

C 545	12.8	0.8	18	1	A39464	ACCESSION:A39464	618	12.4	0.8	14	1	AX007878	ACCESSION:AX007878
C 546	12.8	0.8	18	1	A63131	ACCESSION:A63131	C 619	12.4	0.8	14	1	AX019396	ACCESSION:AX019396
547	12.8	0.8	18	1	A7987	ACCESSION:A7987	C 620	12.4	0.8	14	1	AX028355	ACCESSION:AX028355
548	12.8	0.8	18	1	A8954	ACCESSION:A8954	621	12.4	0.8	14	1	AX419965	ACCESSION:AX419965
C 549	12.8	0.8	18	1	A8954	ACCESSION:A8954	622	12.4	0.8	14	1	BD065423	ACCESSION:BD065423
C 550	12.8	0.8	18	1	AX003675	ACCESSION:AX003675	C 623	12.4	0.8	14	1	BD066715	ACCESSION:BD066715
C 551	12.8	0.8	18	1	AX003677	ACCESSION:AX003677	624	12.4	0.8	14	1	BD0668930	ACCESSION:BD0668930
C 552	12.8	0.8	18	1	AX069474	ACCESSION:AX069474	625	12.4	0.8	14	1	AX7986	ACCESSION:AX7986
C 553	12.8	0.8	18	1	AX070852	ACCESSION:AX070852	626	12.4	0.8	15	1	A89953	ACCESSION:A89953
C 554	12.8	0.8	18	1	AX083621	ACCESSION:AX083621	C 627	12.4	0.8	15	1	AR041268	ACCESSION:AR041268
C 555	12.8	0.8	18	1	AX083623	ACCESSION:AX083623	C 628	12.4	0.8	15	1	AR050983	ACCESSION:AR050983
C 556	12.8	0.8	18	1	AX096629	ACCESSION:AX096629	C 629	12.4	0.8	15	1	AR131823	ACCESSION:AR131823
C 557	12.8	0.8	18	1	AX098791	ACCESSION:AX098791	C 630	12.4	0.8	15	1	AR180559	ACCESSION:AR180559
C 558	12.8	0.8	18	1	AR100282	ACCESSION:AR100282	C 631	12.4	0.8	15	1	AR204601	ACCESSION:AR204601
C 559	12.8	0.8	18	1	AR105370	ACCESSION:AR105370	C 632	12.4	0.8	15	1	AR307316	ACCESSION:AR307316
C 560	12.8	0.8	18	1	AR117923	ACCESSION:AR117923	C 633	12.4	0.8	15	1	AX003643	ACCESSION:AX003643
C 561	12.8	0.8	18	1	AR120115	ACCESSION:AR120115	C 634	12.4	0.8	15	1	AX028356	ACCESSION:AX028356
C 562	12.8	0.8	18	1	AR121115	ACCESSION:AR121115	C 635	12.4	0.8	15	1	AX328726	ACCESSION:AX328726
C 563	12.8	0.8	18	1	AR123810	ACCESSION:AR123810	C 636	12.4	0.8	15	1	AX328727	ACCESSION:AX328727
C 564	12.8	0.8	18	1	AR123812	ACCESSION:AR123812	C 637	12.4	0.8	15	1	AX357594	ACCESSION:AX357594
C 565	12.8	0.8	18	1	AR149937	ACCESSION:AR149937	C 638	12.4	0.8	15	1	AX636188	ACCESSION:AX636188
C 566	12.8	0.8	18	1	AR157304	ACCESSION:AR157304	C 639	12.4	0.8	15	1	BD065499	ACCESSION:BD065499
C 567	12.8	0.8	18	1	AR162791	ACCESSION:AR162791	640	12.4	0.8	15	1	BD132291	ACCESSION:BD132291
C 568	12.8	0.8	18	1	AR196090	ACCESSION:AR196090	C 641	12.4	0.8	15	1	I12919	ACCESSION:I12919
C 569	12.8	0.8	18	1	AR205718	ACCESSION:AR205718	C 642	12.4	0.8	15	1	I51784	ACCESSION:I51784
C 570	12.8	0.8	18	1	AR211741	ACCESSION:AR211741	C 643	12.4	0.8	15	1	I61712	ACCESSION:I61712
C 571	12.8	0.8	18	1	AR258012	ACCESSION:AR258012	C 644	12.4	0.8	15	1	I84393	ACCESSION:I84393
C 572	12.8	0.8	18	1	AR264643	ACCESSION:AR264643	645	12.4	0.8	16	1	AR050052	ACCESSION:AR050052
C 573	12.8	0.8	18	1	AR277996	ACCESSION:AR277996	646	12.4	0.8	16	1	AX007859	ACCESSION:AX007859
C 574	12.8	0.8	18	1	AR293832	ACCESSION:AR293832	C 647	12.4	0.8	16	1	AX042425	ACCESSION:AX042425
C 575	12.8	0.8	18	1	AX004745	ACCESSION:AX004745	C 648	12.4	0.8	16	1	AX317220	ACCESSION:AX317220
C 576	12.8	0.8	18	1	AX047241	ACCESSION:AX047241	649	12.4	0.8	16	1	AX328727	ACCESSION:AX328727
C 577	12.8	0.8	18	1	AX081062	ACCESSION:AX081062	C 650	12.4	0.8	16	1	AX716641	ACCESSION:AX716641
C 578	12.8	0.8	18	1	AX082556	ACCESSION:AX082556	C 651	12.4	0.8	16	1	AX741031	ACCESSION:AX741031
C 579	12.8	0.8	18	1	AX082560	ACCESSION:AX082560	C 652	12.4	0.8	16	1	AX741043	ACCESSION:AX741043
C 580	12.8	0.8	18	1	AX082562	ACCESSION:AX082562	653	12.4	0.8	16	1	BD132292	ACCESSION:BD132292
C 581	12.8	0.8	18	1	AX118127	ACCESSION:AX118127	C 654	12.4	0.8	16	1	I28863	ACCESSION:I28863
C 582	12.8	0.8	18	1	AX147718	ACCESSION:AX147718	C 655	12.4	0.8	16	1	I35381	ACCESSION:I35381
C 583	12.8	0.8	18	1	AX229739	ACCESSION:AX229739	C 656	12.4	0.8	17	1	A25087	ACCESSION:A25087
C 584	12.8	0.8	18	1	AX278630	ACCESSION:AX278630	C 657	12.4	0.8	17	1	A25088	ACCESSION:A25088
C 585	12.8	0.8	18	1	AX284155	ACCESSION:AX284155	658	12.4	0.8	17	1	A76795	ACCESSION:A76795
C 586	12.8	0.8	18	1	AX323452	ACCESSION:AX323452	C 659	12.4	0.8	17	1	AR027367	ACCESSION:AR027367
C 587	12.8	0.8	18	1	AX394481	ACCESSION:AX394481	C 660	12.4	0.8	17	1	AR028821	ACCESSION:AR028821
588	12.8	0.8	18	1	AX356680	ACCESSION:AX356680	C 661	12.4	0.8	17	1	AR034358	ACCESSION:AR034358
589	12.8	0.8	18	1	AX659153	ACCESSION:AX659153	C 662	12.4	0.8	17	1	AR074719	ACCESSION:AR074719
C 590	12.8	0.8	18	1	AX705791	ACCESSION:AX705791	C 663	12.4	0.8	17	1	AR091418	ACCESSION:AR091418
C 591	12.8	0.8	18	1	AX708559	ACCESSION:AX708559	C 664	12.4	0.8	17	1	AR125623	ACCESSION:AR125623
C 592	12.8	0.8	18	1	AX713195	ACCESSION:AX713195	C 665	12.4	0.8	17	1	AR189922	ACCESSION:AR189922
C 593	12.8	0.8	18	1	AX718864	ACCESSION:AX718864	C 666	12.4	0.8	17	1	AR286227	ACCESSION:AR286227
594	12.8	0.8	18	1	AX719127	ACCESSION:AX719127	C 667	12.4	0.8	17	1	AR286325	ACCESSION:AR286325
595	12.8	0.8	18	1	BD012743	ACCESSION:BD012743	668	12.4	0.8	17	1	AR286386	ACCESSION:AR286386
596	12.8	0.8	18	1	BD065500	ACCESSION:BD065500	C 669	12.4	0.8	17	1	AR286446	ACCESSION:AR286446
C 597	12.8	0.8	18	1	BD074290	ACCESSION:BD074290	C 670	12.4	0.8	17	1	AX113912	ACCESSION:AX113912
C 598	12.8	0.8	18	1	BD104198	ACCESSION:BD104198	C 671	12.4	0.8	17	1	AX113921	ACCESSION:AX113921
C 600	12.8	0.8	18	1	BD106627	ACCESSION:BD106627	C 672	12.4	0.8	17	1	AX214848	ACCESSION:AX214848
C 601	12.8	0.8	18	1	BD107307	ACCESSION:BD107307	C 673	12.4	0.8	17	1	AX215461	ACCESSION:AX215461
C 602	12.8	0.8	18	1	BD171754	ACCESSION:BD171754	C 674	12.4	0.8	17	1	AX215462	ACCESSION:AX215462
C 603	12.8	0.8	18	1	E06267	ACCESSION:E06267	C 675	12.4	0.8	17	1	AX215726	ACCESSION:AX215726
C 604	12.8	0.8	18	1	E06463	ACCESSION:E06463	676	12.4	0.8	17	1	AX216348	ACCESSION:AX216348
C 605	12.8	0.8	18	1	E32535	ACCESSION:E32535	677	12.4	0.8	17	1	AX216954	ACCESSION:AX216954
C 606	12.8	0.8	18	1	I34449	ACCESSION:I34449	678	12.4	0.8	17	1	AX216955	ACCESSION:AX216955
C 607	12.8	0.8	18	1	I73252	ACCESSION:I73252	C 679	12.4	0.8	17	1	AX227482	ACCESSION:AX227482
C 608	12.8	0.8	18	1	ADH524348	ACCESSION:ADH524348	C 680	12.4	0.8	17	1	AX227592	ACCESSION:AX227592
609	12.8	0.8	18	1	D0269513	ACCESSION:D0269513	681	12.4	0.8	17	1	AX328728	ACCESSION:AX328728
610	12.8	0.8	18	1	AB069291	ACCESSION:AB069291	682	12.4	0.8	17	1	AX498854	ACCESSION:AX498854
611	12.8	0.8	32	1	A62993	ACCESSION:A62993	683	12.4	0.8	17	1	AX498858	ACCESSION:AX498858
612	12.8	0.8	32	1	AR179068	ACCESSION:AR179068	C 684	12.4	0.8	17	1	AX532312	ACCESSION:AX532312
C 613	12.6	0.8	50	1	AX146616	ACCESSION:AX146616	C 685	12.4	0.8	17	1	AX532313	ACCESSION:AX532313
C 614	12.6	0.8	20	1	BD016571	ACCESSION:BD016571	C 686	12.4	0.8	17	1	AX532314	ACCESSION:AX532314
615	12.4	0.8	47	1	AX146611	ACCESSION:AX146611	C 687	12.4	0.8	17	1	AX532315	ACCESSION:AX532315
C 616	12.4	0.8	14	1	AR7910	ACCESSION:AR7910	688	12.4	0.8	17	1	AX532475	ACCESSION:AX532475
C 617	12.4	0.8	14	1	A89202	ACCESSION:A89202	689	12.4	0.8	17	1	AX532476	ACCESSION:AX532476
			14	1	A89877	ACCESSION:A89877	690	12.4	0.8	17	1	AX532477	ACCESSION:AX532477

691	12.4	0.8	17	1	AX532478	ACCESSION:AX532478	C 764	12.2	0.8	17	1	AR168853	ACCESSION:AR168853
692	12.4	0.8	17	1	AX673727	ACCESSION:AX673727	C 765	12.2	0.8	17	1	AR185983	ACCESSION:AR185983
693	12.4	0.8	17	1	AX687671	ACCESSION:AX687671	C 766	12.2	0.8	17	1	AR188484	ACCESSION:AR188484
694	12.4	0.8	17	1	AX687746	ACCESSION:AX687746	C 767	12.2	0.8	17	1	AR188509	ACCESSION:AR188509
695	12.4	0.8	17	1	AX687750	ACCESSION:AX687750	C 768	12.2	0.8	17	1	AR188587	ACCESSION:AR188587
696	12.4	0.8	17	1	AX688007	ACCESSION:AX688007	C 769	12.2	0.8	17	1	AR191744	ACCESSION:AR191744
697	12.4	0.8	17	1	AX688008	ACCESSION:AX688008	C 770	12.2	0.8	17	1	AR195605	ACCESSION:AR195605
698	12.4	0.8	17	1	AX688009	ACCESSION:AX688009	C 771	12.2	0.8	17	1	AR195753	ACCESSION:AR195753
699	12.4	0.8	17	1	AX688010	ACCESSION:AX688010	C 772	12.2	0.8	17	1	AR195755	ACCESSION:AR195755
700	12.4	0.8	17	1	AX688727	ACCESSION:AX688727	C 773	12.2	0.8	17	1	AR195755	ACCESSION:AR195755
701	12.4	0.8	17	1	AX688728	ACCESSION:AX688728	C 774	12.2	0.8	17	1	AR196227	ACCESSION:AR196227
702	12.4	0.8	17	1	AX688729	ACCESSION:AX688729	C 775	12.2	0.8	17	1	AR200322	ACCESSION:AR200322
703	12.4	0.8	17	1	AX688730	ACCESSION:AX688730	C 776	12.2	0.8	17	1	AR224299	ACCESSION:AR224299
704	12.4	0.8	17	1	AX688735	ACCESSION:AX688735	C 777	12.2	0.8	17	1	AR242713	ACCESSION:AR242713
705	12.4	0.8	17	1	AX688736	ACCESSION:AX688736	C 778	12.2	0.8	17	1	AR243452	ACCESSION:AR243452
706	12.4	0.8	17	1	AX688737	ACCESSION:AX688737	C 779	12.2	0.8	17	1	AR262453	ACCESSION:AR262453
707	12.4	0.8	17	1	AX688738	ACCESSION:AX688738	C 780	12.2	0.8	17	1	AR285947	ACCESSION:AR285947
708	12.4	0.8	17	1	AX690457	ACCESSION:AX690457	C 781	12.2	0.8	17	1	AR286005	ACCESSION:AR286005
709	12.4	0.8	17	1	AX690458	ACCESSION:AX690458	C 782	12.2	0.8	17	1	AR286300	ACCESSION:AR286300
710	12.4	0.8	17	1	AX690459	ACCESSION:AX690459	C 783	12.2	0.8	17	1	AR286317	ACCESSION:AR286317
711	12.4	0.8	17	1	AX690460	ACCESSION:AX690460	C 784	12.2	0.8	17	1	AX060340	ACCESSION:AX060340
712	12.4	0.8	17	1	AX696158	ACCESSION:AX696158	C 785	12.2	0.8	17	1	AX074458	ACCESSION:AX074458
713	12.4	0.8	17	1	AX722711	ACCESSION:AX722711	C 786	12.2	0.8	17	1	AX074465	ACCESSION:AX074465
714	12.4	0.8	17	1	AX724356	ACCESSION:AX724356	C 787	12.2	0.8	17	1	AX133871	ACCESSION:AX133871
715	12.4	0.8	17	1	AX724898	ACCESSION:AX724898	C 788	12.2	0.8	17	1	AX139210	ACCESSION:AX139210
716	12.4	0.8	17	1	AX726731	ACCESSION:AX726731	C 789	12.2	0.8	17	1	AX165743	ACCESSION:AX165743
717	12.4	0.8	17	1	AX727805	ACCESSION:AX727805	C 790	12.2	0.8	17	1	AX173375	ACCESSION:AX173375
718	12.4	0.8	17	1	AX728285	ACCESSION:AX728285	C 791	12.2	0.8	17	1	AX214609	ACCESSION:AX214609
719	12.4	0.8	17	1	AX729359	ACCESSION:AX729359	C 792	12.2	0.8	17	1	AX215322	ACCESSION:AX215322
720	12.4	0.8	17	1	AX729407	ACCESSION:AX729407	C 793	12.2	0.8	17	1	AX215328	ACCESSION:AX215328
721	12.4	0.8	17	1	AX732545	ACCESSION:AX732545	C 794	12.2	0.8	17	1	AX215379	ACCESSION:AX215379
722	12.4	0.8	17	1	AX733202	ACCESSION:AX733202	C 795	12.2	0.8	17	1	AX215409	ACCESSION:AX215409
723	12.4	0.8	17	1	AX735559	ACCESSION:AX735559	C 796	12.2	0.8	17	1	AX215426	ACCESSION:AX215426
724	12.4	0.8	17	1	AX737927	ACCESSION:AX737927	C 797	12.2	0.8	17	1	AX215427	ACCESSION:AX215427
725	12.4	0.8	17	1	AX738886	ACCESSION:AX738886	C 798	12.2	0.8	17	1	AX215459	ACCESSION:AX215459
726	12.4	0.8	17	1	BD013476	ACCESSION:BD013476	C 799	12.2	0.8	17	1	AX216129	ACCESSION:AX216129
727	12.4	0.8	17	1	BD013496	ACCESSION:BD013496	C 800	12.2	0.8	17	1	AX216149	ACCESSION:AX216149
728	12.4	0.8	17	1	BD067380	ACCESSION:BD067380	C 801	12.2	0.8	17	1	AX216199	ACCESSION:AX216199
729	12.4	0.8	17	1	BD067381	ACCESSION:BD067381	C 802	12.2	0.8	17	1	AX216349	ACCESSION:AX216349
730	12.4	0.8	17	1	BD104453	ACCESSION:BD104453	C 803	12.2	0.8	17	1	AX216893	ACCESSION:AX216893
731	12.4	0.8	17	1	BD104759	ACCESSION:BD104759	C 804	12.2	0.8	17	1	AX216928	ACCESSION:AX216928
732	12.4	0.8	17	1	BD132293	ACCESSION:BD132293	C 805	12.2	0.8	17	1	AX218199	ACCESSION:AX218199
733	12.4	0.8	17	1	125290	ACCESSION:125290	C 806	12.2	0.8	17	1	AX262672	ACCESSION:AX262672
734	12.4	0.8	17	1	138725	ACCESSION:138725	C 807	12.2	0.8	17	1	AX262673	ACCESSION:AX262673
735	12.4	0.8	17	1	138726	ACCESSION:138726	C 808	12.2	0.8	17	1	AX262856	ACCESSION:AX262856
736	12.4	0.8	17	1	181334	ACCESSION:181334	C 809	12.2	0.8	17	1	AX262857	ACCESSION:AX262857
737	12.4	0.8	17	1	181335	ACCESSION:181335	C 810	12.2	0.8	17	1	AX263984	ACCESSION:AX263984
738	12.4	0.8	20	1	184401	ACCESSION:184401	C 811	12.2	0.8	17	1	AX263985	ACCESSION:AX263985
739	12.2	0.8	17	1	AX216373	ACCESSION:AX216373	C 812	12.2	0.8	17	1	AX266223	ACCESSION:AX266223
740	12.2	0.8	17	1	AX216946	ACCESSION:AX216946	C 813	12.2	0.8	17	1	AX266224	ACCESSION:AX266224
741	12.2	0.8	17	1	AX216951	ACCESSION:AX216951	C 814	12.2	0.8	17	1	AX266303	ACCESSION:AX266303
742	12.2	0.8	17	1	AX499046	ACCESSION:AX499046	C 815	12.2	0.8	17	1	AX266304	ACCESSION:AX266304
743	12.2	0.8	17	1	A27313	ACCESSION:A27313	C 816	12.2	0.8	17	1	AX266571	ACCESSION:AX266571
744	12.2	0.8	17	1	A87923	ACCESSION:A87923	C 817	12.2	0.8	17	1	AX266572	ACCESSION:AX266572
745	12.2	0.8	17	1	A89890	ACCESSION:A89890	C 818	12.2	0.8	17	1	AX272790	ACCESSION:AX272790
746	12.2	0.8	17	1	AR044080	ACCESSION:AR044080	C 819	12.2	0.8	17	1	AX273293	ACCESSION:AX273293
747	12.2	0.8	17	1	AR039907	ACCESSION:AR039907	C 820	12.2	0.8	17	1	AX273310	ACCESSION:AX273310
748	12.2	0.8	17	1	AR039163	ACCESSION:AR039163	C 821	12.2	0.8	17	1	AX280439	ACCESSION:AX280439
749	12.2	0.8	17	1	AR039607	ACCESSION:AR039607	C 822	12.2	0.8	17	1	AX325917	ACCESSION:AX325917
750	12.2	0.8	17	1	AR039609	ACCESSION:AR039609	C 823	12.2	0.8	17	1	AX325918	ACCESSION:AX325918
751	12.2	0.8	17	1	AR039611	ACCESSION:AR039611	C 824	12.2	0.8	17	1	AX326181	ACCESSION:AX326181
752	12.2	0.8	17	1	AR039615	ACCESSION:AR039615	C 825	12.2	0.8	17	1	AX326182	ACCESSION:AX326182
753	12.2	0.8	17	1	AR039963	ACCESSION:AR039963	C 826	12.2	0.8	17	1	AX406535	ACCESSION:AX406535
754	12.2	0.8	17	1	AR046684	ACCESSION:AR046684	C 827	12.2	0.8	17	1	AX421748	ACCESSION:AX421748
755	12.2	0.8	17	1	AR074706	ACCESSION:AR074706	C 828	12.2	0.8	17	1	AX422335	ACCESSION:AX422335
756	12.2	0.8	17	1	AR074707	ACCESSION:AR074707	C 829	12.2	0.8	17	1	AX422336	ACCESSION:AX422336
757	12.2	0.8	17	1	AR074708	ACCESSION:AR074708	C 830	12.2	0.8	17	1	AX422818	ACCESSION:AX422818
758	12.2	0.8	17	1	AR074709	ACCESSION:AR074709	C 831	12.2	0.8	17	1	AX423030	ACCESSION:AX423030
759	12.2	0.8	17	1	AR107651	ACCESSION:AR107651	C 832	12.2	0.8	17	1	AX423222	ACCESSION:AX423222
760	12.2	0.8	17	1	AR127639	ACCESSION:AR127639	C 833	12.2	0.8	17	1	AX423276	ACCESSION:AX423276
761	12.2	0.8	17	1	AR140636	ACCESSION:AR140636	C 834	12.2	0.8	17	1	AX423546	ACCESSION:AX423546
762	12.2	0.8	17	1	AR159850	ACCESSION:AR159850	C 835	12.2	0.8	17	1	AX474905	ACCESSION:AX474905
763	12.2	0.8	17	1	AR164573	ACCESSION:AR164573	C 836	12.2	0.8	17	1	AX474906	ACCESSION:AX474906

837	12.2	0.8	17	1	AX498859	ACCESSION:AX498859	910	12.2	0.8	17	1	AX737846	ACCESSION:AX737846			
838	12.2	0.8	17	1	AX498979	ACCESSION:AX498979	911	12.2	0.8	17	1	AX738348	ACCESSION:AX738348			
839	12.2	0.8	17	1	AX499230	ACCESSION:AX499230	912	12.2	0.8	17	1	AX738466	ACCESSION:AX738466			
840	12.2	0.8	17	1	AX499231	ACCESSION:AX499231	913	12.2	0.8	17	1	AX738561	ACCESSION:AX738561			
841	12.2	0.8	17	1	AX499490	ACCESSION:AX499490	914	12.2	0.8	17	1	AX739235	ACCESSION:AX739235			
842	12.2	0.8	17	1	AX499660	ACCESSION:AX499660	915	12.2	0.8	17	1	AX739841	ACCESSION:AX739841			
843	12.2	0.8	17	1	AX499661	ACCESSION:AX499661	916	12.2	0.8	17	1	AX741041	ACCESSION:AX741041			
844	12.2	0.8	17	1	AX527194	ACCESSION:AX527194	917	12.2	0.8	17	1	AX744246	ACCESSION:AX744246			
845	12.2	0.8	17	1	AX531219	ACCESSION:AX531219	918	12.2	0.8	17	1	BD001184	ACCESSION:BD001184			
846	12.2	0.8	17	1	AX531299	ACCESSION:AX531299	919	12.2	0.8	17	1	BD001613	ACCESSION:BD001613			
847	12.2	0.8	17	1	AX532022	ACCESSION:AX532022	920	12.2	0.8	17	1	BD011182	ACCESSION:BD011182			
848	12.2	0.8	17	1	AX532235	ACCESSION:AX532235	921	12.2	0.8	17	1	BD013716	ACCESSION:BD013716			
849	12.2	0.8	17	1	AX532237	ACCESSION:AX532237	922	12.2	0.8	17	1	BD012716	ACCESSION:BD012716			
850	12.2	0.8	17	1	AX532413	ACCESSION:AX532413	923	12.2	0.8	17	1	BD013494	ACCESSION:BD013494			
851	12.2	0.8	17	1	AX544648	ACCESSION:AX544648	924	12.2	0.8	17	1	BD065436	ACCESSION:BD065436			
852	12.2	0.8	17	1	AX545028	ACCESSION:AX545028	925	12.2	0.8	17	1	BD067713	ACCESSION:BD067713			
853	12.2	0.8	17	1	AX545089	ACCESSION:AX545089	926	12.2	0.8	17	1	BD067714	ACCESSION:BD067714			
854	12.2	0.8	17	1	AX545145	ACCESSION:AX545145	927	12.2	0.8	17	1	BD104504	ACCESSION:BD104504			
855	12.2	0.8	17	1	AX545188	ACCESSION:AX545188	928	12.2	0.8	17	1	BD104826	ACCESSION:BD104826			
856	12.2	0.8	17	1	AX578339	ACCESSION:AX578339	929	12.2	0.8	17	1	BD105168	ACCESSION:BD105168			
857	12.2	0.8	17	1	AX578995	ACCESSION:AX578995	930	12.2	0.8	17	1	BD182250	ACCESSION:BD182250			
858	12.2	0.8	17	1	AX579172	ACCESSION:AX579172	931	12.2	0.8	17	1	E12897	ACCESSION:E12897			
859	12.2	0.8	17	1	AX579334	ACCESSION:AX579334	932	12.2	0.8	17	1	E36931	ACCESSION:E36931			
860	12.2	0.8	17	1	AX615281	ACCESSION:AX615281	933	12.2	0.8	17	1	E42982	ACCESSION:E42982			
861	12.2	0.8	17	1	AX615838	ACCESSION:AX615838	934	12.2	0.8	17	1	E42982	ACCESSION:E42982			
862	12.2	0.8	17	1	AX648333	ACCESSION:AX648333	935	12.2	0.8	17	1	E14531	ACCESSION:E14531			
863	12.2	0.8	17	1	AX649376	ACCESSION:AX649376	936	12.2	0.8	17	1	E14591	ACCESSION:E14591			
864	12.2	0.8	17	1	AX649524	ACCESSION:AX649524	937	12.2	0.8	17	1	E46955	ACCESSION:E46955			
865	12.2	0.8	17	1	AX671955	ACCESSION:AX671955	938	12.2	0.8	17	1	E53736	ACCESSION:E53736			
866	12.2	0.8	17	1	AX672132	ACCESSION:AX672132	939	12.2	0.8	17	1	I75308	ACCESSION:I75308			
867	12.2	0.8	17	1	AX672333	ACCESSION:AX672333	940	12.2	0.8	17	1	AB068835	ACCESSION:AB068835			
868	12.2	0.8	17	1	AX673341	ACCESSION:AX673341	ALIGNMENTS									
869	12.2	0.8	17	1	AX674701	ACCESSION:AX674701	RESULT 1	AX146582/c	AX146582	Sequence 44 from Patent WO0134654.	50 bp	DNA	linear	PAT 31-MAY-2001		
870	12.2	0.8	17	1	AX687510	ACCESSION:AX687510	LOCUS	AX146582	Sequence 44 from Patent WO0134654.							
871	12.2	0.8	17	1	AX687650	ACCESSION:AX687650	DEFINITION	AX146582	Sequence 44 from Patent WO0134654.							
872	12.2	0.8	17	1	AX687672	ACCESSION:AX687672	ACCESSION	AX146582	Sequence 44 from Patent WO0134654.							
873	12.2	0.8	17	1	AX687673	ACCESSION:AX687673	VERSION	AX146582.1	GI:14284975							
874	12.2	0.8	17	1	AX687674	ACCESSION:AX687674	KEYWORDS		Homo sapiens (human)							
875	12.2	0.8	17	1	AX687675	ACCESSION:AX687675	SOURCE		Homo sapiens							
876	12.2	0.8	17	1	AX687676	ACCESSION:AX687676	ORGANISM		Homo sapiens							
877	12.2	0.8	17	1	AX688006	ACCESSION:AX688006	REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
878	12.2	0.8	17	1	AX688332	ACCESSION:AX688332	AUTHORS		Strauch, K.							
879	12.2	0.8	17	1	AX688570	ACCESSION:AX688570	TITLE		Hedgehog fusion proteins and uses							
880	12.2	0.8	17	1	AX688660	ACCESSION:AX688660	JOURNAL		Patent: WO 0134654-A 44 17-MAY-2001;							
881	12.2	0.8	17	1	AX688669	ACCESSION:AX688669	FEATURES		BIOTEN, INC. (US)							
882	12.2	0.8	17	1	AX688671	ACCESSION:AX688671	source		Location/Qualifiers							
883	12.2	0.8	17	1	AX688672	ACCESSION:AX688672	1..50		/organism="Homo sapiens"							
884	12.2	0.8	17	1	AX688726	ACCESSION:AX688726	11 a		/mol_type="genomic DNA"							
885	12.2	0.8	17	1	AX690657	ACCESSION:AX690657	15 g		/db_xref="taxon:9606"							
886	12.2	0.8	17	1	AX690675	ACCESSION:AX690675	13 t									
887	12.2	0.8	17	1	AX693203	ACCESSION:AX693203	BASE COUNT		11 a 11 c 15 g 13 t							
888	12.2	0.8	17	1	AX711072	ACCESSION:AX711072	Query Match		3.2%; Score 50; DB 1; Length 50;							
889	12.2	0.8	17	1	AX721791	ACCESSION:AX721791	Best Local Similarity		100.0%; Pred. No. 0.00073;							
890	12.2	0.8	17	1	AX723336	ACCESSION:AX723336	Matches		50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
891	12.2	0.8	17	1	AX723519	ACCESSION:AX723519	QY	272	CCTTTAGCCTACAGCAGTTTATCCCAATGTGCGGAGAACCCCTAGG	321						
892	12.2	0.8	17	1	AX724912	ACCESSION:AX724912	Db	50	CCTTTAGCCTACAGCAGTTTATCCCAATGTGCGGAGAACCCCTAGG	1						
893	12.2	0.8	17	1	AX725292	ACCESSION:AX725292	ALIGNMENTS									
894	12.2	0.8	17	1	AX725622	ACCESSION:AX725622	RESULT 2									
895	12.2	0.8	17	1	AX725658	ACCESSION:AX725658	LOCUS	AX146613/c	Sequence 75 from Patent WO0134654.	50 bp	DNA	linear	PAT 31-MAY-2001			
896	12.2	0.8	17	1	AX725998	ACCESSION:AX725998	DEFINITION	AX146613	Sequence 75 from Patent WO0134654.							
897	12.2	0.8	17	1	AX726458	ACCESSION:AX726458	ACCESSION	AX146613	Sequence 75 from Patent WO0134654.							
898	12.2	0.8	17	1	AX726580	ACCESSION:AX726580										
899	12.2	0.8	17	1	AX727491	ACCESSION:AX727491										
900	12.2	0.8	17	1	AX728148	ACCESSION:AX728148										
901	12.2	0.8	17	1	AX728634	ACCESSION:AX728634										
902	12.2	0.8	17	1	AX728654	ACCESSION:AX728654										
903	12.2	0.8	17	1	AX729739	ACCESSION:AX729739										
904	12.2	0.8	17	1	AX731101	ACCESSION:AX731101										
905	12.2	0.8	17	1	AX731108	ACCESSION:AX731108										
906	12.2	0.8	17	1	AX731467	ACCESSION:AX731467										
907	12.2	0.8	17	1	AX733148	ACCESSION:AX733148										
908	12.2	0.8	17	1	AX735717	ACCESSION:AX735717										
909	12.2	0.8	17	1	AX737405	ACCESSION:AX737405										

VERSION AX146613.1 GI:14285006
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Strauch, K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 75 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 6 a 17 c 13 g 14 t

Query Match 3.1%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.0013;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 228 CGGCAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 277
|||||
Db 50 CGGCAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 1

RESULT 3
AX146614/c
LOCUS AX146614 50 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 76 from Patent WO0134654.
ACCESSION AX146614
VERSION AX146614.1 GI:14285007
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Strauch, K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 76 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 6 a 19 c 13 g 12 t

Query Match 3.1%; Score 48.4; DB 1; Length 50;
Best Local Similarity 98.0%; Pred. No. 0.0013;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 228 CGGCAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 277
|||||
Db 50 CGGCAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 1

RESULT 4
AX146616/c
LOCUS AX146616 50 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 78 from Patent WO0134654.
ACCESSION AX146616
VERSION AX146616.1 GI:14285009
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Strauch, K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 71 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES Location/Qualifiers
source 1..47
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 11 a 13 c 20 g 3 t

JOURNAL Patent: WO 0134654-A 78 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 6 a 19 c 15 g 10 t

Query Match 2.9%; Score 45.2; DB 1; Length 50;
Best Local Similarity 94.0%; Pred. No. 0.0045;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 228 CGGCAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 277
|||||
Db 50 CGGCAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 1

RESULT 5
AX146608
LOCUS AX146608 47 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 70 from Patent WO0134654.
ACCESSION AX146608
VERSION AX146608.1 GI:14285001
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Strauch, K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 70 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES Location/Qualifiers
source 1..47
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 13 a 13 c 18 g 3 t

Query Match 2.8%; Score 43.8; DB 1; Length 47;
Best Local Similarity 95.7%; Pred. No. 0.0075;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 225 GACCGGCGAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACC 271
|||||
Db 1 GCGCGGCGAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACC 47

RESULT 6
AX146609
LOCUS AX146609 47 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 71 from Patent WO0134654.
ACCESSION AX146609
VERSION AX146609.1 GI:14285002
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Strauch, K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 71 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES Location/Qualifiers
source 1..47
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 11 a 13 c 20 g 3 t


```

Query Match      2.8%; Score 43.8; DB 1; Length 47;
Best Local Similarity 95.7%; Pred. No. 0.0075;
Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 225 GACCGGCGAGGGGTTCCGGAGAGAGGAGGACCCCAAAAAGCTGACC 271
Db 1 GCGCGGCGAGGGGTTCCGGAGAGGAGGAGGACCCCAAAAAGCTGACC 47

RESULT 7
AX146612/c
LOCUS AX146612 45 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 74 from Patent WO0134654.
ACCESSION AX146612
VERSION AX146612.1 GI:14285005
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Strauch,K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 74 17-MAY-2001;
BIODEN, INC. (US)
FEATURES
source
1..45
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 12 a 14 c 10 g 9 t

Query Match      2.8%; Score 43.4; DB 1; Length 45;
Best Local Similarity 97.8%; Pred. No. 0.0086;
Matches 44; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 272 CCTTAGCCTACAGCAGTTTATCCCAATGTGGCGGAGAGACC 316
Db 1 CCTTAGCCTACAGCAGTTTATCCCAATGTGGCGGAGAGACC 45

RESULT 8
AX146615/c
LOCUS AX146615 50 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 77 from Patent WO0134654.
ACCESSION AX146615
VERSION AX146615.1 GI:14285008
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Strauch,K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 77 17-MAY-2001;
BIODEN, INC. (US)
FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 6 a 16 c 16 g 12 t

Query Match      2.7%; Score 42; DB 1; Length 50;
Best Local Similarity 90.0%; Pred. No. 0.015;
Matches 45; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 228 CGGCGAGGGGTTCCGGAGAGAGGAGGACCCCAAAAAGCTGACCCCTTTA 277
Db 50 CGGCGAGGGGTTCCGGAGAGGAGGAGGACCCCAAAAAGCTGACCCCTTTA 1

Query Match      2.6%; Score 40.6; DB 1; Length 47;
Best Local Similarity 91.5%; Pred. No. 0.026;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 225 GACCGGCGAGGGGTTCCGGAGAGAGGAGGACCCCAAAAAGCTGACC 271
Db 1 GCGCGGCGAGGGGTTCCGGAGAGGAGGAGGACCCCAAAAAGCTGACC 47

RESULT 11
AX146610
LOCUS AX146610 47 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 72 from Patent WO0134654.
ACCESSION AX146610
VERSION AX146610.1 GI:14285003
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Strauch,K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 73 17-MAY-2001;
BIODEN, INC. (US)
FEATURES
source
1..47
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 9 a 15 c 20 g 3 t

Query Match      2.6%; Score 41.4; DB 1; Length 43;
Best Local Similarity 97.7%; Pred. No. 0.018;
Matches 42; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 278 GCCTACAGCAGTTTATCCCAATGTGGCGGAGAGACCCCTAG 320
Db 43 GCCTACAGCAGTTTATCCCAATGTGGCGGAGAGACCCCTAG 1

```



```
BASE COUNT      0 a      11 c      22 g      0 t

Query Match      1.6%; Score 25; DB 1; Length 33;
Best Local Similarity 84.8%; Pred. No. 8.5;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1351 CAGCGCGCGGCGGACCGCGGGCGGGCGGGCGGG 1383
Db 1 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 33

RESULT 16
AR063105 AR063105 24 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 43 from patent US 5844079.
DEFINITION AR063105
ACCESSION AR063105
VERSION AR063105.1 GI:5990796
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ingham,P.W., McMahon,A.P. and Tabin,C.J.
TITLE Vertebrate embryonic pattern-inducing proteins, and uses related thereto
JOURNAL Patent: US 5844079-A 43 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT      6 a      5 c      11 g      2 t

Query Match      1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
Db 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 17
AR122632 AR122632 24 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 43 from patent US 6165747.
DEFINITION AR122632
ACCESSION AR122632
VERSION AR122632.1 GI:14106949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ingham,P.W., McMahon,A.P., Tabin,C.J., Bumcrot,D.A. and Marti-Gorostiza,E.
TITLE Nucleic acids encoding hedgehog proteins
JOURNAL Patent: US 6165747-A 43 26-DEC-2000;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT      6 a      5 c      11 g      2 t

Query Match      1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
Db 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 18
AR164260 AR164260 24 bp DNA linear PAT 17-OCT-2001
LOCUS Sequence 43 from patent US 6271363.
DEFINITION
```

```
AR164260 AR164260.1 GI:16235331
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ingham,P.W., McMahon,A.P. and Tabin,C.J.
TITLE Nucleic acids encoding hedgehog proteins
JOURNAL Patent: US 6271363-A 43 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT      6 a      5 c      11 g      2 t

Query Match      1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
Db 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 19
AR208932 AR208932 24 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 43 from patent US 6384192.
DEFINITION AR208932
ACCESSION AR208932
VERSION AR208932.1 GI:21510216
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ingham,P.W., McMahon,A.P. and Tabin,C.J.
TITLE Vertebrate embryonic pattern-inducing proteins
JOURNAL Patent: US 6384192-A 43 07-MAY-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT      6 a      5 c      11 g      2 t

Query Match      1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
Db 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 20
I84401/I84401/c I84401 30 bp DNA linear PAT 04-APR-1998
LOCUS Sequence 2 from patent US 5695933.
DEFINITION I84401
ACCESSION I84401
VERSION I84401.1 GI:3021921
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Schalling,M., Hudson,T.J. and Housman,D.E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 2 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
BASE COUNT      0 a      20 c      10 g      0 t

Query Match      1.5%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 14;
```

ORGANISM unidentified
JOURNAL submitted (04-OCT-1999)
DATE SUBMISSION MADE Cedars Sinai Medical Center, 8700

Beverly Blvd., Los Angeles, CA 90048, US

COMMENT Related entry: NM 000193.

FEATURES Location/Qualifiers

source 1..23 /organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

misc_feature 1..23

/note="PCR sense primer for sonic hedgehog (Drosophila)

homolog (SHH)"

BASE COUNT 3 a 4 c 10 g 6 t

Query Match 1.4%; Score 22; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGGCGAGATGT 172

Db 2 GATGCTGCTGCTGGCGAGATGT 23

RESULT 26

AX548364

LOCUS 24 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 288 from Patent WO0240716.

AX548364

VERSION AX548364.1 GI:25913398

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

REFERENCE

AUTHORS

Palm, K.

Profiling tumor specific markers for the diagnosis and treatment of

neoplastic disease

Patent: WO 0240716-A 288 23-MAY-2002;

Cemines, LLC (US)

JOURNAL

FEATURES

source

1..24 /organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Probe"

BASE COUNT 4 a 4 c 10 g 6 t

Query Match 1.4%; Score 22; DB 1; Length 24;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGGCGAGATGT 172

Db 3 GATGCTGCTGCTGGCGAGATGT 24

RESULT 27

AX146574/c

LOCUS 29 bp DNA linear PAT 31-MAY-2001

DEFINITION Sequence 36 from Patent WO0134654.

AX146574

VERSION AX146574.1 GI:14284967

KEYWORDS

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Strauch, K.

Hedgehog fusion proteins and uses

Patent: WO 0134654-A 36 17-MAY-2001;

BIOGEN, INC. (US)

JOURNAL

FEATURES

source

/mol_type="genomic DNA"

/db_xref="taxon:9606"

BASE COUNT 3 a 14 c 5 g 7 t

Query Match 1.4%; Score 22; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TGCAGACCGGCGAGGGGTTTCG 242

Db 22 TGCAGACCGGCGAGGGGTTTCG 1

RESULT 28

AX417112/c

LOCUS 29 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 37 from Patent WO0198344.

AX417112

ACCESSION AX417112

VERSION AX417112.1 GI:21449699

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

REFERENCE

AUTHORS

Ling, L.E. and Sanicola-Nadel, M.

Angiogenesis-modulating compositions and uses

Patent: WO 0198344-A 37 27-DEC-2001;

BIOGEN, INC. (US)

JOURNAL

FEATURES

source

1..29

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Oligonucleotide"

BASE COUNT 3 a 14 c 5 g 7 t

Query Match 1.4%; Score 22; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 25;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TGCAGACCGGCGAGGGGTTTCG 242

Db 22 TGCAGACCGGCGAGGGGTTTCG 1

RESULT 29

AX327693

LOCUS 24 bp DNA linear PAT 07-JAN-2002

DEFINITION Sequence 29 from Patent WO0183715.

AX327693

ACCESSION AX327693

VERSION AX327693.1 GI:18098024

KEYWORDS

synthetic construct

synthetic construct

artificial sequences.

ORGANISM

REFERENCE

AUTHORS

Lee, S.H., Lumelesky, N., Studer, L. and McKay, R.D.

Derivation of midbrain dopaminergic neurons from embryonic stem

cells

Patent: WO 0183715-A 29 08-NOV-2001;

THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US);

Lee, Sang-Hun (KR); Lumelesky, Nadya (US); Studer, Lorenz (US);

McKay, Ron D. G. (US)

JOURNAL

FEATURES

source

1..24

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

BASE COUNT 11 a 6 c 5 g 2 t

Query Match 1.2%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 67;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

342 GGAAGATCTCCAGAACTCCGAGC 365
|||||
Db 1 GGAAGATCACAGAACTCCGAGC 24

RESULT 30
AR154250
LOCUS AR154250 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6238876.
ACCESSION AR154250
VERSION AR154250.1 GI:15122303
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Altaba,A,Ruizi.
TITLE Methods and materials for the diagnosis and treatment of sporadic
JOURNAL basal cell carcinoma
FEATURES Patent: US 6238876-A 5 29-MAY-2001;
Location/Qualifiers
source 1..19
/organism="unknown"
BASE COUNT 7 a 6 c 3 g 3 t
Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

343 GAAGATCTCCAGAACTCC 361
|||||
Db 1 GAAGATCTCCAGAACTCC 19

RESULT 31
AR154254
LOCUS AR154254 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 9 from patent US 6238876.
ACCESSION AR154254
VERSION AR154254.1 GI:15122307
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Altaba,A,Ruizi.
TITLE Methods and materials for the diagnosis and treatment of sporadic
JOURNAL basal cell carcinoma
FEATURES Patent: US 6238876-A 9 29-MAY-2001;
Location/Qualifiers
source 1..19
/organism="unknown"
BASE COUNT 3 a 5 c 5 g 6 t
Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

167 AGATGTCGCTGCTAGTCC 185
|||||
Db 1 AGATGTCGCTGCTAGTCC 19

RESULT 32
AR028113
LOCUS AR028113 25 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5858649.
ACCESSION AR028113
VERSION AR028113.1 GI:5940086
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Asgari,M., Blick,M., Bresser,J., Cubbage,M.Lee. and Prashad,N.
TITLE Amplification of mRNA for distinguishing fetal cells in maternal
JOURNAL blood
FEATURES Patent: US 5858649-A 3 12-JAN-1999;
Location/Qualifiers
source 1..25
/organism="unknown"
BASE COUNT 0 a 9 c 16 g 0 t
Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 85;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1357 CGGCGGGGACCGCGGGCGCGCGC 1381
|||||
Db 1 CGGCGGGGCGCGCGCGCGCGCGC 25

RESULT 33
AR030289
LOCUS AR030289 25 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5861253.
ACCESSION AR030289
VERSION AR030289.1 GI:5943503
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Asgari,M., Blick,M., Bresser,J., Cubbage,M.Lee. and Prashad,N.
TITLE Intracellular antigens for identifying fetal cells in maternal
JOURNAL blood
FEATURES Patent: US 5861253-A 3 19-JAN-1999;
Location/Qualifiers
source 1..25
/organism="unknown"
BASE COUNT 0 a 9 c 16 g 0 t
Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 85;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1357 CGGCGGGGACCGCGGGCGCGCGC 1381
|||||
Db 1 CGGCGGGGCGCGCGCGCGCGCGC 25

RESULT 34
AX689173
LOCUS AX689173 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1905 from Patent EP1281758.
ACCESSION AX689173
VERSION AX689173.1 GI:29411881
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Patent: EP 1281758-A 1905 05-FEB-2003;
FEATURES mdz12
Location/Qualifiers
source 1..25
/organism="Homo sapiens"
/ mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 11 c 4 g 6 t
```

Query Match 1.2%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 85;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 861 ACTTCTCACTTTCCTGGACCGCA 885
 Db 1 AGTCTCTCACTATCTCTGCCCGCA 25

RESULT 35
 LOCUS 142108 25 bp DNA linear PAT 07-OCT-1997
 DEFINITION Sequence 3 from patent US 5629147.
 ACCESSION I42108
 VERSION I42108.1 GI:2467603
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Asgari,M., Blick,M., Bresser,J., Cubbage,M.L. and Prashad,N.
 TITLE Enriching and identifying fetal cells in maternal blood for in situ hybridization
 JOURNAL Patent: US 5629147-A 3 13-MAY-1997;
 FEATURES Location/Qualifiers
 source 1..25
 BASE COUNT 0 a 9 c 16 g 0 t

Query Match 1.2%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 85;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGGGGACCGGGGGCGCGGC 1381
 Db 1 CGCGGGGCGGGGGCGGGCGGC 25

RESULT 36
 LOCUS AR063245 24 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 6 from patent US 5844110.
 ACCESSION AR063245
 VERSION AR063245.1 GI:5990936
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Gold,B.I.
 TITLE Synthetic triple helix-forming compound precursors
 JOURNAL Patent: US 5844110-A 6 01-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..24
 BASE COUNT 3 a 9 c 10 g 2 t

Query Match 1.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 97;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1001 GAGCCGAGGCGTCTCGGGTC 1023
 Db 2 GAGCCGAGGCGGCTCGGGTC 24

RESULT 37
 LOCUS AX689174 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1906 from Patent EP1281758.
 ACCESSION AX689174
 VERSION AX689174.1 GI:29411882
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 1906 05-FEB-2003;
 FEATURES Location/Qualifiers
 source 1..25
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 3 a 11 c 5 g 6 t

Query Match 1.2%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 99;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 863 TTCCTCACTTTCCTGGACCGCA 885
 Db 2 TTCCTCACTATCTCTGCCCGCA 24

RESULT 38
 LOCUS AX689175 25 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1907 from Patent EP1281758.
 ACCESSION AX689175
 VERSION AX689175.1 GI:29411883
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 1907 05-FEB-2003;
 FEATURES Location/Qualifiers
 source 1..25
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 BASE COUNT 3 a 11 c 4 g 7 t

Query Match 1.2%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 99;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 863 TTCCTCACTTTCCTGGACCGCA 885
 Db 1 TTCCTCACTATCTCTGCCCGCA 23

RESULT 39
 LOCUS E16681/c 25 bp DNA linear PAT 28-JUL-1999
 DEFINITION Primer.
 ACCESSION E16681
 VERSION E16681.1 GI:5711364
 KEYWORDS JP 1998215867-A/3.
 SOURCE unidentified
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Momoi,T., Kumagai,H., Higashida,H. and Hama,Y.
 TITLE PROTEIN DERIVATIVE, GENE CODING FOR THE PROTEIN AND PRODUCTION OF THE PROTEIN

JOURNAL Patent: JP 1998215867-A 3 18-AUG-1998;
ASahi GLASS CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1998215867-A/3
PD 18-AUG-1998
PF 04-FEB-1997 JP 1997021811
PI MOMOI TAKASHI, KIMAGAI HIROMICHI, HIGASHIDA HIDEKI, HAMA YUKO
PC C12N15/09.C07K14/52.C07K16/24.C12N1/19.C12P21/02.C12P21/08, PC
G01N33/53;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FT source 1..25
FT Location/Qualifiers
FT /organism='Artificial sequences'.
FEATURES source
1..25
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
BASE COUNT 3 a 9 c 8 g 5 t
Query Match 1.2%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 722 GTGGCGGCCAATCGGAGGCTG 744
|||||
DB 24 GTGGCGGCCAATCGGAGGCTG 2
|||||
RESULT 40
AR154251/c 18 bp DNA linear PAT 08-AUG-2001
LOCUS AR154251
DEFINITION Sequence 6 from patent US 6238876.
ACCESSION AR154251
VERSION AR154251.1 GI:15122304
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Altaba, A. Ruiz.
TITLE Methods and materials for the diagnosis and treatment of sporadic
basal cell carcinoma
JOURNAL Patent: US 6238876-A 6 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..18
/organism='unknown'
BASE COUNT 4 a 5 c 5 g 4 t
Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 559 GGAGTCTCTGCCTACTACGA 576
|||||
DB 18 GGAGTCTCTGCCTACTACGA 1
|||||
RESULT 41
AR177692/c 21 bp DNA linear PAT 17-DEC-2001
LOCUS AR177692
DEFINITION Sequence 24 from patent US 6312949.
ACCESSION AR177692
VERSION AR177692.1 GI:17920047
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)

AUTHORS Sakurada, K., Palmer, T. and Gage, F.H.
TITLE Regulation of tyrosine hydroxylase expression
JOURNAL Patent: US 6312949-A 24 08-NOV-2001;
FEATURES Location/Qualifiers
source 1..21
/organism='unknown'
BASE COUNT 2 a 7 c 5 g 7 t
Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 604 TGACCGGACCGCAGCAAGTA 624
|||||
DB 21 TGACCGGACCGCAGCAAGTA 1
|||||
RESULT 42
AX616896 21 bp DNA linear PAT 20-FEB-2003
LOCUS AX616896
DEFINITION Sequence 7 from Patent WO02094123.
ACCESSION AX616896
VERSION AX616896.1 GI:28447727
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Bojlsen, K., Poulsen, C.H. and Soe, J.B.
TITLE Method of preparing a dough with an enzyme
JOURNAL Patent: WO 02094123-A 7 28-NOV-2002;
FEATURES Location/Qualifiers
source 1..21
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
/note='oligonucleotide primer'
BASE COUNT 0 a 7 c 9 g 5 t
Query Match 1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1020 GCTCGGGCGCGCTTCGGGG 1040
|||||
DB 1 GCTCGGGCGCGCTTCGGGG 21
|||||
RESULT 43
AX548233 25 bp DNA linear PAT 26-NOV-2002
LOCUS AX548233
DEFINITION Sequence 157 from Patent WO0240716.
ACCESSION AX548233
VERSION AX548233.1 GI:25613267
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.
AUTHORS Palm, K.
TITLE Profiling tumor specific markers for the diagnosis and treatment of
neoplastic disease
JOURNAL Patent: WO 0240716-A 157 23-MAY-2002;
FEATURES Location/Qualifiers
source 1..25
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
/note='probe'
BASE COUNT 4 a 6 c 9 g 6 t

Query Match 1.1%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 195 CGCTGCTGGTATGCTCGGAGCTGG 218
Db 1 CACTGCTGCTGCTGCTGAGGACTGG 24

RESULT 44
AX689172
LOCUS AR689172 25 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1904 from Patent EP1281758.
ACCESSION AX689172
VERSION AX689172.1 GI:29411880
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1904 05-FEB-2003;
FEATURES Aeomica, Inc. (US)
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 12 c 4 g 6 t

Query Match 1.1%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 861 ACTTCTCACTTTCTGACCGCG 884
Db 2 AGTTCTCACTATCTGCCCCGCG 25

RESULT 45
AR028416/c
LOCUS AR028416 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 31 from patent US 5858671.
ACCESSION AR028416
VERSION AR028416.1 GI:5940389
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Jones, D.H.
TITLE Iterative and regenerative DNA sequencing method
JOURNAL Patent: US 5858671-A 31 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 4 a 6 c 11 g 2 t 1 others

Query Match 1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1305 CGCTCCTGGCTGCACTGGCGCC 1327
Db 24 CACTCTCGCTGCTGCTGCGCAC 2

RESULT 46
AR130926/c
LOCUS AR130926 24 bp DNA linear PAT 16-MAY-2001

Query Match 1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1305 CGCTCCTGGCTGCACTGGCGCC 1327
Db 24 CACTCTCGCTGCTGCTGCGCAC 2

RESULT 47
AR161892/c
LOCUS AR161892 24 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 31 from patent US 6258533.
ACCESSION AR161892
VERSION AR161892.1 GI:16228893
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Jones, D.H.
TITLE Iterative and regenerative DNA sequencing method
JOURNAL Patent: US 6258533-A 31 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 4 a 6 c 11 g 2 t 1 others

Query Match 1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1305 CGCTCCTGGCTGCACTGGCGCC 1327
Db 24 CACTCTCGCTGCTGCTGCGCAC 2

RESULT 48
AR240225
LOCUS AR240225 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 12 from patent US 6468756.
ACCESSION AR240225
VERSION AR240225.1 GI:27285302
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Bonini, J.A., Borowsky, B.E., Adham, N., Boyle, N. and Thompson, T.O.
TITLE Methods of identifying compounds that bind to SNORF25 receptors
JOURNAL Patent: US 6468756-A 12 22-OCT-2002;
FEATURES Location/Qualifiers
source 1..24
/organism="unknown"
BASE COUNT 10 a 4 c 9 g 1 t

SEQUENCE	Sequence 23 from patent US 6197312.									
ACCESSION	AR137168									
VERSION	AR137168.1 GI:14478677									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unknown.									
REFERENCE	Unclassified									
AUTHORS	1 (bases 1 to 18)									
TITLE	Peak,I.Richard,Anselm., Jennings,M.Paul. and Moxon,E.Richard.									
JOURNAL	Surface antigen									
FEATURES	Patent: US 6197312-A 23 06-MAR-2001;									
source	Location/Qualifiers									
	1..18									
	/organism="unknown"									
BASE COUNT	3 a 9 c 0 g 6 t									
Query Match	1.0%; Score 16.4; DB 1; Length 18;									
Best Local Similarity	94.4%; Pred. No. 1.7e+02;									
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	329 GGAAGGTATGAAGGGAAG 346									
Db	18 GGAAGGTTTGAAGGGAAG 1									
LOCUS	BD136502 18 bp DNA linear PAT 18-SEP-2002									
DEFINITION	Novel surface antigen.									
ACCESSION	BD136502									
VERSION	BD136502.1 GI:23231447									
KEYWORDS	JP 2002508394-A/13.									
SOURCE	synthetic construct									
ORGANISM	artificial construct									
REFERENCE	1 (bases 1 to 18)									
AUTHORS	Peak,I.R., Jennings,M.P. and Moxon,R.E.									
TITLE	Novel surface antigen									
JOURNAL	Patent: JP 2002508394-A 13 19-MAR-2002;									
COMMENT	THE UNIVERSITY OF QUEENSLAND									
	OS Artificial Sequence									
	PN JP 2002508394-A/13									
	PD 19-MAR-2002									
	PF 14-DEC-1998 JP 2000539055									
	PR 12-DEC-1997 GB 9726398.2									
	PI IAN RICHARD PEAK,MICHAEL PAUL JENNINGS,RICHARD E MOXON PC									
	C07K14/22,A61K38/00,A61K39/395,A61P31/04,C07K16/12,C12N1/21, PC									
	C12N15/09,									
	PC C12Q1/68//C12P21/08,A61K37/02,C12N15/00									
	CC Description of Artificial Sequence: 3' oligonucleotide primer									
	CC for PCR									
PH	Key									
FT	Location/Qualifiers									
	1..18									
	/organism='Artificial Sequence'.									
FEATURES	Location/Qualifiers									
source	1..18									
	/organism="synthetic construct"									
	/mol_type="genomic DNA"									
	/db_xref="taxon:32630"									
BASE COUNT	3 a 9 c 0 g 6 t									
Query Match	1.0%; Score 16.4; DB 1; Length 18;									
Best Local Similarity	94.4%; Pred. No. 1.7e+02;									
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	329 GGAAGGTATGAAGGGAAG 346									
Db	18 GGAAGGTTTGAAGGGAAG 1									
LOCUS	AX537662 20 bp DNA linear PAT 23-NOV-2002									
DEFINITION	Novel surface antigen.									
ACCESSION	AX537662									
VERSION	AX537662.1 GI:14478677									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unknown.									
REFERENCE	Unclassified									
AUTHORS	1 (bases 1 to 18)									
TITLE	Peak,I.Richard,Anselm., Jennings,M.Paul. and Moxon,E.Richard.									
JOURNAL	Surface antigen									
FEATURES	Patent: US 6197312-A 23 06-MAR-2001;									
source	Location/Qualifiers									
	1..18									
	/organism="unknown"									
BASE COUNT	3 a 9 c 0 g 6 t									
Query Match	1.0%; Score 16.4; DB 1; Length 18;									
Best Local Similarity	94.4%; Pred. No. 1.7e+02;									
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	329 GGAAGGTATGAAGGGAAG 346									
Db	18 GGAAGGTTTGAAGGGAAG 1									
LOCUS	AX537662 20 bp DNA linear PAT 23-NOV-2002									

DEFINITION Sequence 12 from Patent EP1241269.

ACCESSION AX537662

VERSION AX537662.1 GI:25269615

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Heiskala,M.

TITLE Method for detecting reg-like protein and nucleic acids coding

JOURNAL therefor

DEFINITION Patent: EP 1241269-A 12 18-SEP-2002;

FEATURES Ortho-Clinical Diagnostics, Inc. (US)

source Location/Qualifiers

1. .20

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Artificial"

2 a 5 c 7 g 6 t

BASE COUNT

Query Match 1.0%; Score 16.4; DB 1; Length 20;

Best Local Similarity 94.4%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1249 CATCGAGGACACAGCTG 1266

Db 18 CATCGAGGACACAGCTG 1

RESULT 54

A58260

LOCUS A58260 21 bp DNA linear PAT 05-MAR-1998

DEFINITION Sequence 1 from Patent WO9635793.

ACCESSION A58260

VERSION A58260.1 GI:3713937

KEYWORDS unidentified

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1

AUTHORS Gagne,M.

TITLE ANIMAL GENE THERAPY

JOURNAL Patent: WO 9635793-A 1 14-NOV-1996;

COMMENT IMMUNOVA (CA)

Other publication AU 5641696 961129.

FEATURES Location/Qualifiers

source 1. .21

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

10 a 1 c 4 g 6 t

BASE COUNT

Query Match 1.0%; Score 16.4; DB 1; Length 21;

Best Local Similarity 94.4%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 408 TTAAGGATGAAGAAACA 425

Db 1 TTAAGGTTGAAGAAACA 18

RESULT 55

AX244168

LOCUS AX244168 21 bp DNA linear PAT 28-SEP-2001

DEFINITION Sequence 13 from Patent WO0166754.

ACCESSION AX244168

VERSION AX244168.1 GI:15859223

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .21

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Primer"

3 a 4 c 11 g 3 t

BASE COUNT

Query Match 1.0%; Score 16.4; DB 1; Length 21;

Best Local Similarity 94.4%; Pred. No. 1.8e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 763 GGTGCACCTGGAGCAGGG 780

Db 4 GGTGCTCTGGAGCAGGG 21

RESULT 56

AR084563/c

LOCUS AR084563 21 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 52 from patent US 5981185.

ACCESSION AR084563

VERSION AR084563.1 GI:10011334

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)

AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.

TITLE Oligonucleotide repeat arrays

JOURNAL Patent: US 5981185-A 52 09-NOV-1999;

FEATURES Location/Qualifiers

source 1. .21

/organism="unknown"

0 a 14 c 7 g 0 t

BASE COUNT

Query Match 1.0%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1342 CGCGGGGACACAGCGCGCGG 1362

Db 21 CGCGGGGACACAGCGCGCGG 1

RESULT 57

AR084566/c

LOCUS AR084566 21 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 55 from patent US 5981185.

ACCESSION AR084566

VERSION AR084566.1 GI:10011337

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)

AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.

TITLE Oligonucleotide repeat arrays

JOURNAL Patent: US 5981185-A 55 09-NOV-1999;

FEATURES Location/Qualifiers

source 1. .21

/organism="unknown"

0 a 14 c 7 g 0 t

BASE COUNT

Query Match 1.0%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1341 GCGGGGGACACAGCGCGCGG 1361

REFERENCE	1 (bases 1 to 21)
AUTHORS	Matson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE	Oligonucleotide repeat arrays

RESULT 63

TITLE	Iterative and regenerative DNA sequencing method
JOURNAL	Patent: US 5858671-A 32 12-JAN-1999;
FEATURES	Location/Qualifiers
source	1..22
BASE COUNT	2 a 10 c 6 g 4 t
Query Match	1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity	85.7%; Pred. No. 2e+02;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1307 CTCCTGGCTGCACTGGCGCC 1327
Db	1 CTCCTCGCTGCACTGGCGCAC 21
RESULT 66	
LOCUS	AR028420 22 bp DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 35 from patent US 5858671.
ACCESSION	AR028420
VERSION	AR028420.1 GI:5940393
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 22)
AUTHORS	Jones,D.H.
TITLE	Iterative and regenerative DNA sequencing method
JOURNAL	Patent: US 5858671-A 35 12-JAN-1999;
FEATURES	Location/Qualifiers
source	1..22
BASE COUNT	4 a 6 c 10 g 2 t
Query Match	1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity	85.7%; Pred. No. 2e+02;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1307 CTCCTGGCTGCACTGGCGCC 1327
Db	22 CTCCTCGCTGCACTGGCGCAC 2
RESULT 67	
LOCUS	AR130927 32 bp DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 32 from patent US 6190889.
ACCESSION	AR130927
VERSION	AR130927.1 GI:14119252
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 22)
AUTHORS	Jones,D.H.
TITLE	Methods for removing primer sequences and blocking restriction
JOURNAL	endonuclease recognition domains
FEATURES	Location/Qualifiers
source	1..22
BASE COUNT	2 a 10 c 6 g 4 t
Query Match	1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity	85.7%; Pred. No. 2e+02;
Matches	18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	1307 CTCCTGGCTGCACTGGCGCC 1327
Db	1 CTCCTCGCTGCACTGGCGCAC 21

```
RESULT 68
AR130930/c
LOCUS AR130930 22 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 35 from patent US 6190889.
ACCESSION AR130930
VERSION AR130930.1 GI:14119255
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Jones,D.H.
TITLE Methods for removing primer sequences and blocking restriction
endonuclease recognition domains
JOURNAL Patent: US 6190889-A 35 20-FEB-2001;
FEATURES
source
location/Qualifiers
BASE COUNT 4 a 6 c 10 g 2 t
Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1307 CTCCTGGCTGCACTGGCGCC 1327
Db 22 CTCCTGGCTGCACTGGCGCAC 2
RESULT 69
AR161893
LOCUS AR161893 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 32 from patent US 6258533.
ACCESSION AR161893
VERSION AR161893.1 GI:16228895
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Jones,D.H.
TITLE Iterative and regenerative DNA sequencing method
JOURNAL Patent: US 6258533-A 32 10-JUL-2001;
FEATURES
source
location/Qualifiers
BASE COUNT 2 a 10 c 6 g 4 t
Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1307 CTCCTGGCTGCACTGGCGCC 1327
Db 1 CTCCTGGCTGCACTGGCGCAC 21
RESULT 70
AR161896/c
LOCUS AR161896 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 35 from patent US 6258533.
ACCESSION AR161896
VERSION AR161896.1 GI:16228901
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Jones,D.H.
TITLE Iterative and regenerative DNA sequencing method
JOURNAL Patent: US 6258533-A 35 10-JUL-2001;
FEATURES
source
location/Qualifiers
BASE COUNT 2 a 10 c 6 g 4 t
Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1307 CTCCTGGCTGCACTGGCGCC 1327
Db 1 CTCCTGGCTGCACTGGCGCAC 21
RESULT 71
BD066182
LOCUS BD066182 22 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066182
VERSION BD066182.1 GI:22611785
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 817 07-AUG-2001;
COMMENT BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
FN JP 2001511000-A/817
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FEATURES
source
location/Qualifiers
BASE COUNT 1 a 4 c 16 g 1 t
Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1368 GCGGGGCGCGCGCGCAGAG 1368
Db 2 GAGGGGCGCGCGCGCGGTG 22
RESULT 72
E41382
LOCUS E41382 23 bp DNA linear PAT 31-JAN-2002
DEFINITION Amino acid transporting protein and gene thereof.
ACCESSION E41382
VERSION E41382.1 GI:18627516
KEYWORDS JP 2000157286-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Endo,H. and Kanai,Y.
TITLE Amino acid transporting protein and gene thereof
JOURNAL Patent: JP 2000157286-A 14 13-JUN-2000;
COMMENT SCIENCE & TECH AGENCY
OS Artificial Sequence
FN JP 2000157286-A/14
PD 13-JUN-2000
PF 02-SEP-1999 JP 1999248546
```



```

ACCESSION AR271204
VERSION AR271204.1 GI:29702507
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pelz,D.T.
TITLE Putting trainer
JOURNAL Patent: US 6503152-A 147 07-JAN-2003;
FEATURES
    source
    location/Qualifiers
BASE COUNT 4 a 7 c 5 g 4 t
    Query Match 1.0%; Score 15.8; DB 1; Length 20;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 522 TGACCGAGGCTGGGACGA 540
DB 19 TGACCGAGTCTGGGACCA 1

RESULT 78
AX104051
LOCUS AX104051 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 243 from Patent WO0122972.
ACCESSION AX104051
VERSION AX104051.1 GI:13920248
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    REFERENCE 1
    AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
    TITLE Immunostimulatory nucleic acids
    JOURNAL Patent: WO 0129972-A 243 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
    GmbH (DE)
FEATURES
    source
    location/Qualifiers
BASE COUNT 0 a 6 c 14 g 0 t
    Query Match 1.0%; Score 15.8; DB 1; Length 20;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGCGGCGGCGAG 1386
DB 2 GCGGGGCGGCGGCGGCGGCG 20

RESULT 79
AX355382
LOCUS AX355382 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 410 from Patent WO0197843.
ACCESSION AX355382
VERSION AX355382.1 GI:18620050
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    REFERENCE 1
    AUTHORS Weiner,G. and Hartmann,G.
    TITLE Methods for enhancing antibody-induced cell lysis and treating
    cancer
    JOURNAL Patent: WO 0197843-A 410 27-DEC-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
    location/Qualifiers

```

```

source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-phosphodiester backbone"
BASE COUNT 0 a 6 c 14 g 0 t
    Query Match 1.0%; Score 15.8; DB 1; Length 20;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGCGGCGGCGAG 1386
DB 2 GCGGGGCGGCGGCGGCGGCG 20

RESULT 80
AX547104
LOCUS AX547104 20 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 243 from Patent WO02053141.
ACCESSION AX547104
VERSION AX547104.1 GI:25812248
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    REFERENCE 1
    AUTHORS Bratzler,R.L.
    TITLE Inhibition of angiogenesis by nucleic acids
    JOURNAL Patent: WO 02053141-A 243 11-JUL-2002;
    Coley Pharmaceutical Group, Inc. (US)
FEATURES
    source
    location/Qualifiers
BASE COUNT 0 a 6 c 14 g 0 t
    Query Match 1.0%; Score 15.8; DB 1; Length 20;
    Best Local Similarity 89.5%; Pred. No. 2.2e+02;
    Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGCGGCGGCGAG 1386
DB 2 GCGGGGCGGCGGCGGCGGCG 20

RESULT 81
BD069976
LOCUS BD069976 20 bp DNA linear PAT 27-AUG-2002
DEFINITION Use of nucleic acids containing unmethylated CPG dinucleotide in
the treatment of LPS-associated disorders.
ACCESSION BD069976
VERSION BD069976.1 GI:22615579
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
    REFERENCE 1 (bases 1 to 20)
    AUTHORS Schwartz,D.A. and Krieg,A.M.
    TITLE Use of nucleic acids containing unmethylated CPG dinucleotide in
    the treatment of LPS-associated disorders
    JOURNAL Patent: JP 2001513776-A 65 04-SEP-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION
    COMMENT
    OS Artificial Sequence
    PN JP 2001513776-A/65
    PD 04-SEP-2001
    PF 25-FEB-1998 JP 1998537810
    PR 28-FEB-1997 US 60/039405
    PI DAVID A SCHWARTZ,ARTHUR M KRIEG
    PC A61K49/00,C07H21/02,C07H21/04,A01N43/04
    CC synthetic oligonucleotide

```



```

FH Key      Location/Qualifiers
FT source   1..20 /organism='Artificial Sequence'.
FT          Location/Qualifiers
FEATURES
    source   1..20 /organism='synthetic construct'
              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
BASE COUNT    0 a 6 c 14 g 0 t

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGCGGGCGGGCGGGCGAG 1386
Db      |||||
        2 GCGGGCGGGCGGGCGGGCGG 20

RESULT 82
LOCUS      AR109586                21 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 11 from patent US 6114129.
ACCESSION  AR109586
VERSION     AR109586.1 GI:12825862
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 21)
AUTHORS   Agrawal, B. and Longenecker, B. Michael.
TITLE     Methods of detecting T-cell activation and treating disorders
          associated with T-cell dysfunction
JOURNAL   Patent: US 6114129-A 11-05-SEP-2000;
FEATURES   Location/Qualifiers
    source   1..21
              /organism='unknown'
BASE COUNT    4 a 5 c 5 g 7 t

Query Match      1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AAATCGGAGGCTGCTTCC 749
Db      |||||
        3 ATATCGAGAGGCTGCTTCC 21

RESULT 83
LOCUS      AX094992/c              21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 170 from Patent WO0118250.
ACCESSION  AX094992
VERSION     AX094992.1 GI:13511195
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Lander, E.S., Gargill, M., Ireland, J.S., Bolck, S., Daley, G.Q. and
          McCarthy, J.J.
TITLE     Single nucleotide polymorphisms in genes
JOURNAL   Patent: WO 0118250-A 170 15-MAR-2001;
          WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
          Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
    source   1..21
              /organism='Homo sapiens'
              /mol_type='genomic DNA'
              /db_xref='taxon:9606'
BASE COUNT    4 a 7 c 7 g 2 t 1 others

Query Match      1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1164 GCGAGGAGCGCGGGCGGCC 1183

```

```

Query Match      1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1484 TGCTCTCTGGACAGCGAGGCC 1504
Db      |||||
        21 TGTGTCTCTGGACAGCGAGGCC 1

RESULT 84
LOCUS      AX095827/c              21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 1005 from Patent WO0118250.
ACCESSION  AX095827
VERSION     AX095827.1 GI:13512054
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Lander, E.S., Gargill, M., Ireland, J.S., Bolck, S., Daley, G.Q. and
          McCarthy, J.J.
TITLE     Single nucleotide polymorphisms in genes
JOURNAL   Patent: WO 0118250-A 1005 15-MAR-2001;
          WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
          Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
    source   1..21
              /organism='Homo sapiens'
              /mol_type='genomic DNA'
              /db_xref='taxon:9606'
BASE COUNT    4 a 7 c 8 g 1 t 1 others

Query Match      1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1026 GGCGCGCTTCGGGGCGGCAC 1046
Db      |||||
        21 GGCGCGCTTCGGGGCGGCAC 1

RESULT 85
LOCUS      AX146231                21 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 422 from Patent WO0134840.
ACCESSION  AX146231
VERSION     AX146231.1 GI:14284749
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Au, K.G., Chen, J.G., Patil, N. and Thomas, D.
TITLE     Genetic compositions and methods
JOURNAL   Patent: WO 0134840-A 422 17-MAY-2001;
          GLAXO GROUP LIMITED (GB) ; Affymetrix, Inc. (US)
FEATURES   Location/Qualifiers
    source   1..21
              /organism='Homo sapiens'
              /mol_type='genomic DNA'
              /db_xref='taxon:9606'
          variation 1..21
              /note='n' represents a polymorphic base"
BASE COUNT    0 a 9 c 11 g 0 t 1 others

Query Match      1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1164 GCGAGGAGCGCGGGCGGCC 1183

```

Db 1 GC GCGGGCGGCGGCGGCGC 20
|||||

RESULT 86

E08187/c LOCUS DOG2016P01 21 bp DNA linear PAT 29-SEP-1997
DEFINITION Primer for isolation of the promoter in rice starch-branching enzyme.

ACCESSION E08187

VERSION E08187.1 GI:2176308

KEYWORDS JP 1994261767-A/5.

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 21)

AUTHORS Baba, T. and Shimada, H.

TITLE NEW RICE PLANT STARCH-BRANCHED ENZYMIC GENE

JOURNAL PATENT: JP 1994261767-A 5 20-SEP-1994;

COMMENT MITSUI GIYOUSAI SHOKUBUTSU BIO KENKUSHO:KK

OS None

OC Artificial sequences.

PN JP 1994261767-A/5

PD 20-SEP-1994

PF 22-OCT-1993 JP 1993265171

PR 29-OCT-1992 JP 92P 291719

PI BABA TADASHI, SHIMADA HIROAKI

PC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

CC C12N15/54;A01H5/00;C12N5/10;C12P19/16//A23L1/10;C12N9/10; CC

primer_bind 7 a 3 c 6 g
/db_xref="taxon:9615"
/clone="2016P"
complement(1..22)
/note="2016P"
/evidence=experimental

BASE COUNT

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 403 CATATTTAAGGATGAAGAAAC 424

Db 1 CATTTTAAGGATGAAGACGC 22

RESULT 88

A88670

LOCUS A88670

DEFINITION Sequence 818 from Patent WO9833904.

ACCESSION A88670

VERSION A88670.1

KEYWORDS GI:6737240

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)

AUTHORS Brysch, W. and Schlingensiepen, K.

TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD

JOURNAL Patent: WO 9833904-A 818 06-AUG-1998;

BIODIVERSITY GENES (DE); BRYSCH WOLFGANG (DE)

FEATURES Location/Qualifiers

1..17

source

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

0 a 4 c 13 g 0 t

BASE COUNT

Query Match 1.0%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGCGGCGGCGGCGG 1386

Db 1 GGGGGCGGCGGCGGCGG 17

RESULT 89

A90637

LOCUS A90637

DEFINITION Sequence 818 from Patent EP0856579.

ACCESSION A90637

VERSION A90637.1

KEYWORDS GI:6739151

SOURCE unidentified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 17)

AUTHORS Brysch, W.D. and Schlingensiepen, K.D.

TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: EP 0856579-A 818 05-AUG-1998;

BIODIVERSITY GENES (DE)

FEATURES Location/Qualifiers

1..17

source

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

0 a 4 c 13 g 0 t

BASE COUNT

Query Match 1.0%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DOG2016P01 LOCUS DOG2016P01 22 bp DNA linear MAM 29-NOV-1996

DEFINITION Canis familiaris (clone 2016P) DNA, STS primer.

ACCESSION L78581

VERSION L78581.1 GI:11372870

KEYWORDS genetic marker; microsatellite; tetranucleotide repeat.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

TITLE 1 (bases 1 to 22)

JOURNAL Francisco, L.V., Langston, A.A., Mellersh, C.S., Neal, C.L. and

OSTRANDER, E.A.

TITLE A class of highly polymorphic tetranucleotide repeats for canine

JOURNAL Genetic mapping

Mamm. Genome 7 (5), 359-362 (1996)

KEYWORDS 96269603

FEATURES Location/Qualifiers

1..22

source

/organism="Canis familiaris"

/mol_type="genomic DNA"

```

QY 1370 GGGGGGGGGGGGGGGG 1386
Db 1 GGGGGGGGGGGGGGGG 17

RESULT 90
BD066183 17 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066183
ACCESSION BD066183
VERSION 1 GI:22611786
KEYWORDS JP 2001511000-A/818.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlingensiefen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 818 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/818
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FT Location/Qualifiers
FT source 1..17
FT /organism='Unknown'.

FEATURES
source
1..17 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 0 a 4 c 13 g 0 t

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGGGGGGGGGGGG 1386
Db 1 GGGGGGGGGGGGGGGG 17

RESULT 91
BD141639/c
LOCUS p53-Dependent novel apoptosis-associated protein and method of
DEFINITION BD141639 screening apoptosis controller.
ACCESSION BD141639
VERSION 1 GI:23236584
KEYWORDS WO 0212496-A/17.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nakamura,Y. and Arakawa,H.
TITLE p53-Dependent novel apoptosis-associated protein and method of
JOURNAL screening apoptosis controller
JOURNAL Patent: WO 0212496-A 17 14-FEB-2002;
JOURNAL JAPAN AS REPRESENTED BY THE PRESIDENT OF THE UNIVERSITY OF TOKYO,
JOURNAL CENTER FOR ADVANCED SCIENCE AND TECHNOLOGY INCUBATION LTD, YUSUKE
JOURNAL NAKAMURA, HIROFUMI ARAKAWA
COMMENT OS Artificial Sequence
PN WO 0212496-A/17
PD 14-FEB-2002
PF 02-AUG-2001 WO 2001JP066666
PR 03-AUG-2000 JP 00P 240399
PI YUSUKE NAKAMURA,HIROFUMI ARAKAWA
PC C12N15/12,C07K14/47,C07K16/18,C12P21/02,C12Q1/68,G01N33/50, PC

G01N33/15,
PC A61K45/00,A61K48/00,A61K38/17,A61P43/00,A61P35/00 CC
Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.

FEATURES
source
1..17 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 2 a 6 c 2 g 7 t

Query Match 1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 706 GARAGCAGAGAACTCGG 722
Db 17 GARAGCAGAGAACTTGG 1

RESULT 92
A67594
LOCUS A67594 18 bp DNA linear PAT 05-MAY-1999
DEFINITION Sequence 14 from Patent WO9744485.
ACCESSION A67594
VERSION A67594.1 GI:4756457
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Goodfellow,P.N.
TITLE METHODS FOR IDENTIFYING A MUTATION IN A GENE OF INTEREST
JOURNAL Patent: WO 9744485-A 14 27-NOV-1997;
JOURNAL HEXAGEN TECHNOLOGY LIMITED (GB)

FEATURES
source
1..18 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 0 a 7 c 11 g 0 t

Query Match 1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 GCGGGGGGGGGGGGGG 1384
Db 1 GCGGGGGGGGGGGGGG 17

RESULT 93
AR089732
LOCUS AR089732 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 14 from patent US 5994075.
ACCESSION AR089732
VERSION AR089732.1 GI:10016487
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Goodfellow,P.N.
TITLE Methods for identifying a mutation in a gene of interest without a
JOURNAL phenotypic guide
JOURNAL Patent: US 5994075-A 14 30-NOV-1999;
JOURNAL Location/Qualifiers
FEATURES
source
1..18
/organism="unknown"
BASE COUNT 0 a 7 c 11 g 0 t

```

Query Match 1.0%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 GCGGGGCGCGCGCGC 1384
 |||||
 Db 1 GCGGGGCGCGCGCGC 17

RESULT 94
 LOCUS AR315298/c
 DEFINITION Sequence 5835 from patent US 6559294.
 ACCESSION AR315298
 VERSION AR315298.1 GI:31708724
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Griffais, R., Hoise, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
 TITLE Chlamydia pneumoniae polynucleotides and uses thereof
 JOURNAL Patent: US 6559294-A 5835 06-MAY-2003;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 6 a 4 c 7 g 3 t
 Query Match 1.0%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 2.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 190 CTCCTCGCTGCTGTAT 206
 |||||
 Db 18 CTCCTCGCTGCTGCAT 2

RESULT 95
 LOCUS BD139686
 DEFINITION Novel guaA.
 ACCESSION BD139686
 VERSION BD139686.1 GI:23234631
 KEYWORDS JP 2002504309-A/3.
 SOURCE Streptococcus pneumoniae
 ORGANISM Streptococcus pneumoniae
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Zalacain, M., Brown, J.R., Biswas, S., Warren, R.L. and Shilling, L.K.
 JOURNAL Novel guaA
 COMMENT Patent: JP 2002504309-A 3 12-FEB-2002;
 SMITHKLINE BEECHAM CORP
 OS Streptococcus pneumoniae
 PN JP 2002504309-A/3
 PD 12-FEB-2002
 PF 20-NOV-1998 JP 2000522247
 PR 21-NOV-1997 US 60/066350
 PI MAGDALENA ZALACAIN, JAMES R BROWN, SANJOY BISWAS, RICHARD L PI WARREN,
 PI LISA K SHILLING
 PC C12N15/09, A61K38/00, A61P31/04, A61P37/02, C07K14/315, C07K16/12, C12N1/15,
 PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/15, G01N33/PC 50,
 PC G01N33/53, G01N33/68/C12P21/08, (C12N15/09, C12R1:46), C12N15/00, PC A61K37/02,
 PC C12N5/00, (C12N15/00, C12R1:46)
 CC Novel guaA
 FH Key Location/Qualifiers

FT source 1..22
 FT /organism='Streptococcus pneumoniae'.
 FEATURES Location/Qualifiers
 source 1..22
 /organism='Streptococcus pneumoniae'
 /mol_type='genomic DNA'
 /db_xref='taxon:1313'
 BASE COUNT 7 a 6 c 5 g 4 t
 Query Match 1.0%; Score 15.4; DB 1; Length 22;
 Best Local Similarity 94.1%; Pred. No. 2.6e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1520 ATGGCGGTCAAGTCCAG 1536
 |||||
 Db 6 ATGGCGGTCAAGTCCAG 22

RESULT 96
 LOCUS AR137400
 DEFINITION Sequence 15 from patent US 6197507.
 ACCESSION AR137400
 VERSION AR137400.1 GI:14478909
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Berg, T., Tollersrud, O., Kristien, and Nilsen, O.
 TITLE Genetic test for alpha-mannosidosis
 JOURNAL Patent: US 6197507-A 15 06-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 2 a 5 c 11 g 2 t
 Query Match 1.0%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.7e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGGCGCGCGCGCAGA 1387
 |||||
 Db 1 GTGGCGCGCGCGCGTGCAGA 20

RESULT 97
 LOCUS AR174482/c
 DEFINITION Sequence 6 from patent US 6306831.
 ACCESSION AR174482
 VERSION AR174482.1 GI:17914802
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Roberts, P.C. and Driver, S.B.
 TITLE Transplacental delivery of oligonucleotides
 JOURNAL Patent: US 6306831-A 6 23-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 0 a 11 c 4 g 5 t
 Query Match 1.0%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 2.7e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 CGAGCGGAGCGAGGAGG 53
 |||||
 Db 20 CGAGCGGAGGAGGAGG 1

```

RESULT 98
AR212475/c
LOCUS AR212475 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6399763.
ACCESSION AR212475
VERSION AR212475.1 GI:21516059
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Frenken,L. and van der Logt,C.P.E.
TITLE Method for producing antibody fragments
JOURNAL Patent: US 6399763-A 7 04-JUN-2002;
FEATURES
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 2 a 7 c 3 t 1 others
Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 769 CCTGGAGCGCGGCACCA 788
Db 20 CCTGGAGCGCGGCACCA 1

RESULT 99
AR217890
LOCUS AR217890 20 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6417169.
ACCESSION AR217890
VERSION AR217890.1 GI:23318015
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Insulin-like growth factor II antisense oligonucleotide sequences
JOURNAL Patent: US 6417169-A 8 09-JUL-2002;
FEATURES
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 3 a 4 c 12 g 1 t
Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1540 AGCCGGGGCGCGGGGAG 1559
Db 1 ACCTCGAGGGCGCGGGGAG 20

RESULT 100
AX027702/c
LOCUS AX027702 20 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 7 from Patent WO0043507.
ACCESSION AX027702
VERSION AX027702.1 GI:10188569
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Frenken,L.G. and Van Der Logt,C.P.E.
TITLE Method for producing antibody fragments
JOURNAL Patent: WO 0043507-A 7 27-JUL-2000;
UNILEVER PLC (GB) ; LEVER HINDUSTAN LTD (IN) ; UNILEVER NV (NL)

```

```

FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="PRIMER"
7 c 3 t 1 others
BASE COUNT 2 a 7 c 3 t 1 others
Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 769 CCTGGAGCGCGGCACCA 788
Db 20 CCTGGAGCGCGGCACCA 1

RESULT 101
AR001196
LOCUS AR001196 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 9 from patent US 5738993.
ACCESSION AR001196
VERSION AR001196.1 GI:3963263
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 21)
AUTHORS Fugono,N., Kurusu,Y., Terasawa,M. and Yukawa,H.
TITLE Oligonucleotide and method for analyzing base sequence of nucleic acid
JOURNAL Patent: US 5738993-A 9 14-APR-1998;
FEATURES
Location/Qualifiers
1..21
/organism="unknown"
BASE COUNT 11 a 0 c 10 g 0 t
Query Match 1.0%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 50 AGGGAAGCGCAGAGAGAG 69
Db 1 AGGAAGAGCGGAGAGAG 20

RESULT 102
AX154080
LOCUS AX154080 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 178 from Patent WO0138576.
ACCESSION AX154080
VERSION AX154080.1 GI:14535694
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Cargill,M., Ireland,J.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 178 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 11 c 0 t 1 others
Query Match 1.0%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 979 GCACACGACTCGCCACCG 998
    |||||
Db 1 GCACACACACGCGCCACCG 20

RESULT 103
E11034
LOCUS E11034 21 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide as a probe for sequencing by hybridization.
ACCESSION E11034
VERSION E11034.1 GI:22024675
KEYWORDS JP 1996070900-A/9.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 21)
AUTHORS Fugono,N., Kuruai,Y., Terasawa,M. and Yugawa,H.
TITLE ANALYSIS OF BASE SEQUENCE OF OLIGONUCLEOTIDE AND NUCLEIC ACID
JOURNAL Patent: JP 1996070900-A 9 19-MAR-1996;
COMMENT MITSUBISHI CHEM CORP
OS None
OC Artificial sequences.
PN JP 1996070900-A/9
PD 19-MAR-1996
PF 13-FEB-1995 JP 1995024410
PR 22-FEB-1994 JP 94P 24168, 29-JUN-1994 JP 94P 147291 PI
FUGONO NOBUTAKE, KURUSU YASUO, TERASAWA MASATO, PI YUGAWA
HIDEAKI
PC C1201/68, C12N15/09;
CC strandedness: Single;
CC topology: linear;
FH Key Location/Qualifiers
FT source
    1..21
    /organism="Artificial sequences".
    /location/Qualifiers
    1..21
    /organism="unclassified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
BASE COUNT 11 a 0 c 10 g 0 t
    Query Match 1.0%; Score 15.2; DB 1; Length 21;
    Best Local Similarity 85.0%; Pred. No. 2.7e+02;
    Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 50 AGGAAAGCGCAAGAGAGAG 69
    |||||
Db 1 AGGAAAGCGCAAGAGAGAG 20

RESULT 104
I07164/c
LOCUS I07164/c 16 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 10 from Patent EP 0331356.
ACCESSION I07164
VERSION I07164.1 GI:590048
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gorman,J., Clark,P.E., Fornwald,J.A., Brawner,M.E., Deen,K.C.,
TITLE Expression of HIV binding proteins
JOURNAL Gorman,J.A., Sathe,G.M., Sweet,R.W. and Taylor,D.P.
FEATURES
    Patent: EP 0331356-A2 10 06-SEP-1989;
    Location/Qualifiers
    1..16
    /organism="unknown"
    /db_xref="taxon:32644"
BASE COUNT 0 a 10 c 6 g 0 t
    Query Match 1.0%; Score 15; DB 1; Length 16;
    Best Local Similarity 100.0%; Pred. No. 2.7e+02;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 979 GCACACGACTCGCCACCG 998
    |||||
Db 1 GCACACACACGCGCCACCG 20

RESULT 105
SSAJ793/c
LOCUS SSAJ793 19 bp mRNA linear MAM 29-JUL-1997
DEFINITION Sus scrofa EST 3'UTR SLC3A1 forward primer.
ACCESSION AJ000793
VERSION AJ000793.1 GI:2286016
KEYWORDS PCR primer.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 19)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Fridolfsson,A.K., Hori,T., Wintero,A.K., Fredholm,M., Yarle,M.,
Robic,A., Andersson,L. and Ellegren,H.
TITLE Expansion of the pig comparative map by expressed sequence tags
    (EST) mapping
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 19)
AUTHORS Fridolfsson,A.K.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-1997) Fridolfsson A.K., Animal Breeding and
Genetics, Swedish University of Agricultural Sciences, Biomedical
Center, Box 597, S-751 24 Uppsala, SWEDEN
FEATURES
    1..19
    Location/Qualifiers
    1..19
    /organism="Sus scrofa"
    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /chromosome="3"
    /map="q21-q23"
BASE COUNT 5 a 7 c 5 g 2 t
    Query Match 1.0%; Score 15; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 2.9e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 AGATGCTGCTGCTGG 164
    |||||
Db 16 AGATGCTGCTGCTGG 2

RESULT 106
A51144
LOCUS A51144 21 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 13 from Patent WO9616175.
ACCESSION A51144
VERSION A51144.1 GI:2303915
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Beckmann,J. and Richard,I.
TITLE LGMD gene
JOURNAL Patent: WO 9616175-A 13 30-MAY-1996;
ASS FRANCAISE CONTRE LES MYOPA (FR)
FEATURES
    Location/Qualifiers
    1..21
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
BASE COUNT 1 a 7 c 3 g 10 t
    Query Match 1.0%; Score 15; DB 1; Length 21;
    Best Local Similarity 100.0%; Pred. No. 2.9e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1341 GCGGGGGGACGGGGC 1358
Db 1 GCGGGGGGACGGGGC 18

RESULT 112
AX063650
LOCUS AX063650
DEFINITION Sequence 34 from patent US 6297013.
ACCESSION AR171053
VERSION AR171053.1 GI:17910003
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Morgan, A.R. and Severini, A.
TITLE Compositions and methods for determining the activity of
DNA-binding proteins and of initiation of transcription
JOURNAL Patent: US 6297013-A 34 02-OCT-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 1 a 4 c 13 g 0 t

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1359 GCGGGGACCGGGGGC 1376
Db 1 GCGGGGACCGGGGGC 18

RESULT 113
AX063650
LOCUS AX063650
DEFINITION Sequence 34 from Patent WO0100817.
ACCESSION AX063650
VERSION AX063650.1 GI:12541374
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Morgan, A.R. and Severini, A.
TITLE Compositions and methods for determining the activity of
dna-binding proteins and of initiation of transcription
JOURNAL Patent: WO 0100817-A 34 04-JAN-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 1 a 4 c 13 g 0 t

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1359 GCGGGGACCGGGGGC 1376
Db 1 GCGGGGACCGGGGGC 18

RESULT 114
AX115187
LOCUS AX115187/c
DEFINITION Sequence 310 from Patent WO0129262.

AX115187
VERSION AX115187.1 GI:14032129
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 310 26-APR-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 0 a 2 c 9 g 7 t

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 69 GCGCACGCGCACACCC 86
Db 18 GCGCACGCGCACACAC 1

RESULT 115
BD178357
LOCUS BD178357
DEFINITION Method of screening drug for preventing/treating proliferative
glomerular nephritis.
ACCESSION BD178357
VERSION BD178357.1 GI:30015622
KEYWORDS WO 02077642-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Takagaki, K., Katsuma, S. and Tsujimoto, G.
TITLE Method of screening drug for preventing/treating proliferative
glomerular nephritis
JOURNAL Patent: WO 02077642-A 15 03-OCT-2002;
COMMENT NIPPON SHINYAKU CO LTD, THE JAPAN HEALTH SCIENCES FOUNDATION,
KAZUCHIKA TAKAGAKI, SUSUMU KATSUMA, GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 02077642-A/15
PD 03-OCT-2002
PF 25-MAR-2001 JP 01P 088018, 06-SEP-2001 JP 01P 270551 P1
PR 26-MAR-2001 JP 01P 088018, 06-SEP-2001 JP 01P 270551 P1
KAZUCHIKA TAKAGAKI, SUSUMU KATSUMA, GOZO TSUJIMOTO PC
G01N33/50 G01N33/15 G01N33/566 A61P13/12 A61K45/00 CC Description
of Artificial Sequence: Reverse primer for PCR FH Key
FEATURES Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
source 1..18
BASE COUNT 2 a 5 c 7 g 4 t

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1403 CCAGGTGCTGCGGAGCT 1420
Db 1 CTAGGTGCTGCGGAGCT 18

Db 20 GCGCGCGCGGAGAGCC 3

RESULT 121
AX250649/c
LOCUS
DEFINITION Sequence 45 from Patent WO0168921.
ACCESSION AX250649
VERSION AX250649.1 GI:15984393
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFICIAL SEQUENCES.

REFERENCE 1
AUTHORS Koshinsky, H., Zwick, M.S. and Mccue, K.F.
TITLE Compositions and methods for simultaneous detection of multiple biological entities
JOURNAL Patent: WO 0168921-A 45 20-SEP-2001;
INVESTIGATOR (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

BASE COUNT 5 a 5 c 7 g 3 t
Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 119 GACAGCTCGGAGTCATC 136
|||||
Db 20 GACCGCTCGGAGTCTTC 3

RESULT 122
AX250651/c
LOCUS
DEFINITION Sequence 47 from Patent WO0168921.
ACCESSION AX250651
VERSION AX250651.1 GI:15984395
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFICIAL SEQUENCES.

REFERENCE 1
AUTHORS Koshinsky, H., Zwick, M.S. and Mccue, K.F.
TITLE Compositions and methods for simultaneous detection of multiple biological entities
JOURNAL Patent: WO 0168921-A 47 20-SEP-2001;
INVESTIGATOR (US)

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="PCR Primer"

BASE COUNT 5 a 5 c 7 g 3 t
Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 119 GACAGCTCGGAGTCATC 136
|||||
Db 20 GACCGCTCGGAGTCTTC 3

RESULT 123
BD001973
LOCUS
DEFINITION Process for the preparation and improvement of pantothenic acid-producing microorganisms, plasmid vector, E. coli K12 strain, microorganism, C. glutamicum and process for the preparation of pantothenic acid.

ACCESSION BD001973
VERSION BD001973.1 GI:18628713
KEYWORDS JP 2000116387-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFICIAL SEQUENCES.

REFERENCE 1 (bases 1 to 20)
AUTHORS Erishevski, F., Kalinowski, J., Puehler, A., Dushu, N., Doomen, J., Fawick, M. and Thiabach, G.
TITLE Process for the preparation and improvement of pantothenic acid-producing microorganisms, plasmid vector, E. coli K12 strain, microorganism, C. glutamicum and process for the preparation of pantothenic acid.

JOURNAL Patent: JP 2000116387-A 4 25-APR-2000;
DEGUSSA HUELS AG

COMMENT OS Artificial Sequence
PN JP 2000116387-A/4
PD 25-APR-2000
PF 06-OCT-1999 JP 1999285925
PI FRANK ERISHEVSKI, JOERN KALINOWSKI, ALFRED PUEHLER, NICOLE DUSCHU,
PI JURGEN DOOMEN, MAIK FAWICK, GEORG THIABACH
PC C12N15/09, C12N1/21, C12N9/00, C12N9/04, C12N9/88, C12P13/02, PC (C12N1/21, C12R1/15), (C12N1/21, C12R1/19), (C12P13/02, C12R1/19), PC (C12P13/02, C12R1/15), (C12P13/02, C12R1/645), C12N15/00 CC

PH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".

FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT 4 a 7 c 3 g 6 t
Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 561 AGTCTCTGCACTACGAGG 578
|||||
Db 3 AGTCTCTGCACTACGAGG 20

RESULT 124
BD178509/c
LOCUS
DEFINITION Method of detecting nucleic acid relating to disease.
ACCESSION BD178509
VERSION BD178509.1 GI:30015775
KEYWORDS WO 02077281-A/15.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Hashimoto, K., Hashimoto, M., Mishihiro, S. and Ota, Y.
TITLE Method of detecting nucleic acid relating to disease
JOURNAL Patent: WO 02077281-A 15 03-OCT-2002;
TOSHIBA CORP, KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA

COMMENT OS Hepatitis virus (hepatitis C virus)
PN WO 02077281-A/15
PD 03-OCT-2002
PF 05-MAR-2002 WO 2002JP002030
PI 27-MAR-2001 JP 01P 090053.18-SEP-2001 JP 01P 284112 PI KOJI HASHIMOTO, MICHIE HASHIMOTO, SHUNJI MISHIRO, YASUHIKO OTA PC C12Q1/68, C12N15/09, C12M1/00, G01N33/53, G01N33/543, G01N33/566, PC G01N33/576,
PC G01N37/00
CC Method of detecting nucleic acid relating to disease FH Key

```

SOURCE ORGANISM
Unknown.
Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Okamoto, H. and Nakamura, T.
TITLE Oligonucleotides and determination system of HCV genotypes
JOURNAL Patent: US 5427909-A 19 27-JUN-1995;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 5 a 5 c 7 g 3 t
Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 119 GACAGCTCGGAAGTCATC 136
||| ||||| ||||| |||
Db 20 GACCGCTCGGAAGTCTTC 3
||| ||||| ||||| |||

RESULT 125
E31674/c
LOCUS E31674 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for distinguishing eucaryotic individual based on PCR finger
print with the use of restriction primer of inter-SINE sequences
and primer to be used therein.
ACCESSION E31674
VERSION E31674.1 GI:13018594
KEYWORDS JP 2000023671-A/47.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ichiro, O., Ichiro, N. and Hiroshi, Y.
TITLE Method for distinguishing eucaryotic individual based on PCR finger
print with the use of restriction primer of inter-SINE sequences
and primer to be used therein
JOURNAL Patent: JP 200023671-A 47 25-JAN-2000;
COMMENT NATIONAL RESEARCH INSTITUTE OF AQUACULTURE
OS Artificial Sequence
PN JP 2000023671-A/47
PD 25-JAN-2000
PF 10-JUL-1998 JP 1998195692
PR ICHIRO OHARA, ICHIRO NAKAYAMA, HIROSHI YASUE
PC C12N15/09, C12Q1/68, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
FEATURES
source 1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 2 a 4 g 3 t
Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1376 GCGCGGGCAGAGTAGCC 1393
||| ||||| ||||| |||
Db 20 GCGCGGGCAGAGTAGCC 3
||| ||||| ||||| |||

RESULT 126
I12609/c
LOCUS I12609 20 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 19 from patent US 5427909.
ACCESSION I12609
VERSION I12609.1 GI:909991
KEYWORDS

```

```

SOURCE ORGANISM
Unknown.
Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Okamoto, H. and Nakamura, T.
TITLE Oligonucleotides and determination system of HCV genotypes
JOURNAL Patent: US 5427909-A 19 27-JUN-1995;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 5 a 5 c 7 g 3 t
Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 119 GACAGCTCGGAAGTCATC 136
||| ||||| ||||| |||
Db 20 GACCGCTCGGAAGTCTTC 3
||| ||||| ||||| |||

RESULT 127
A56957/c
LOCUS A56957 21 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 15 from Patent WO9629091.
ACCESSION A56957
VERSION A56957.1 GI:3712940
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stanley, M.A. and Scarpini, C.G.
TITLE TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED LESIONS USING INTERLEUKIN-12
JOURNAL Patent: WO 9629091-A 15 26-SEP-1996;
COMMENT UNIV CAMBRIDGE TECH (GB)
Other publication AU 5151596 961008.
FEATURES Location/Qualifiers
source 1..21
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 4 a 6 c 6 g 5 t
Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 118 GGACAGCTCGGAAGTCAT 135
||| ||||| ||||| |||
Db 18 GGCCAGCTTGGGAAGTCAT 1
||| ||||| ||||| |||

RESULT 128
AR052917/c
LOCUS AR052917 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 41 from patent US 5833976.
ACCESSION AR052917
VERSION AR052917.1 GI:5977779
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Malefyt, Rde, Waal, Howard, M., Hsu, D.-H., Ishida, H., O'Garra, A.,
Spits, H. and Zlotnik, A.
TITLE Use of interleukin-10 (IL-10) to treat endotoxin- or
superantigen-induced toxicity
JOURNAL Patent: US 5833976-A 41 10-NOV-1998;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
BASE COUNT 4 a 6 c 6 g 5 t

```

```

Query Match          0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GGACAGCTCGGAAGTCAT 135
  |||||
Db 18 GGCCAGCTTGGAGTCAT 1

RESULT 129
AR054280/c
LOCUS AR054280 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 41 from patent US 5837232.
ACCESSION AR054280
VERSION AR054280.1 GI:5979857
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS De Waal Malefyt, R., Howard, M., Hsu, D.-H., Ishida, H., O'Garra, A.,
TITLE Spits, H. and Zlotnik, A.
TITLE Use of an interleukin-10 antagonist to treat a B cell mediated
autoimmune disorder
JOURNAL Patent: US 5837232-A 41 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
BASE COUNT 4 a 6 c 6 g 5 t

Query Match          0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GGACAGCTCGGAAGTCAT 135
  |||||
Db 18 GGCCAGCTTGGAGTCAT 1

RESULT 130
AR054482/c
LOCUS AR054482 21 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 41 from patent US 5837293.
ACCESSION AR054482
VERSION AR054482.1 GI:5980059
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS De Waal Malefyt, R., Howard, M., Hsu, D.-H., Ishida, H., O'Garra, A.,
TITLE Spits, H. and Zlotnik, A.
TITLE Use of interleukin-10 analogs for antagonists to treat endotoxin-
or superantigen-induced toxicity
JOURNAL Patent: US 5837293-A 41 17-NOV-1998;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
BASE COUNT 4 a 6 c 6 g 5 t

Query Match          0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GGACAGCTCGGAAGTCAT 135
  |||||
Db 18 GGCCAGCTTGGAGTCAT 1

RESULT 131
AR148289
LOCUS AR148289 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 20 from patent US 6225082.
ACCESSION AR148289
VERSION AR148289.1 GI:15112379
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Carson, J., Kwon, S., Ainger, K. and Avossa, D.
TITLE Myelin basic protein mRNA transport and translation enhancer
sequences
JOURNAL Patent: US 6225082-A 20 01-MAY-2001;
FEATURES
source Location/Qualifiers
1..21
/organism="unknown"
BASE COUNT 5 a 7 c 9 g 0 t

Query Match          0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCCAGCGAGGAGAGAGC 26
  |||||
Db 1 GCCAGCGAGGAGAGAGC 18

RESULT 132
AX133267
LOCUS AX133267 21 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 4485 from Patent WO0130362.
ACCESSION AX133267
VERSION AX133267.1 GI:14139577
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 4485 03-MAY-2001;
FEATURES
source Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="PDGF A ribozyme recognition site"
BASE COUNT 1 a 11 c 7 g 2 t

Query Match          0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1055 CGGGCGCTGTTCGCCAGC 1072
  |||||
Db 1 CGGGCGCTGTTCGCCAGC 18

RESULT 133
A31925/c
LOCUS A31925 17 bp DNA linear PAT 04-DEC-1995
DEFINITION Synthetic BamHI-PvuII insert sequence.
ACCESSION A31925
VERSION A31925.1 GI:1249466
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS
JOURNAL Patent: BE 901119-A 3 15-MAR-1985;

```

```

FEATURES
  source
    Location/Qualifiers
      1..17
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
      2 a 7 c 6 g 2 t
BASE COUNT      2 a 7 c 6 g 2 t
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 3.4e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1432 GGCACCGCGGGGATC 1447
Db 16 GGCACCGCGGGGATC 1

RESULT 134
AR053075/c
LOCUS      AR053075      17 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 45 from patent US 5834181.
ACCESSION AR053075
VERSION AR053075.1 GI:5977937
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Shuber,A.P.
TITLE     High throughput screening method for sequences or genetic
          alterations in nucleic acids
JOURNAL   Patent: US 5834181-A 45 10-NOV-1998;
FEATURES   Location/Qualifiers
  source
    1..17
      /organism="unknown"
      /db_xref="taxon:32630"
BASE COUNT      3 a 6 c 6 g 2 t
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 3.4e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1514 CTGGCGCATGGCGGTCA 1529
Db 17 CTGGCGCATGGCGGTCA 2

RESULT 135
AR065036/c
LOCUS      AR065036      17 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 45 from patent US 5849483.
ACCESSION AR065036
VERSION AR065036.1 GI:5995252
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Shuber,A.P.
TITLE     High throughput screening method for sequences or genetic
          alterations in nucleic acids
JOURNAL   Patent: US 5849483-A 45 15-DEC-1998;
FEATURES   Location/Qualifiers
  source
    1..17
      /organism="unknown"
      /db_xref="taxon:32630"
BASE COUNT      3 a 6 c 6 g 2 t
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 3.4e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1514 CTGGCGCATGGCGGTCA 1529
Db 17 CTGGCGCATGGCGGTCA 2

RESULT 136
AX423136
LOCUS      AX423136      17 bp      mRNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 1472 from Patent WO0188124.
ACCESSION AX423136
VERSION AX423136.1 GI:21526518
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Jarvis,T., von Carlwiltz,I., Mswiggen,J.A., McLaughlin,F.G. and
          Randi,A.M.
TITLE     Method and reagent for the inhibition of erg
          Patent: WO 0188124-A 1472 22-NOV-2001;
          RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
BASE COUNT      2 a 7 c 4 t
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 3.4e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 967 CTTTGTGGCGCGGCAC 982
Db 2 CTTTGTGGCGCGGCAC 17

RESULT 137
I32581/c
LOCUS      I32581      17 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 45 from patent US 5589330.
ACCESSION I32581
VERSION I32581.1 GI:1823372
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Shuber,A.P.
TITLE     High-throughput screening method for sequence or genetic
          alterations in nucleic acids using elution and sequencing of
          complementary oligonucleotides
JOURNAL   Patent: US 5589330-A 45 31-DEC-1996;
FEATURES   Location/Qualifiers
  source
    1..17
      /organism="unknown"
BASE COUNT      3 a 6 c 6 g 2 t
  Query Match      0.9%; Score 14.4; DB 1; Length 17;
  Best Local Similarity 93.8%; Pred. No. 3.4e+02;
  Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1514 CTGGCGCATGGCGGTCA 1529
Db 17 CTGGCGCATGGCGGTCA 2

RESULT 138
AR181637/c
LOCUS      AR181637      18 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 99 from patent US 6335194.
ACCESSION AR181637
VERSION AR181637.1 GI:20223851
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.

```

```

Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C. Frank., Ackermann, E.J., Swayze, E.E. and Cowsert, L.M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 99 01-JAN-2002;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 11 c 4 g 1 t
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1370 GCGGGCGCGGCGGCA 1385
Db 18 GGTGGCGGCGGCGGCA 3

RESULT 139
ARI96700/c
LOCUS ARI96700 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1165 from patent US 6350934.
ACCESSION ARI96700
VERSION ARI96700.1 GI:20246137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P. Ann. Owens., Guo, L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1165 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 0 a 12 c 6 g 0 t
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1368 GCGGGCGGCGGCGGCGG 1383
Db 18 GCGGGCGGCGGCGGCGG 3

RESULT 140
AR295385
LOCUS AR295385 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7120 from patent US 6537751.
ACCESSION AR295385
VERSION AR295385.1 GI:31682669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7120 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..19
BASE COUNT 6 a 2 c 8 g 3 t
Query Match 0.9%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 445 GACTCAGAGGTGTAAG 460

Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett, C. Frank., Ackermann, E.J., Swayze, E.E. and Cowsert, L.M.
TITLE Antisense modulation of survivin expression
JOURNAL Patent: US 6335194-A 99 01-JAN-2002;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 11 c 4 g 1 t
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1370 GCGGGCGGCGGCGGCA 1385
Db 18 GGTGGCGGCGGCGGCA 3

RESULT 139
ARI96700/c
LOCUS ARI96700 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1165 from patent US 6350934.
ACCESSION ARI96700
VERSION ARI96700.1 GI:20246137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P. Ann. Owens., Guo, L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1165 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 0 a 12 c 6 g 0 t
Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1368 GCGGGCGGCGGCGGCGG 1383
Db 18 GCGGGCGGCGGCGGCGG 3

RESULT 140
AR295385
LOCUS AR295385 19 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7120 from patent US 6537751.
ACCESSION AR295385
VERSION AR295385.1 GI:31682669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 7120 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..19
BASE COUNT 6 a 2 c 8 g 3 t
Query Match 0.9%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 445 GACTCAGAGGTGTAAG 460

Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Moni, B.P., Butler, M.M. and Wyatt, J.
TITLE Antisense inhibition of C/EBP beta expression
JOURNAL Patent: US 6271030-A 37 07-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 0 a 6 c 14 g 0 t
Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1368 GCGGGCGGCGGCGGCGG 1383
Db 5 GCGGGCGGCGGCGGCGG 20

RESULT 143
ARI63929/c
LOCUS ARI63929 20 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 127 from patent US 6271030.
ACCESSION ARI63929
VERSION ARI63929.1 GI:16234767
KEYWORDS

```


DEFINITION Method for detecting and assaying methane bacteria.

ACCESSION BD090479

VERSION BD090479.1 GI:22636089

KEYWORDS JP 2001327290-A/1.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 20)

AUTHORS Nakamura,T.

TITLE Method for detecting and assaying methane bacteria

JOURNAL Patent: JP 2001327290-A 1 27-NOV-2001;

COMMENT MITSUBISHI HEAVY INDUSTRIES LTD

OS Methane bacteria

PN JP 2001327290-A/1

PD 27-NOV-2001

PF 22-MAY-2000 JP 2000150109

PI TSUYOSHI NAKAMURA

PC C12N15/09,C12Q1/68,G01N33/569// (C12N15/09,C12R1:01), (C12Q1/68,

PC C12R1:01), (C12N15/00,C12R1:01)

PC C12N15/00, (C12N15/00,C12R1:01)

CC 1

CC 1

FT Key

FT Location/Qualifiers

FT 1..20

FT /organism="Methane bacteria".

FEATURES

source

BASE COUNT 0 a 10 c 5 g 4 t 1 others

Query Match 0.9%; Score 14.4; DB 1; Length 20;

Best Local Similarity 98.2%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 937 GCGCTCTGCTCACCG 953

Db 3 GCGCTCTGCTGCCCG 19

RESULT 149

BD096469

LOCUS

DEFINITION

20 bp DNA linear PAT 27-AUG-2002

BD096469

Diagnosis of migraine with aura, depression and anxiety from

allelic variations in dopaminergic genes.

ACCESSION BD096469

VERSION BD096469.1 GI:22642057

KEYWORDS JP 2001527520-A/10.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 20)

AUTHORS Peroutka,S.J.

TITLE Diagnosis of migraine with aura, depression and anxiety from

allelic variations in dopaminergic genes

JOURNAL Patent: JP 2001527520-A 10 25-DEC-2001;

COMMENT GLAXO GROUP LTD

OS Unidentified

PN JP 2001527520-A/10

PD 25-DEC-2001

PF 21-AUG-1997 JP 1998511012

PI 22-AUG-1996 US 60/024399,17-JAN-1997 US 60/036091 PI

PC A61K1/445

CC Strandedness: Single;

CC Topology: Linear;

CC Diagnosis of migraine with aura, depression and anxiety from

allelic variations in dopaminergic genes

CC variations in dopaminergic genes

FT Key

FT Location/Qualifiers

FT 1..20

FT /organism="Unidentified".

FEATURES

source

BASE COUNT 0 a 10 c 5 g 4 t 1 others

Query Match 0.9%; Score 14.4; DB 1; Length 20;

Best Local Similarity 98.2%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 937 GCGCTCTGCTCACCG 953

Db 3 GCGCTCTGCTGCCCG 19

source

BASE COUNT 7 a 3 c 7 g 3 t

Query Match 0.9%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 704 GTGAAGCAGAGACT 719

Db 4 GTGAATGCAGAGACT 19

RESULT 150

E31668/c

LOCUS

DEFINITION

20 bp DNA linear PAT 18-JUN-2001

E31668

Method for distinguishing eucaryotic individual based on PCR finger

print with the use of restriction primer of inter-SINE sequences

and primer to be used therein.

ACCESSION E31668

VERSION E31668.1 GI:13018578

KEYWORDS JP 2000023671-A/41.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 20)

AUTHORS Ichiho,O., Ichiho,N. and Hiroshi,Y.

TITLE Method for distinguishing eucaryotic individual based on PCR finger

print with the use of restriction primer of inter-SINE sequences

JOURNAL Patent: JP 2000023671-A 41 25-JAN-2000;

COMMENT NATIONAL RESEARCH INSTITUTE OF AQUACULTURE

OS Artificial Sequence

PN JP 2000023671-A/41

PD 25-JAN-2000

PF 10-JUL-1998 JP 1998195692

PI ICHIRO OHARA, ICHIRO NAKAYAMA, HIROSHI YASUE

PC C12N15/09,C12Q1/68,C12N15/00

CC Key

FT Location/Qualifiers

FT 1..20

FT /organism="Artificial Sequence".

FEATURES

source

BASE COUNT 3 a 9 c 5 g 3 t

Query Match 0.9%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 3.6e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1378 CGCGCGCAGTAGCC 1393

Db 20 CGCGCGCAGGTAGCC 5

RESULT 151

AR161796/c

LOCUS

DEFINITION

Sequence 106 from patent US 6358529.

ACCESSION AR161796

VERSION AR161796.1 GI:16228746

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)

AUTHORS Berdoz,J. and Kraehenbuhl,J.-P.

RESULT 151

AR161796/c

LOCUS

DEFINITION

Sequence 106 from patent US 6358529.

ACCESSION AR161796

VERSION AR161796.1 GI:16228746

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)

AUTHORS Berdoz,J. and Kraehenbuhl,J.-P.

TITLE PCR amplification of rearranged genomic variable regions of immunoglobulin genes

JOURNAL Patent: US 6258529-A 106 10-JUL-2001;

FEATURES Location/Qualifiers

source 1..19

BASE COUNT 2 a 5 c 8 g 4 t

Query Match 0.9%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 3.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1198 GCGCCAGGCGCACATCTC 1216

Db 19 GCGCCAGGCGCACACTCTC 1

RESULT 152

AX468761

LOCUS AX468761 19 bp DNA linear PAT 16-JUL-2002

DEFINITION Sequence 18 from Patent WO218574.

ACCESSION AX468761

VERSION AX468761.1 GI:21901529

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Chu, C.C., Chavan, S.S. and Mason, J.M.

TITLE Human interleukin-four induced protein

JOURNAL Patent: WO 0218574-A 18 07-MAR-2002;

North Shore-Long Island Jewish Research Institute (US)

FEATURES Location/Qualifiers

source 1..19

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Primer"

BASE COUNT 4 a 4 c 8 g 3 t

Query Match

Best Local Similarity 0.9%; Score 14.2; DB 1; Length 19;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1515 TGGGATGGCGGTCAAGTC 1533

Db 1 TGGAGACGGGTCAAGTC 19

RESULT 153

AX535777

LOCUS AX535777 19 bp DNA linear PAT 22-NOV-2002

DEFINITION Sequence 16 from Patent WO2068684.

ACCESSION AX535777

VERSION AX535777.1 GI:25262228

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Lundberg, J., Ahmadian, A. and Nyren, P.

TITLE Allele-specific primer extension assay

JOURNAL Patent: WO 02068684-A 16 06-SEP-2002;

Pyrosequencing AB (SE); DZIEGLEWSKA, Hanna Eva (GB)

FEATURES Location/Qualifiers

source 1..19

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Primer"

BASE COUNT 2 a 5 c 9 g 3 t

Query Match

Best Local Similarity 0.9%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 3.8e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1418 GCTCCGGTGGCGGGGCCA 1436

Db 1 GCTGCTGGTGCAGGGGCCA 19

RESULT 154

AX557192

LOCUS AX557192 19 bp DNA linear PAT 27-NOV-2002

DEFINITION Sequence 90 from Patent WO244353.

ACCESSION AX557192

VERSION AX557192.1 GI:25900191

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Wolffe, A.P.

TITLE Human heparanase gene regulatory sequences

JOURNAL Patent: WO 0244353-A 90 06-JUN-2002;

Sangamo Biosciences Inc. (US)

FEATURES Location/Qualifiers

source 1..19

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="SBS# 5349 target"

BASE COUNT 4 a 3 c 12 g 0 t

Query Match

Best Local Similarity 0.9%; Score 14.2; DB 1; Length 19;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1544 CCGGGGGCGGGGGAGGG 1562

Db 1 CCGGAGGCCAGGGAGGAG 19

RESULT 155

BD094590/c

LOCUS BD094590 19 bp DNA linear PAT 27-AUG-2002

DEFINITION Substrate for immobilizing ligand.

ACCESSION BD094590

VERSION BD094590.1 GI:22640178

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Kato, I., Izu, H. and Asada, K.

TITLE Substrate for immobilizing ligand

JOURNAL Patent: WO 0135098-A 28 17-MAY-2001;

TAKARA SHUZO CO LTD, IKUNOSHIN KATO, HIROYUKI IZU, KIYOZO ASADA

COMMENT CS Artificial Sequence

PN WO 0135098-A/28

PD 17-MAY-2001

PF 24-OCT-2000 WO 2000JP007415

PR 05-NOV-1999 JP 99P 315610

PI IKUNOSHIN KATO, HIROYUKI IZU, KIYOZO ASADA

PC GOIN33/543, GOIN33/521, GOIN33/53, GOIN33/566, GOIN37/00 CC

Designed oligonucleotide primer for amplifying a portion of CC insulin receptor gene.

CC receptor gene.

FT Key

FT source 1..19

Location/Qualifiers

/organism="Artificial Sequence".

FEATURES

source 1..19

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

```

BASE COUNT      4 a      8 c      3 g      4 t

Query Match      0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 137 AGTTCCATGGCGGAGATGC 155
|||||
Db 19 AGTTCGATGGCGGAGATGC 1

RESULT 156
DOGP18802/c
LOCUS      DOGP18802      20 bp      DNA      linear      MAM 11-MAR-1996
DEFINITION Dog (Clone: CXX.188) primer for STS 188, 3' end.
ACCESSION L24215
VERSION L24215.1 GI:401865
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 2 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ostrander, E.A.; Mapa, F.A.; Yee, M. and Rins, J.
TITLE One hundred and one new simple sequence repeat-based markers for
the canine genome
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)
MEDLINE 95268214
PUBMED 7749226
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOstrander@lbl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.
FEATURES
source
1..20
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/tissue_type="spleen"
/dev_stage="adult"
/tissue_lib="E. Ostrander, in pBluescript+"
primer_bind complement(1..20)
BASE COUNT      0 a      12 c      0 g      8 t

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GAGCGAGGAGGGAAGCG 59
|||||
Db 20 GAGAGAGGAGGAGAGGG 2

RESULT 157
AR027799/c
LOCUS      AR027799      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 30 from patent US 5856458.
ACCESSION AR027799
VERSION AR027799.1 GI:5938619
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 20)
Okamoto, H. and Nakamura, T.
Oligonucleotide primers, and their application for high-fidelity
detection of non-A, non-B hepatitis virus
Patent: US 5856458-A 30 05-JAN-1999;
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT      5 a      6 c      6 g      3 t

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 117 GGGACAGCTCGGAAGTCAT 135
|||||
Db 19 GCGACCGCTCGGAAGTCAT 1

RESULT 158
AR028728/c
LOCUS      AR028728      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5858760.
ACCESSION AR028728
VERSION AR028728.1 GI:5940701
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 20)
Daib, O. slashed, ge, H., Kofod, L. Venke., Kauppinen, M. Sakari.,
Andersen, L. Nonboe., Christgau, S. and Heidt-Hansen, H. Peter.
Enzyme with pectin lyase activity
Patent: US 5858760-A 17 12-JAN-1999;
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT      3 a      8 c      6 g      3 t

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 816 ACCGGGTGCTGGCGCGGA 834
|||||
Db 20 ACGACGTGCTGGCGCGCGA 2

RESULT 159
AR036620/c
LOCUS      AR036620      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5872242.
ACCESSION AR036620
VERSION AR036620.1 GI:5953288
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
1 (bases 1 to 20)
Monia, B. P., Cowsett, L. M. and Manoharan, M.
Antisense oligonucleotide inhibition of ras
Patent: US 5872242-A 20 16-FEB-1999;
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT      0 a      12 c      6 g      2 t

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1368 GCGGGGGCGGGCGGCGAG 1386

```

Db 19 GCCGGGGGGGGGGGGGAG 1
|||||
|||

RESULT 160
AR037348
LOCUS AR037348 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5801154.
ACCESSION AR037348
VERSION AR037348.1 GI:5955204
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini, E., Bennett, C. Frank, and Dean, N.M.
TITLE Antisense oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5801154-A 23 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 8 c 6 g 4 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 GCTGTGGGCGGCTCTCT 1311
|||||
|||

Db 1 GCCAGGCTCAGGGCTGCT 19
|||||
|||

RESULT 161
AR040631
LOCUS AR040631 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5807838.
ACCESSION AR040631
VERSION AR040631.1 GI:5959994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Baracchini, E. Jr. and Bennett, C. Frank.
TITLE Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL Patent: US 5807838-A 23 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 8 c 6 g 4 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 GCTGTGGGCGGCTCTCT 1311
|||||
|||

Db 1 GCCAGGCTCAGGGCTGCT 19
|||||
|||

RESULT 162
AR060544/c
LOCUS AR060544 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 45 from patent US 5840693.
ACCESSION AR060544
VERSION AR060544.1 GI:5986994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)

AUTHORS Eriksson, U., Olofsson, B., Alitalo, K. and Pajusola, K.
TITLE Vascular endothelial growth factor-B
JOURNAL Patent: US 5840693-A 45 24-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 9 c 7 g 2 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1331 CGCAGGACCGCGCGGG 1349
|||||
|||

Db 19 CGCAGGTACCTGGCGGG 1
|||||
|||

RESULT 163
AR068763/c
LOCUS AR068763 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5854049.
ACCESSION AR068763
VERSION AR068763.1 GI:6000970
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, G.L.
TITLE Plasmin-resistant streptokinase
JOURNAL Patent: US 5854049-A 12 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 3 a 7 c 7 g 3 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 960 ACCTGCTCTTGTGGCGCC 978
|||||
|||

Db 19 ACCTGCTCATGGCGGCC 1
|||||
|||

RESULT 164
AR069073/c
LOCUS AR069073 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 23 from patent US 5854410.
ACCESSION AR069073
VERSION AR069073.1 GI:6001280
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Arnold, L.J. Jr., Reynolds, M.A., Schwartz, D.A. and Daily, W.J.
TITLE Oligonucleoside cleavage compounds and therapies
JOURNAL Patent: US 5854410-A 23 29-DEC-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 1 a 9 c 1 g 9 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 CAGCGAGGAGAGAGCGAG 29
|||||
|||

Db 20 CAGAGAGAGAGAGAGAG 2
|||||
|||

```

RESULT 165
AR079640/c
LOCUS AR079640 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 20 from patent US 5965722.
ACCESSION AR079640
VERSION AR079640.1 GI:10006381
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Ecker,D.J., Cook,P.Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
TITLE Antisense inhibition of ras gene with chimeric and alternating
oligonucleotides
JOURNAL Patent: US 5965722-A 20 12-OCT-1999;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 0 a 12 c 6 g 2 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1368 GCGGGGGGGGGGGGGGCGAG 1386
Db 19 GCGGGGGGGGGGGGGGCGAG 1

RESULT 166
AR088462
LOCUS AR088462 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 48 from patent US 5989885.
ACCESSION AR088462
VERSION AR088462.1 GI:10015226
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Teng,D.H.-F., Tavtigian,S.V., Perry,W.L. III and Skolnick,M.H.
TITLE Specific mutations of map kinase 4 (MK4) in human tumor cell lines
identify it as a tumor suppressor in various types of cancer
JOURNAL Patent: US 5989885-A 48 23-NOV-1999;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 6 a 1 c 13 g 0 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 CAGCGAGGAGAGAGAGCGAG 29
Db 1 CGGGAGGAGAGAGAGAGAGAG 19

RESULT 167
AR100185/c
LOCUS AR100185 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 35 from patent US 6080567.
ACCESSION AR100185
VERSION AR100185.1 GI:12810633
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Kofod,L.Venke., Kauppinen,M.Sakari., Christgau,S.,
Heldt-Hansen,H.Peter., Dalb.o slashed.Ge.H., Andersen,L.Nonboe.,
Si,J.Qi., Jacobsen,T.Sejersgaard., Munk,N. and Mullertz,A.
TITLE Enzymes with xylanase activity from Aspergillus aculeatus

```

```

JOURNAL Patent: US 6080567-A 35 27-JUN-2000;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 0 a 13 c 4 g 3 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1373 GCGGGGGGGGGGGGGGAGTAG 1391
Db 20 GCGGGGGGGGGGGGGGAGAG 2

RESULT 168
AR102403/c
LOCUS AR102403 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 28 from patent US 6083923.
ACCESSION AR102403
VERSION AR102403.1 GI:12813201
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and
Mehta,R.C.
TITLE Liposomal oligonucleotide compositions for modulating RAS gene
expression
JOURNAL Patent: US 6083923-A 28 04-JUL-2000;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 0 a 12 c 6 g 2 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1368 GCGGGGGGGGGGGGGGCGAG 1386
Db 19 GCGGGGGGGGGGGGGGCGAG 1

RESULT 169
AR124487/c
LOCUS AR124487 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 56 from patent US 6171860.
ACCESSION AR124487
VERSION AR124487.1 GI:14109848
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense inhibition of rank expression
JOURNAL Patent: US 6171860-A 56 09-JAN-2001;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 1 a 13 c 5 g 1 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1368 GCGGGGGGGGGGGGGGCGAG 1386
Db 19 GAGGGGGGGGGGGGGGCGGCTG 1

```

RESULT 170
LOCUS ARI30116 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 19 from patent US 6187587.
ACCESSION ARI30116
VERSION ARI30116.1 GI:14118013
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Popoff, I., Brown-Driver, V.L. and Cowse, L.M.
TITLE Antisense inhibition of e2f transcription factor 1 expression
JOURNAL Patent: US 6187587-A 19 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 1 a 5 c 13 g 1 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1123 CGCGGGCTCTCCGCGCC 1141
Db 20 CGCGGGCTCTCCGCGCC 2
RESULT 171
LOCUS ARI37875 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 35 from patent US 6197564.
ACCESSION ARI37875
VERSION ARI37875.1 GI:14479384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kofod, L., Venke, Kauppinen, M., Sakari, Christgau, S.,
Heldt-Hansen, H., Peter, Dalb. o slashed, ge, H., Andersen, L., Nonboe.,
Si, J., Qi., Jacobsen, T., Sejersgaard, Munk, N. and Mullertz, A.
TITLE Enzymes with xylanase activity from Aspergillus aculeatus
JOURNAL Patent: US 6197564-A 35 06-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 0 a 13 c 4 g 3 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1373 GCGGGGGCGGCGAGTAG 1391
Db 20 GCGGGGGCGGCGAGTAG 2
RESULT 172
LOCUS ARI39321 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 29 from patent US 6207372.
ACCESSION ARI39321
VERSION ARI39321.1 GI:14481817
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Shuber, A.P.
TITLE Universal primer sequence for multiplex DNA amplification
JOURNAL Patent: US 6207372-A 29 27-MAR-2001;
FEATURES Location/Qualifiers

source 1..20
/organism="unknown"
BASE COUNT 0 a 9 c 11 g 0 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1344 GCGGGGACGCGGCGCGG 1362
Db 2 GCGGGGCGGCGGCGCGG 20
RESULT 173
LOCUS ARI49869 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 35 from patent US 6228630.
ACCESSION ARI49869
VERSION ARI49869.1 GI:15114460
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kofod, L., Venke, Kauppinen, M., Sakari, Christgau, S.,
Heldt-Hansen, H., Peter, Dalb. o slashed, ge, H., Andersen, L., Nonboe.,
Si, J., Qi., Jacobsen, T., Sejersgaard, Munk, N. and Mullertz, A.
TITLE Enzymes with xylanase activity from Aspergillus aculeatus
JOURNAL Patent: US 6228630-A 35 08-MAY-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 0 a 13 c 4 g 3 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1373 GCGGGGCGGCGGAGTAG 1391
Db 20 GCGGGGCGGCGGAGTAG 2
RESULT 174
LOCUS ARI78908 20 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 154 from patent US 6319906.
ACCESSION ARI78908
VERSION ARI78908.1 GI:20220046
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett, C., Frank, and Vickers, T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6319906-A 154 20-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 6 a 8 c 3 g 3 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 898 GAAGTCTTCTACGTATC 916
Db 19 GAAGTGTCTTCTCGTATC 1
RESULT 175

AR201438/c AR201438 20 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 20 from patent US 6359124.
DEFINITION AR201438
ACCESSION AR201438
VERSION AR201438.1 GI:20252326
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Ecker,D.J., Cook,P., Dan., Monia,B.P., Freier,S.M. and Sanghvi,Y.S.
TITLE Antisense inhibition of ras gene with chimeric and alternating oligonucleotides
JOURNAL Patent: US 6359124-A 20 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 0 a 12 c 6 g 2 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1368 GCGGGGGCGGCGCGGCGAG 1386
Db 19 GCCGCGGCGGCGGAGGCG 1
RESULT 176
AR206614
LOCUS AR206614 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 34 from patent US 6372433.
ACCESSION AR206614
VERSION AR206614.1 GI:21505271
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Baker,B.F., Bennett,C.Frank. and Wyatt,J.
TITLE Antisense modulation of inhibitor of DNA binding-1 expression
JOURNAL Patent: US 6372433-A 34 16-APR-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 3 a 7 c 6 g 4 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 958 GCACCTGCTCTTGTGGCG 976
Db 1 GCACGAGCTCTTGAGCG 19
RESULT 177
AR220167/c
LOCUS AR220167 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 32 from patent US 6423543.
ACCESSION AR220167
VERSION AR220167.1 GI:23324610
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Marcotte,P.A. and Cowseert,L.M.
TITLE Antisense modulation of hepsin expression
JOURNAL Patent: US 6423543-A 32 23-JUL-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 9 c 5 g 2 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 808 CCCCGGGGACCGGCTGCTG 826
Db 20 CTCGGGGGACTGGTGCTG 2
RESULT 178
AR221462/c
LOCUS AR221462 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 12 from patent US 6426221.
ACCESSION AR221462
VERSION AR221462.1 GI:23328512
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Ward,D.T. and Cowseert,L.M.
TITLE Antisense modulation of RIP2 expression
JOURNAL Patent: US 6426221-A 12 30-JUL-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 1 a 8 c 8 g 3 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 800 GACCTGAGCCCGGGGACC 818
Db 20 GGCCTGAGCGCGGGGACC 2
RESULT 179
AR224718
LOCUS AR224718 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6440739.
ACCESSION AR224718
VERSION AR224718.1 GI:23333558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Freier,S.M.
TITLE Antisense modulation of glioma-associated oncogene-2 expression
JOURNAL Patent: US 6440739-A 23 27-AUG-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 5 c 7 g 6 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 150 AGATGCTGCTGCTGGCGAG 168
Db 1 AGTTGCTGCTGCTGCTGAG 19
RESULT 180
AR234546
LOCUS AR234546 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6458590.
ACCESSION AR234546
VERSION AR234546.1 GI:27277250

```

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Mukherjee,A.B., Kundu,G.C. and Panda,D.K.
TITLE       Methods and compositions for treatment of restenosis
JOURNAL     Patent: US 6458590-A 2 01-OCT-2002;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
BASE COUNT      5 a      6 c      4 g      5 t
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 548 CACCACCTCAGAGAGTCTC 566
Db 1 CACCAGTCTGATGAGTCTC 19

RESULT 181
LOCUS      AR262768      20 bp      DNA      linear      PAT 29-JAN-2003
DEFINITION Sequence 45 from patent US 6331301.
ACCESSION  AR262768
VERSION     AR262768.1 GI:28074441
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Eriksson,U., Olofsson,B., Alitalo,K. and Pajusola,K.
TITLE       Antibodies specific for vascular endothelial growth factor-B
JOURNAL     Patent: US 6331301-A 45 18-DEC-2001;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
BASE COUNT      2 a      9 c      7 g      2 t
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1331 CGCAGCAGCGCGCGCGGG 1349
Db 19 CGCAGCTACCTGGCGCGGG 1

RESULT 182
LOCUS      AR271767/c      20 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 11 from patent US 6503754.
ACCESSION  AR271767
VERSION     AR271767.1 GI:29703335
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Zhang,H. and Wyatt,J.
TITLE       Antisense modulation of BHS interacting domain death agonist
JOURNAL     Patent: US 6503754-A 11 07-JAN-2003;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
BASE COUNT      7 a      5 c      6 g      2 t
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Mukherjee,A.B., Kundu,G.C. and Panda,D.K.
TITLE       Methods and compositions for treatment of restenosis
JOURNAL     Patent: US 6458590-A 2 01-OCT-2002;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"
BASE COUNT      5 a      6 c      4 g      5 t
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 170 TGTCTGCTCTAGTCTCTCG 188
Db 20 TGTCTGAGCTCTGCTCTCG 2

RESULT 183
LOCUS      AX008654/c      20 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9966037.
ACCESSION  AX008654
VERSION     AX008654.1 GI:9996178
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Renzi,P.
TITLE       Antisense oligonucleotides for treating or preventing atopic
JOURNAL     diseases and neoplastic cell proliferation
            Patent: WO 9966037-A 7 23-DEC-1999;
            RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA)
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32830"
            /note="Antisense oligonucleotide inhibiting the common
            subunit of IL-4 and IL-13 human receptor"
BASE COUNT      0 a      16 c      4 g      0 t
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1546 GGGCGCGCGGGGAGGGGCG 1564
Db 19 GGGCGCGGGGCGGGGCGG 1

RESULT 184
LOCUS      AX009450      20 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9961662.
ACCESSION  AX009450
VERSION     AX009450.1 GI:9996736
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Shchepinov,M.S. and Southern,E.M.
TITLE       Polynucleotide multimers and their use in hybridisation assays
JOURNAL     Patent: WO 9961662-A 3 02-DEC-1999;
            SHCHEPINOV MIKHAIL SERGEEVICH (GB); SOUTHERN EDWIN MELLOR (GB);
            ISIS INNOVATION (GB)
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide"
BASE COUNT      0 a      10 c      0 g      10 t
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GAGCGAGGAAGGGAAGCG 59
Db 20 GAGGAAGGAAGGGAAGAG 2

```

```

RESULT 185
AX037348/c
LOCUS AX037348 20 bp DNA linear PAT 15-NOV-2000
DEFINITION Sequence 1 from Patent WO0058506.
ACCESSION AX037348
VERSION AX037348.1 GI:11226773
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Barker, J.N. and Trembath, R.C.
TITLE Susceptibility to psoriasis
JOURNAL Patent: WO 0058506-A 1 05-OCT-2000;
KING S COLLEGE LONDON (GB); UNIV LEICESTER (GB); BARKER JONATHAN
NICHOLAS WILLI (GB); TREMBATH RICHARD CHARLES (GB)
FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a _10 c 0 g 7 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 235 GGGGTTCCGGAGAGGAGG 253
Db 20 GAGGTTGGGAGAGGAG 2

RESULT 186
AX048785/c
LOCUS AX048785 20 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 56 from Patent WO0070059.
ACCESSION AX048785
VERSION AX048785.1 GI:12225930
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Helentjaris, T.G.
TITLE Signal transduction genes and methods of use
JOURNAL Patent: WO 0070059-A 56 23-NOV-2000;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
BASE COUNT 3 a _8 c 5 g 4 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 639 GCCTGGCGGTGGAGCGG 657
Db 20 GCCTGGCGGTGGAAACCTG 2

RESULT 187
AX224942/c
LOCUS AX224942 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 96 from Patent WO0161030.
ACCESSION AX224942
VERSION AX224942.1 GI:15555015
KEYWORDS

```

```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Gray, D.M. and Bollon, A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
for control of gene expression
JOURNAL Patent: WO 0161030-A 96 23-AUG-2001;
Cytoconal Pharmaceuticals, Inc. (US); University of Texas at
Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a _8 c 10 g 0 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1283 GGGCCCTTCGCTGGCGC 1301
Db 19 GGGCCCGCTGCTGGCGC 1

RESULT 188
AX224943/c
LOCUS AX224943 20 bp DNA linear PAT 10-SEP-2001
DEFINITION Sequence 97 from Patent WO0161030.
ACCESSION AX224943
VERSION AX224943.1 GI:15555016
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Gray, D.M. and Bollon, A.P.
TITLE Libraries of optimum subsequence regions of mrna and genomic dna
for control of gene expression
JOURNAL Patent: WO 0161030-A 97 23-AUG-2001;
Cytoconal Pharmaceuticals, Inc. (US); University of Texas at
Dallas, Dept. of Molecular and Cell Biology (US); Lab. of
Experimental Carcinogenesis, National Cancer Institute/NIH (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a _7 c 11 g 0 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1283 GGGCCCTTCGCTGGCGC 1301
Db 20 GGGCCCGCTGCTGGCGC 2

RESULT 189
AX293815/c
LOCUS AX293815 20 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 5577 from Patent WO0179548.
ACCESSION AX293815
VERSION AX293815.1 GI:17055498
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

```



```

1
REFERENCE Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
AUTHORS Method of designing addressable array for detection of nucleic acid
TITLE sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179348-A 5577 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES Location/Qualifiers
source 1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/notes="Hypothetical Probe Sequence"
BASE COUNT 2 a 8 c 4 g 6 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 525 CCGAGGCTGGGACGAGA 543
Db 20 CCGTGGATAGGACGAAGA 2
RESULT 190
AX299012/c 20 bp DNA linear PAT 26-NOV-2001
LOCUS Sequence 646 from Patent WO0183749.
DEFINITION AX299012
ACCESSION AX299012.1 GI:17129002
VERSION
KEYWORDS Mus sp.
SOURCE ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S.,
Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G.
TITLE Gene and sequence variation associated with sensing carbohydrate
compounds and other sweeteners
JOURNAL Patent: WO 0183749-A 646 08-NOV-2001;
WARNER-LAMBERT COMPANY (US); The Monell Chemical Senses Center
(US)
FEATURES Location/Qualifiers
source 1..20
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
BASE COUNT 8 a 5 c 6 g 1 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 186 TCGTCTCCTCGTCTGCT 204
Db 20 TGGTCTCCTCTCTGCAGGT 2
RESULT 191
AX671167/c 20 bp DNA linear PAT 27-MAR-2003
LOCUS Sequence 7 from Patent WO03004511.
DEFINITION AX671167
ACCESSION AX671167.1 GI:29329623
VERSION
KEYWORDS synthetic construct
SOURCE ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Renzi, P., Allam, M. and Allakhverdi, Z.
TITLE Methods for increasing in vivo efficacy of oligonucleotides and
inhibiting inflammation in mammals
JOURNAL Patent: WO 03004511-A 7 16-JAN-2003;
Topigen Pharmaceuticals Inc (CA)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Sequence is completely synthesized"
BASE COUNT 0 a 16 c 4 g 0 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1546 GGGGGCGGGGGGGGGG 1564
Db 19 GGGGGCGGGGGGGGGGCG 1
RESULT 192
BD006253/c 20 bp DNA linear PAT 31-JAN-2002
LOCUS Antisense inhibition of ras gene with chimeric and alternating
oligonucleotides.
DEFINITION BD006253
ACCESSION BD006253.1 GI:18634624
VERSION
KEYWORDS JP 2001500530-A/20.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ecker, D.J., Cook, P.D., Monia, B.P., Freier, S.M. and Sang, Y.S.
TITLE Antisense inhibition of ras gene with chimeric and alternating
oligonucleotides
JOURNAL Patent: JP 2001500530-A 20 16-JAN-2001;
ISIS PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
FN JP 2001500530-A/20
PD 16-JAN-2001
PF 30-APR-1998 JP 1998547418
PR 30-APR-1997 US 08/848840
PI DAVID J ECKER, PHILIP DAN COOK, BRETT P MONIA, SUSAN M FREIER, PI
YOGESH S SANGHVI
PC C12Q1/68, C12P19/34, C07H19/16, C07H19/167, C07H19/173, C07H19/067,
PC C07H19/06,
PC C07H19/09, C07H21/04, A61K48/00
CC CC
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 0 a 12 c 6 g 2 t
Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1368 GCGGGGGCGGGGGGGG 1386
Db 19 GCCCGCGGGGGGGGGGAG 1
RESULT 193
BD073147/c 20 bp DNA linear PAT 27-AUG-2002
LOCUS Antisense oligonucleotide inhibition of RAS.
DEFINITION BD073147
ACCESSION BD073147.1 GI:22618750
VERSION
KEYWORDS JP 2001509394-A/20.
SOURCE unidentified

```

[illegible]

```

PD 12-OCT-1993
PF 16-MAR-1992 JP 1992090268
PI MATSUMOTO TOSHIYA, KURIMURA TAKASHI, KITA HIROSHI PC
C12Q1/68, C12N15/10, C12N15/38, C12Q1/70;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
BASE COUNT      2 a      6 c      12 g      0 t
    Query Match      0.9%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 3.8e+02;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 85 CGCGCGCGCGCACTCGGC 103
Db 19 CGCGCGCGCGCCTTCGCG 1
RESULT 197
E34262
LOCUS      E34262      20 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION E34262
VERSION E34262.1 GI:18624267
KEYWORDS JP 2000106879-A/6.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM    1 (bases 1 to 20)
REFERENCE   Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
AUTHORS     Gunji,S., Obayashi,I., Imai,Y., No.N. and Ogawa,K.
TITLE       Pollinosis-associated gene
JOURNAL     Patent: JP 2000106879-A 6 18-APR-2000;
COMMENT     GENOX RESEARCH INC
OS Artificial Sequence
PN JP 2000106879-A/6
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO.
PI KAGURU OGAWA
PC C12N15/09, A61K31/00, A61K39/36, A61K45/00, C12Q1/68, C12N15/00 CC
FH Key      Location/Qualifiers
FT source   1..20
            /organism='Artificial Sequence'.
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
BASE COUNT      1 a      9 c      3 g      7 t
    Query Match      0.9%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 3.8e+02;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 954 CGCGCACCTGCTCTTTGT 972
Db 1 CCTGGCACCTGCTCTTTCT 19
RESULT 198
I12355/c
LOCUS      I12355      20 bp      DNA      linear      PAT 26-JUL-1995
DEFINITION Sequence 10 from patent US 5422265.
ACCESSION I12355
VERSION I12355.1 GI:910378
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Civelli,O. and Van Tol,H.H.
TITLE       DNA sequence for the human dopamine receptor D.sub.4 and expression thereof in mammalian cells
JOURNAL     Patent: US 5422265-A 10 06-JUN-1995;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
BASE COUNT      0 a      10 c      7 g      3 t
    Query Match      0.9%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 3.8e+02;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1355 GCGCGCGCGGACCCGCGG 1373
Db 20 GCGCGCAGGACCCGCGG 2
RESULT 199
I19642
LOCUS      I19642      20 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 23 from patent US 5510239.
ACCESSION I19642
VERSION I19642.1 GI:1599997
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Baracchini,E. Jr. and Bennett,C.F.
TITLE       Oligonucleotide modulation of multidrug resistance-associated protein
JOURNAL     Patent: US 5510239-A 23 23-APR-1996;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"
BASE COUNT      2 a      8 c      6 g      4 t
    Query Match      0.9%; Score 14.2; DB 1; Length 20;
    Best Local Similarity 84.2%; Pred. No. 3.8e+02;
    Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1293 GCCTGGCGCACGCGTCTCT 1311
Db 1 GCGAGGCTCACGCGTCTCT 19
RESULT 200
I27426/c
LOCUS      I27426      20 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 62 from patent US 5565323.
ACCESSION I27426
VERSION I27426.1 GI:1818202
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Parker,W.Davis. and Herrnstadt,C.
TITLE       Cytochrome oxidase mutations aiding diagnosis of sporadic alzheimer's disease
JOURNAL     Patent: US 5565323-A 62 15-OCT-1996;
FEATURES
    source
        Location/Qualifiers
            1..20
                /organism="unknown"

```

```
BASE COUNT      4 a      7 c      5 g      4 t

Query Match
Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 656 GGCTTCGACTGGGTACT 674
19 GGCTTCACCGGAGTACT 1

Db

RESULT 201
LOCUS      127459
DEFINITION Sequence 95 from patent US 5565323.
ACCESSION  I27459
VERSION     I27459.1 GI:1818235
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Parker,W.Davis, and Herntstadt,C.
TITLE       Cytochrome oxidase mutations aiding diagnosis of sporadic
            alzheimer's disease
JOURNAL     Patent: US 5565323-A 95 15-OCT-1996;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"

BASE COUNT      4 a      5 c      7 g      4 t

Query Match
Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 656 GGCTTCGACTGGGTACT 674
2 GGCTTCACCGGAGTACT 20

Db

RESULT 202
LOCUS      I33964
DEFINITION Sequence 10 from patent US 5594108.
ACCESSION  I33964
VERSION     I33964.1 GI:1824755
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Civealli,O. and Van Tol,H.H.
TITLE       Human dopamine receptor and its uses
JOURNAL     Patent: US 5594108-A 10 14-JAN-1997;
FEATURES    Location/Qualifiers
            source
            1..20
            /organism="unknown"

BASE COUNT      0 a      10 c      7 g      3 t

Query Match
Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1355 GGCGCGGGGACCGCGGG 1373
20 GGCGCAGGACCGCGGG 2

Db

RESULT 203
LOCUS      I77271/c
DEFINITION Sequence 35 from patent US 5693518.
ACCESSION  I77271

Qy 1371 GGCGCGCGCGCGGC 1384
1 GGCGCGCGCGCGGC 14

Db

RESULT 205
LOCUS      A90638
DEFINITION Sequence 819 from Patent EP0856579.
ACCESSION  A90638
VERSION     A90638.1 GI:6739152
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W.D. and Schlingensiepen,K.D.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: EP 0856579-A 819 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
            1..15

Qy 1373 GGCGCGCGCGAGTAG 1391
20 GGCGCGCGCGAGTAG 2

Db

RESULT 204
LOCUS      A88671
DEFINITION Sequence 819 from Patent WO9833904.
ACCESSION  A88671
VERSION     A88671.1 GI:6737241
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 819 08-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

BASE COUNT      0 a      4 c      11 g      0 t

Query Match
Best Local Similarity 0.9%; Score 14; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1371 GGCGCGCGCGCGGC 1384
1 GGCGCGCGCGCGGC 14

Db

RESULT 205
LOCUS      A90638
DEFINITION Sequence 819 from Patent EP0856579.
ACCESSION  A90638
VERSION     A90638.1 GI:6739152
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W.D. and Schlingensiepen,K.D.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: EP 0856579-A 819 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
            1..15
```

```
VERSION      I77271.1 GI:3013425
KEYWORDS      Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Kofod,L.Venke., Kauppinen,M.Sakari., Christgau,S.,
            Helldt-Hansen,H.Peter., Dalb.O slashed.ge,H., Andersen,L.Nonboe.,
            Si,J.Oi., Jacobsen,T.Sejersgaard., Munk,N. and Mullertz,A.
            Enzymes with xylanase activity from Aspergillus aculeatus
            Patent: US 5693518-A 35 02-DEC-1997;
            Location/Qualifiers
            1..20
            /organism="unknown"

BASE COUNT      0 a      13 c      4 g      3 t

Query Match
Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1373 GGCGCGCGCGAGTAG 1391
20 GGCGCGCGCGAGTAG 2

Db

RESULT 204
LOCUS      A88671
DEFINITION Sequence 819 from Patent WO9833904.
ACCESSION  A88671
VERSION     A88671.1 GI:6737241
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 819 08-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

BASE COUNT      0 a      4 c      11 g      0 t

Query Match
Best Local Similarity 0.9%; Score 14; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1371 GGCGCGCGCGCGGC 1384
1 GGCGCGCGCGCGGC 14

Db

RESULT 205
LOCUS      A90638
DEFINITION Sequence 819 from Patent EP0856579.
ACCESSION  A90638
VERSION     A90638.1 GI:6739152
KEYWORDS   unidentified
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Brysch,W.D. and Schlingensiepen,K.D.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: EP 0856579-A 819 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES    Location/Qualifiers
            source
            1..15
```

BASE COUNT 0 a 4 c 11 g 0 t
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.9%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1371 GGGGGGGGGGGC 1384

Db 1 GGGGGGGGGGGC 14

RESULT 206
 LOCUS AR116349 15 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 37 from patent US 6133031.
 ACCESSION AR116349
 VERSION AR116349.1 GI:14096671
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)
 AUTHORS Monia,B.P. and Gaarde,W.A.
 TITLE Antisense inhibition of focal adhesion kinase expression
 JOURNAL Patent: US 6133031-A 37 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unknown"

BASE COUNT 0 a 5 c 5 g 5 t

Query Match 0.9%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TCCTCGCTGCTGCT 204

Db 1 TCCTCGCTGCTGCT 14

RESULT 207
 LOCUS AR131625 15 bp DNA linear PAT 16-MAY-2001
 DEFINITION Sequence 50 from patent US 6194150.
 ACCESSION AR131625
 VERSION AR131625.1 GI:14120528
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)
 AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
 TITLE Nucleic acid based inhibition of CD40
 JOURNAL Patent: US 6194150-A 50 27-FEB-2001;
 FEATURES Location/Qualifiers
 source 1..15
 /organism="unknown"

BASE COUNT 2 a 3 c 5 g 5 t

Query Match 0.9%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 901 GGTCCTCTACGTGA 914

Db 2 GGTCCTCTACGTGA 15

RESULT 208
 BD066184 15 bp DNA linear PAT 27-AUG-2002
 LOCUS

DEFINITION An antisense oligonucleotide preparation method.
 ACCESSION BD066184
 VERSION BD066184.1 GI:22611787
 KEYWORDS JP 2001511000-A/819.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 15)
 AUTHORS Schlingensiefen,K.H. and Brysch,W.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: JP 2001511000-A 819 07-AUG-2001;
 COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
 OS Unknown
 PN JP 2001511000-A/819
 PD 07-AUG-2001
 PF 30-JAN-1998 JP 1998532533
 PR 31-JAN-1997 EP 97101531.8
 PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
 PC CL2N15/11.C07H21/04.A61K31/70
 CC An antisense oligonucleotide preparation method FH Key
 FT source 1..15
 FT Location/Qualifiers
 /organism="Unknown".

FEATURES source
 1..15
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

BASE COUNT 0 a 4 c 11 g 0 t

Query Match 0.9%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1371 GGGCGCGCGCGGC 1384

Db 1 GGGCGCGCGCGGC 14

RESULT 209
 AX007862 16 bp DNA linear PAT 06-SEP-2000
 LOCUS AX007862
 DEFINITION Sequence 404 from Patent WO9967428.
 ACCESSION AX007862
 VERSION AX007862.1 GI:9995559
 KEYWORDS
 SOURCE Aids-associated retrovirus
 ORGANISM Aids-associated retrovirus
 Viruses; Retrovirdae.

REFERENCE 1
 AUTHORS Stuyver,L.
 TITLE Method for detection of drug-selected mutations in the hiv protease gene
 JOURNAL Patent: WO 9967428-A 404 29-DEC-1999;
 INNOGENETICS NV (BE); STUYVER LIEVEN (BE)

FEATURES Location/Qualifiers
 source 1..16
 /organism="Aids-associated retrovirus"
 /mol_type="genomic DNA"
 /db_xref="taxon:11966"

BASE COUNT 5 a 3 c 4 g 4 t

Query Match 0.9%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 CTGATGACTCAGG 453

Db 3 CTGATGACTCAGG 16

RESULT 210
 AX216347

LOCUS AX216347 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 1789 from Patent WO0159103.
ACCESSION AX216347
VERSION AX216347.1 GI:15526408
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 1789 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
LOCATION/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 2 a 6 c 0 t
Query Match 0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1373 GCGCGCGCGGCAG 1386
|||||
Db 2 GCGCGCGCGGCAG 15
RESULT 211
AX216895
LOCUS AX216895 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2337 from Patent WO0159103.
ACCESSION AX216895
VERSION AX216895.1 GI:15526956
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 2337 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
LOCATION/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 1 a 7 c 0 t
Query Match 0.9%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1373 GCGCGCGCGGCAG 1386
|||||
Db 3 GCGCGCGCGGCAG 16
RESULT 212
AR029261/c
LOCUS AR029261 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5859223.
ACCESSION AR029261
VERSION AR029261.1 GI:5941234
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kniss, D.A.
TITLE Antisense oligonucleotides to suppress eicosanoid formation
JOURNAL Patent: US 5859229-A 12 12-JAN-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
BASE COUNT 2 a 5 c 11 g 0 t
Query Match 0.9%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1132 CCTGCCCGCGCTG 1145
|||||
Db 15 CCTGCCCGCGCTG 2
RESULT 213
AR141675/c
LOCUS AR141675 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6146871.
ACCESSION AR141675
VERSION AR141675.1 GI:15101191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Garcia Lopez, J. Luis., Cortes Rubio, E., Guisan Seijas, J. Manuel.,
Barredo Fuente, J. Luis., Diez Garcia, B., Collados de la Vieja, A.,
Vitalier Alba, A. and Salto Maldonado, F.
TITLE Process for modifying the enzyme 7.beta.-(4-carboxybutanamide)
cephalosporin acylase and purifying said enzyme in a single
chromatographic step
JOURNAL Patent: US 6146871-A 6 14-NOV-2000;
FEATURES Location/Qualifiers
source
1..19
/organism="unknown"
BASE COUNT 1 a 7 c 8 g 2 t 1 others
Query Match 0.9%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 748 CCGGGCTCGGCCA 761
|||||
Db 15 CCGGGCTCGGCCA 2
RESULT 214
AX052895
LOCUS AX052895 19 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 1 from Patent WO0071755.
ACCESSION AX052895
VERSION AX052895.1 GI:12226997
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES
REFERENCE 1
AUTHORS Kwach, J. G., Macklin, J. J., Mitsis, P. G. and Ulmer, K. M.
TITLE Method for sequence and characterizing polymeric biomolecules using
aptamers and a method for producing aptamers
JOURNAL Patent: WO 0071755-A 1 30-NOV-2000;
FEATURES Location/Qualifiers
source
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"

```
/db.xref="taxon:32630"
/note="Synthetic DNA sequence"
BASE COUNT      3 a      2 c      11 g      0 t      3 others
Query Match      0.9%; Score 14; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4e+02;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1552 CGGGGAGGGCGGGGAG 1570
Db 1 CGGRGAGGNACGGGGAG 19

RESULT 215
AR086184/c
LOCUS      AR086184      20 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5985558.
ACCESSION  AR086184
VERSION     AR086184.1 GI:10012950
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE      Antisense oligonucleotide compositions and methods for the
           inhibition of c-Jun and c-Fos
JOURNAL    Patent: US 5985558-A 5 16-NOV-1999;
           Location/Qualifiers
           1..20
           /organism="unknown"
BASE COUNT      1 a      12 c      5 g      2 t
Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1351 CAGCGCGGGCGGGG 1364
Db 16 CAGCGCGGGCGGGG 3

RESULT 216
AR116329
LOCUS      AR116329      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 17 from patent US 6133031.
ACCESSION  AR116329
VERSION     AR116329.1 GI:14096651
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Monia,B.P. and Gaarde,W.A.
TITLE      Antisense inhibition of focal adhesion kinase expression
JOURNAL    Patent: US 6133031-A 17 17-OCT-2000;
           Location/Qualifiers
           1..20
           /organism="unknown"
BASE COUNT      3 a      5 c      6 g      6 t
Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 TCCTCGTGTGTGGT 204
Db 3 TCCTCGTGTGTGGT 16

RESULT 217
AR172916
LOCUS      AR172916      20 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 41 from patent US 6303374.
ACCESSION  AR172916
VERSION     AR172916.1 GI:17912407
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Zhang,H. and Cowsett,L.M.
TITLE      Antisense modulation of caspase 3 expression
JOURNAL    Patent: US 6303374-A 41 16-OCT-2001;
           Location/Qualifiers
           1..20
           /organism="unknown"
BASE COUNT      5 a      5 c      6 g      4 t
Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1442 GGCATCCACTGGTA 1455
Db 7 GGCATCCACTGGTA 20

RESULT 218
AR176750/c
LOCUS      AR176750      20 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 5 from patent US 6312900.
ACCESSION  AR176750
VERSION     AR176750.1 GI:17919105
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Dean,N.M., McKay,R., Miraglia,L. and Baker,B.
TITLE      Antisense oligonucleotide compositions and methods for the
           modulation of activating protein 1
JOURNAL    Patent: US 6312900-A 5 06-NOV-2001;
           Location/Qualifiers
           1..20
           /organism="unknown"
BASE COUNT      1 a      12 c      5 g      2 t
Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1351 CAGCGCGGGCGGGG 1364
Db 16 CAGCGCGGGCGGGG 3

RESULT 219
AR296674/c
LOCUS      AR296674      20 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 8409 from patent US 6537751.
ACCESSION  AR296674
VERSION     AR296674.1 GI:31683958
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
           disequilibrium map of the human genome
JOURNAL    Patent: US 6537751-A 8409 25-MAR-2003;
           Location/Qualifiers
           1..20
           /organism="unknown"
BASE COUNT      3 a      5 c      3 g      9 t
```

```
Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 705 TGAAGCAGAGAAC 718
Db 14 TGAAGCAGAGAAC 1

RESULT 220
AX360175      20 bp      DNA      linear      PAT 13-FEB-2002
LOCUS
DEFINITION Sequence 131 from Patent WO0200860.
ACCESSION AX360175
VERSION AX360175.1 GI:18675742
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Plowman,G., Whyte,D., Sudarsanam,S., Manning,G., Caenepee,S. and Charlyczak,G.
TITLE Novel proteases
JOURNAL Patent: WO 0200860-A 131 03-JAN-2002;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="SNP"

BASE COUNT      4 a      11 c      2 g      2 t      1 others
Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1458 CGCAGCTGCTCTACCA 1473
Db 1 CGCACCTGCTCTACCA 16

RESULT 221
BD016571      20 bp      DNA      linear      PAT 27-AUG-2002
LOCUS
DEFINITION Genes and proteins participating in the upstream of degradation
ACCESSION BD016571
VERSION BD016571.1 GI:22557747
KEYWORDS JP 2001245662-A/59.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Saito,A., Tamatsubo,K. and Adachi,K.
TITLE passage of aromatic polycyclic compound in the upstream of degradation
JOURNAL passage of aromatic polycyclic compound
MARINE BIOTECHNOLOGY INST CO LTD
Patent: JP 2001245662-A 59 11-SEP-2001;
OS Artificial Sequence
PN JP 2001245662-A/59
PD 11-SEP-2001
PF 03-MAR-2000 JP 2000059523
PI ATSUSHI SAITO,KAZUAKI TAMATSUBO,KYOKO ADACHI
PC C12N15/09,C12N9/02,C12N15/00
CC Description of Artificial Sequence: Synthetic primer KP205. FH
Key Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source

Query Match      0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1489 CCTGCAGCAGG 1502
Db 5 CCTGCAGCAGG 18

RESULT 222
AR190074      17 bp      DNA      linear      PAT 20-APR-2002
LOCUS
DEFINITION Sequence 5562 from patent US 6346398.
ACCESSION AR190074
VERSION AR190074.1 GI:20236039
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5562 12-FEB-2002;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"

BASE COUNT      3 a      5 c      6 g      3 t
Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1447 CCACGTGCTACTGCAGC 1463
Db 1 CCAGTGTGCTACTGCAGC 17

RESULT 223
AR285007      17 bp      DNA      linear      PAT 10-APR-2003
LOCUS
DEFINITION Sequence 86 from patent US 6528261.
ACCESSION AR285007
VERSION AR285007.1 GI:29721913
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS De Canck,I., Mersch,G. and Rossau,R.
TITLE Method for typing of HLA alleles
JOURNAL Patent: US 6528261-A 86 04-MAR-2003;
Sugen, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"

BASE COUNT      3 a      5 c      6 g      3 t
Query Match      0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 798 AGGACCTGAGCCCGGG 814
Db 1 AGGACCTGAGCTCCTGG 17

RESULT 224
AR300148/c      17 bp      DNA      linear      PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 16 from patent US 6537766.
ACCESSION AR300148
```



```

VERSION      AR300148.1  GI:31687467.
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Uckun,F.M. and Crotty,M.L.
TITLE        Ikarois isoforms and mutants
JOURNAL      Patent: US 6537766-A 16 25-MAR-2003;
FEATURES     Location/Qualifiers
             1..17
             /organism="unknown"
BASE COUNT   3 a      5 c      8 g      1 t
             0.9%; Score 13.8; DB 1; Length 17;
             Best Local Similarity 88.2%; Pred. No. 4.2e+02;
             Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1499 GAGGCCCTGCACCGCT 1515
Db 17 GAGTCCCTGCGCCGCT 1

RESULT 225
AX012584
LOCUS       AX012584               17 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 86 from Patent WO9954496.
ACCESSION   AX012584
VERSION     AX012584.1  GI:9998578
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE    1
AUTHORS      De Cancke,I., Rossau,R. and Merssch,G.
TITLE        Method for typing of hla alleles
JOURNAL      Patent: WO 9954496-A 86 28-OCT-1999;
             CANCK ILSE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE); MERSCH
             GUY (BE)
FEATURES     Location/Qualifiers
             1..17
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
BASE COUNT   3 a      5 c      6 g      3 t
             0.9%; Score 13.8; DB 1; Length 17;
             Best Local Similarity 88.2%; Pred. No. 4.2e+02;
             Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 798 AGGACCTGAGCCCCGG 814
Db 1 AGGACCTGAGCTCTGG 17

RESULT 226
AX139249
LOCUS       AX139249               17 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 97 from Patent EP1076099.
ACCESSION   AX13249
VERSION     AX13249.1  GI:14274922
KEYWORDS    Mycobacterium tuberculosis
SOURCE      Mycobacterium tuberculosis
ORGANISM    Mycobacterium tuberculosis
REFERENCE    1
AUTHORS      Suzuki,Y., Nishida,M. and Takenishi,S.
TITLE        Kit for diagnosis of tubercle bacilli
JOURNAL      Patent: EP 1076099-A 97 14-FEB-2001;
             NISSHINO INDUSTRIES, INC. (JP) ; System Research Incorporation

VERSION      AR300148.1  GI:31687467.
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Uckun,F.M. and Crotty,M.L.
TITLE        Ikarois isoforms and mutants
JOURNAL      Patent: US 6537766-A 16 25-MAR-2003;
FEATURES     Location/Qualifiers
             1..17
             /organism="unknown"
BASE COUNT   3 a      5 c      8 g      1 t
             0.9%; Score 13.8; DB 1; Length 17;
             Best Local Similarity 88.2%; Pred. No. 4.2e+02;
             Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1499 GAGGCCCTGCACCGCT 1515
Db 17 GAGTCCCTGCGCCGCT 1

RESULT 225
AX012584
LOCUS       AX012584               17 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 86 from Patent WO9954496.
ACCESSION   AX012584
VERSION     AX012584.1  GI:9998578
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE    1
AUTHORS      De Cancke,I., Rossau,R. and Merssch,G.
TITLE        Method for typing of hla alleles
JOURNAL      Patent: WO 9954496-A 86 28-OCT-1999;
             CANCK ILSE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE); MERSCH
             GUY (BE)
FEATURES     Location/Qualifiers
             1..17
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
BASE COUNT   3 a      5 c      6 g      3 t
             0.9%; Score 13.8; DB 1; Length 17;
             Best Local Similarity 88.2%; Pred. No. 4.2e+02;
             Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 798 AGGACCTGAGCCCCGG 814
Db 1 AGGACCTGAGCTCTGG 17

RESULT 226
AX139249
LOCUS       AX139249               17 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 97 from Patent EP1076099.
ACCESSION   AX13249
VERSION     AX13249.1  GI:14274922
KEYWORDS    Mycobacterium tuberculosis
SOURCE      Mycobacterium tuberculosis
ORGANISM    Mycobacterium tuberculosis
REFERENCE    1
AUTHORS      Suzuki,Y., Nishida,M. and Takenishi,S.
TITLE        Kit for diagnosis of tubercle bacilli
JOURNAL      Patent: EP 1076099-A 97 14-FEB-2001;
             NISSHINO INDUSTRIES, INC. (JP) ; System Research Incorporation

```

```

FEATURES     Location/Qualifiers
             1..17
             /organism="Mycobacterium tuberculosis"
             /mol_type="genomic DNA"
             /db_xref="taxon:1773"
             /note="capture"
BASE COUNT   2 a      6 c      8 g      1 t
             0.9%; Score 13.8; DB 1; Length 17;
             Best Local Similarity 88.2%; Pred. No. 4.2e+02;
             Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1365 ACCGCGGGCGCGCGC 1381
Db 1 ACCGCGGGCGCGCGC 17

RESULT 227
AX215377/c
LOCUS       AX215377               17 bp      mRNA      linear      PAT 07-SEP-2001
DEFINITION Sequence 819 from Patent WO0159103.
ACCESSION   AX215377
VERSION     AX215377.1  GI:15525420
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS      Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
             nogo gene expression
JOURNAL      Patent: WO 0159103-A 819 16-AUG-2001;
             RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
             McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES     Location/Qualifiers
             1..17
             /organism="synthetic construct"
             /mol_type="mRNA"
             /db_xref="taxon:32630"
             /note="Nucleic Acid"
BASE COUNT   1 a      10 c      5 g      1 t
             0.9%; Score 13.8; DB 1; Length 17;
             Best Local Similarity 88.2%; Pred. No. 4.2e+02;
             Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1041 GCGCACTGGGCGCTCGG 1057
Db 17 GCGCACTGGGCGCGCGG 1

RESULT 228
AX215399
LOCUS       AX215399               17 bp      mRNA      linear      PAT 07-SEP-2001
DEFINITION Sequence 841 from Patent WO0159103.
ACCESSION   AX215399
VERSION     AX215399.1  GI:15525442
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS      Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE        Method and reagent for the modulation and diagnosis of cd20 and
             nogo gene expression
JOURNAL      Patent: WO 0159103-A 841 16-AUG-2001;
             RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
             McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES     Location/Qualifiers
             1..17
             /organism="synthetic construct"
             /mol_type="mRNA"

```

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Indels	Gaps
BASE COUNT	1 a	9 c	0 t				
Query Match	0.9%	Score 13.8	DB 1	Length 17			
Best Local Similarity	88.2%	Pred. No. 4.2e+02					
Matches	15	Conservative 0	Mismatches 2	Indels 0	Gaps 0		
QY	802	CTTGAGCCCGGGGACC 818					
Db	1	CCGCGCCCGGGGACC 17					
RESULT 229							
LOCUS	AX216373/c	17 bp	mRNA	linear	PAT 07-SEP-2001		
DEFINITION	Sequence 1815 from Patent WO0159103.						
ACCESSION	AX216373						
VERSION	AX216373.1	GI:15526434					
KEYWORDS	synthetic construct						
SOURCE	synthetic construct						
ORGANISM	artificial sequences.						
REFERENCE	1						
AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.						
TITLE	Method and reagent for the modulation and diagnosis of cd20 and						
JOURNAL	nogo gene expression						
FEATURES	Patent: WO 0159103-A 1815 16-AUG-2001;						
source	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;						
BASE COUNT	0 a	9 c	1 t				
Query Match	0.9%	Score 13.8	DB 1	Length 17			
Best Local Similarity	88.2%	Pred. No. 4.2e+02					
Matches	15	Conservative 0	Mismatches 2	Indels 0	Gaps 0		
QY	1369	CGGCGCGCGCGCGGCA 1385					
Db	17	CCGCGCGCGCGCGGCA 1					
RESULT 230							
LOCUS	AX216946/c	17 bp	mRNA	linear	PAT 07-SEP-2001		
DEFINITION	Sequence 2388 from Patent WO0159103.						
ACCESSION	AX216946						
VERSION	AX216946.1	GI:15527007					
KEYWORDS	synthetic construct						
SOURCE	synthetic construct						
ORGANISM	artificial sequences.						
REFERENCE	1						
AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.						
TITLE	Method and reagent for the modulation and diagnosis of cd20 and						
JOURNAL	nogo gene expression						
FEATURES	Patent: WO 0159103-A 2388 16-AUG-2001;						
source	RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;						
BASE COUNT	0 a	10 c	6 g	1 t			
Query Match	0.9%	Score 13.8	DB 1	Length 17			
Best Local Similarity	88.2%	Pred. No. 4.2e+02					
Matches	15	Conservative 0	Mismatches 2	Indels 0	Gaps 0		
QY	1370	GGGCGCGCGCGCGGAC 1386					
Db	17	GGGCGCGCGCGCGGAC 1					
RESULT 231							
LOCUS	AX273287/c	17 bp	mRNA	linear	PAT 29-OCT-2001		
DEFINITION	Sequence 856 from Patent WO0162911.						
ACCESSION	AX273287						
VERSION	AX273287.1	GI:16546024					
KEYWORDS	Homo sapiens (human)						
SOURCE	Homo sapiens						
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
REFERENCE	1						
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.						
TITLE	Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and						
JOURNAL	Ellis, J.H.						
FEATURES	Method and reagent for the inhibition of grid						
source	Patent: WO 0162911-A 856 30-AUG-2001;						
BASE COUNT	2 a	6 c	8 g	1 t			
Query Match	0.9%	Score 13.8	DB 1	Length 17			

```

RESULT 233
AX326058/c
LOCUS AX326058 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2196 from Patent WO0192512.
ACCESSION AX326058
VERSION AX326058.1 GI:18096819
KEYWORDS
SOURCE Brassica rapa
ORGANISM Brassica rapa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
AUTHORS Kniec,E.B., Ganper,H.B., Rice,M.C. and Kim,J.
TITLE Targeted chromosomal genomic alterations in plants using modified
single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 2196 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:3711"
BASE COUNT 6 a 2 c 4 g 5 t
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1211 ATTCTCATCAACCGGGT 1227
Db 17 ATTCTCATTAACCGAT 1
RESULT 234
AX422333
LOCUS AX422333 17 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 669 from Patent WO0188124.
ACCESSION AX422333
VERSION AX422333.1 GI:21525715
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 669 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 9 c 2 t
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 377 CTCACCCCAATTACAA 393
Db 1 CTCACCCCAAGTACAA 17
RESULT 235
AX422334
LOCUS AX422334 17 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 670 from Patent WO0188124.

```

```

ACCESSION AX422334
VERSION AX422334.1 GI:21525716
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 670 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 9 c 1 g 2 t
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 378 TCACCCCAATTACAAAC 394
Db 1 TCACCCCAAGTACAAAC 17
RESULT 236
AX422337
LOCUS AX422337 17 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 673 from Patent WO0188124.
ACCESSION AX422337
VERSION AX422337.1 GI:21525719
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 673 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 7 c 2 g 3 t
Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 389 TACAACCCCGACATCAT 405
Db 1 TACAACCCCGACATCCT 17
RESULT 237
AX499047
LOCUS AX499047 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 354 from Patent EP1299046.
ACCESSION AX499047
VERSION AX499047.1 GI:23381340
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```
REFERENCE
AUTHORS      Zhan,J.
TITLE        Human testis expressed patched like protein
JOURNAL      Patent: EP 1229046-A 354 07-AUG-2002;
              Aecomica, Inc. (US)
FEATURES
  source      1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 8 c 6 g 2 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 636 CCGCGCTGGCGGTGGAG 652
      |||||
Db 1 CCGCGCTGGCGGTGGAG 17

RESULT 238
AX530992
LOCUS        AX530992 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 501 from Patent EP1239051.
ACCESSION   AX530992
VERSION     AX530992.1 GI:25253771
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 501 11-SEP-2002;
             Aecomica, Inc. (US)
FEATURES
  source      1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   2 a 4 c 10 g 1 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1418 GCTCGGCGTGGCGGCG 1434
      |||||
Db 1 GCTCGGCGAGGGGGC 17

RESULT 239
AX531303/c
LOCUS        AX531303 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 812 from Patent EP1239051.
ACCESSION   AX531303
VERSION     AX531303.1 GI:25254392
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 812 11-SEP-2002;
             Aecomica, Inc. (US)
FEATURES
  source      1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 8 c 6 g 2 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1370 GCGGCGCGCGCGCGAG 1386
      |||||
Db 17 GCGGCGCGCTGGGGCAG 1

RESULT 240
AX531304/c
LOCUS        AX531304 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 813 from Patent EP1239051.
ACCESSION   AX531304
VERSION     AX531304.1 GI:25254394
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 813 11-SEP-2002;
             Aecomica, Inc. (US)
FEATURES
  source      1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 11 c 4 g 1 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1369 CGGCGCGCGCGCGGCA 1385
      |||||
Db 17 CGGCGCGCGCTGGGGCA 1

RESULT 241
AX531305/c
LOCUS        AX531305 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 814 from Patent EP1239051.
ACCESSION   AX531305
VERSION     AX531305.1 GI:25254396
KEYWORDS    Homo sapiens (human)
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 814 11-SEP-2002;
             Aecomica, Inc. (US)
FEATURES
  source      1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   1 a 12 c 4 g 0 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1368 GCGGCGCGCGCGCGGC 1384
      |||||
```

Db	17	GGCGGGGGCGGCTGGGGGC	1
RESULT 242	AX531620/c		
LOCUS	AX531620	17 bp	DNA
DEFINITION	Sequence 1129 from Patent EP1239051.		
ACCESSION	AX531620		
VERSION	AX531620.1	GI:25255030	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Shannon,M.		
AUTHORS	Human posh-like protein 1		
TITLE	Patent: EP 1239051-A 1129 11-SEP-2002;		
JOURNAL	Neomica, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	4 a 3 c 8 g 2 t		
Query Match	0.9%;	Score 13.8;	DB 1; Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.2e+02;	
Matches	15;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	1479	GCACCTGGCTCTCTGGAC	1495
Db	17	GCACCTCTCTCTCTGGAC	1
LOCUS	AX531621/c		
DEFINITION	Sequence 1130 from Patent EP1239051.		
ACCESSION	AX531621		
VERSION	AX531621.1	GI:25255032	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Shannon,M.		
AUTHORS	Human posh-like protein 1		
TITLE	Patent: EP 1239051-A 1130 11-SEP-2002;		
JOURNAL	Neomica, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	4 a 4 c 7 g 2 t		
Query Match	0.9%;	Score 13.8;	DB 1; Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.2e+02;	
Matches	15;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	1478	GGCACCTGGCTCTCTGGA	1494
Db	17	GGCACCTCTCTCTCTGGA	1
LOCUS	AX531622/c		
DEFINITION	Sequence 1131 from Patent EP1239051.		
ACCESSION	AX531622		
VERSION	AX531622.1	GI:25255034	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Shannon,M.		
AUTHORS	Human posh-like protein 1		
TITLE	Patent: EP 1239051-A 1131 11-SEP-2002;		
JOURNAL	Neomica, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	4 a 4 c 7 g 2 t		
Query Match	0.9%;	Score 13.8;	DB 1; Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.2e+02;	
Matches	15;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	1477	AGGCACCTGGCTCTCTGG	1493
Db	17	AGGCACCTCTCTCTCTGG	1
LOCUS	AX531927/c		
DEFINITION	Sequence 1436 from Patent EP1239051.		
ACCESSION	AX531927		
VERSION	AX531927.1	GI:25255624	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Shannon,M.		
AUTHORS	Human posh-like protein 1		
TITLE	Patent: EP 1239051-A 1436 11-SEP-2002;		
JOURNAL	Neomica, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	4 a 6 c 5 g 2 t		
Query Match	0.9%;	Score 13.8;	DB 1; Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.2e+02;	
Matches	15;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	132	TCATCAGTTCCTCATGGGC	148
Db	17	TCATCGGTCTCTCTGGGC	1
LOCUS	AX532239/c		
DEFINITION	Sequence 1748 from Patent EP1239051.		
ACCESSION	AX532239		
VERSION	AX532239.1	GI:25255626	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Shannon,M.		
AUTHORS	Human posh-like protein 1		
TITLE	Patent: EP 1239051-A 1748 11-SEP-2002;		
JOURNAL	Neomica, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	4 a 6 c 5 g 2 t		
Query Match	0.9%;	Score 13.8;	DB 1; Length 17;
Best Local Similarity	88.2%;	Pred. No. 4.2e+02;	
Matches	15;	Conservative 0;	Mismatches 2; Indels 0; Gaps 0;
Qy	1477	AGGCACCTGGCTCTCTGG	1493
Db	17	AGGCACCTCTCTCTCTGG	1


```

VERSION      BD105163.1  GI:22650737
KEYWORDS     WO 0192572-A/1267.
SOURCE       synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
              Nishida,M.
TITLE        Kit and method for determining HLA type
JOURNAL      Patent: WO 0192572-A 1267 06-DEC-2001;
              MISSHINO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
              KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
              NISHIDA
COMMENT      OS Artificial Sequence
              PN WO 0192572-A/1267
              PD 06-DEC-2001
              PF 01-JUN-2001 WO 2001JP004662
              PR 01-JUN-2000 JP 00P 164798
              PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
              MATSUMURA,
              SHOGO MORIYA,MICHIO NISHIDA
              PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
              CC Description of Artificial Sequence:capture
              FH Key Location/Qualifiers
              FT source
              FT Location/Qualifiers
              /organism='Artificial Sequence'.

FEATURES     source
              1..17
              Location/Qualifiers
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
BASE COUNT   3 a 5 c 6 g 3 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 798 AGGACCTGAGCCCGG 814
|||||
Db 1 AGGACCTGAGCTCTGG 17

RESULT 251
I46478/c
LOCUS       I46478 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 457 from patent US 5639612.
ACCESSION  I46478
VERSION    I46478.1 GI:2470443
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Mitsuhashi,M. and Cooper,A.
TITLE      Method for detecting polynucleotides with immobilized
JOURNAL    polynucleotide probes identified based on T.sub.m
JOURNAL    Patent: US 5639612-A 457 17-JUN-1997;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
BASE COUNT 2 a 8 c 5 g 2 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CTGCGGTTGGAGCCGG 657
|||||
Db 17 CTGCGGTTGGAGCCCG 1

RESULT 252
I46479/c
LOCUS       I46479 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 458 from patent US 5639612.
ACCESSION  I46479
VERSION    I46479.1 GI:2470444
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Mitsuhashi,M. and Cooper,A.
TITLE      Method for detecting polynucleotides with immobilized
JOURNAL    polynucleotide probes identified based on T.sub.m
JOURNAL    Patent: US 5639612-A 458 17-JUN-1997;
FEATURES   Location/Qualifiers
              1..17
              /organism="unknown"
BASE COUNT 2 a 8 c 5 g 2 t
Query Match  0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CTGCGGTTGGAGCCGG 657
|||||
Db 17 CTGCGGTTGGAGCCCG 1

RESULT 253
A88003
LOCUS       A88003 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 151 from Patent WO9833904.
ACCESSION  A88003
VERSION    A88003.1 GI:6736573
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 18)
AUTHORS    Brysch,W. and Schlingensiepen,K.
TITLE      AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL    Patent: WO 9833904-A 151 06-AUG-1998;
JOURNAL    BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
              1..18
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT 1 a 5 c 11 g 1 t
Query Match  0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 919 GACGCGGAGCGCGCG 935
|||||
Db 2 GACGCGGAGCGCGCGCG 18

RESULT 254
A89970
LOCUS       A89970 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 151 from Patent EP0856579.
ACCESSION  A89970
VERSION    A89970.1 GI:6738484
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 18)
AUTHORS    Brysch,W.D. and Schlingensiepen,K.D.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: EP 0856579-A 151 05-AUG-1998;
JOURNAL    BIOGNOSTIK GES (DE)

```

FEATURES	source	Location/Qualifiers	1. .18	5 c	11 g	1 t	0.9%; Score 13.8; DB 1; Length 18; Best Local Similarity 88.2%; Pred. No. 4.3e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
RESULT 257	AR073408	Sequence 48 from patent US 5951455.	18 bp	DNA	linear		
LOCUS	AR073408						
DEFINITION	AR073408						
ACCESSION	AR073408						
VERSION	AR073408.1	GI:10000172					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 18)						
AUTHORS	Cowsert, L.M.						
TITLE	Antisense modulation of G-alpha-11 expression						
JOURNAL	Patent: US 5951455-A 48 14-SEP-1999;						
FEATURES	source	Location/Qualifiers	1. .18				
BASE COUNT	1 a	/organism="unknown"	7 c	6 g	4 t		
Query Match			0.9%; Score 13.8; DB 1; Length 18;				
Best Local Similarity			88.2%; Pred. No. 4.3e+02;				
Matches	15;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Qy	1450	CTGGTACTCGCAGCTGC 1466					
Db	2	CTGGTACTCGCGCTGC 18					
RESULT 258	AR098790	Sequence 45 from patent US 6077672.	18 bp	DNA	linear		
LOCUS	AR098790						
DEFINITION	AR098790						
ACCESSION	AR098790						
VERSION	AR098790.1	GI:12808556					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 18)						
AUTHORS	Monia, B.P. and Cowsert, L.M.						
TITLE	Antisense modulation of TRADD expression						
JOURNAL	Patent: US 6077672-A 45 20-JUN-2000;						
FEATURES	source	Location/Qualifiers	1. .18				
BASE COUNT	0 a	/organism="unknown"	5 c	12 g	1 t		
Query Match			0.9%; Score 13.8; DB 1; Length 18;				
Best Local Similarity			88.2%; Pred. No. 4.3e+02;				
Matches	15;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Qy	1368	GCGGGGCGCGCGCGC 1384					
Db	2	GTGGCGCGCGCGCGC 18					
RESULT 259	AR187553	Sequence 3041 from patent US 6346398.	18 bp	DNA	linear		
LOCUS	AR187553						
DEFINITION	AR187553						
ACCESSION	AR187553						
VERSION	AR187553.1	GI:20233518					
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 18)						
AUTHORS	Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.						
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor						
JOURNAL	Patent: US 6346398-A 3041 12-FEB-2002;						


```

FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="unknown"
BASE COUNT
  0 a 10 c 5 g 3 t
Query Match
  Score 13.8; DB 1; Length 18;
  Best Local Similarity 88.2%; Pred. No. 4.3e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 939 GCGTCTGCTCACC GCC 955
  |||||
Db 1 GCGTCTGCTCACC GCC 17
  |||||
RESULT 260
LOCUS
  AR196702 18 bp DNA linear PAT 20-APR-2002
DEFINITION
  Sequence 1167 from patent US 6350934.
ACCESSION
  AR196702
VERSION
  AR196702.1 GI:20246139
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 18)
AUTHORS
  Zwick, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P., Ann. Owens.,
  Guo, L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.
TITLE
  Nucleic acid encoding delta-9 desaturase
JOURNAL
  Patent: US 6350934-A 1167 26-FEB-2002;
FEATURES
  Location/Qualifiers
    1..18
      /organism="unknown"
BASE COUNT
  1 a 11 c 6 g 0 t
Query Match
  Score 13.8; DB 1; Length 18;
  Best Local Similarity 88.2%; Pred. No. 4.3e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1368 GCGGGGGCGGGCGGC 1384
  |||||
Db 18 GCTGGCGGGCGGGCGGC 2
  |||||
RESULT 261
LOCUS
  AR208235 18 bp DNA linear PAT 20-JUN-2002
DEFINITION
  Sequence 14 from patent US 6380170.
ACCESSION
  AR208235
VERSION
  AR208235.1 GI:21508199
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 18)
AUTHORS
  Muller, R., Liu, N., Zwicker, J. and Sedlacek, H.-H.
TITLE
  Nucleic acid construct for the cell cycle regulated expression of
  structural genes
JOURNAL
  Patent: US 6380170-A 14 30-APR-2002;
FEATURES
  Location/Qualifiers
    1..18
      /organism="unknown"
BASE COUNT
  4 a 1 c 9 g 4 t
Query Match
  Score 13.8; DB 1; Length 18;
  Best Local Similarity 88.2%; Pred. No. 4.3e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 327 GCGAAGGTATGAAGG 343
  |||||
Db 2 GCGAAGGTATGAAGG 18
  |||||
RESULT 262

```

```

AR264376/c
LOCUS
  AR264376 18 bp DNA linear PAT 29-JAN-2003
DEFINITION
  Sequence 2 from patent US 6331662.
ACCESSION
  AR264376
VERSION
  AR264376.1 GI:28076504
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 18)
AUTHORS
  Wright, D.A. and Voytas, D.F.
TITLE
  Plant retroelements
JOURNAL
  Patent: US 6331662-A 2 18-DEC-2001;
FEATURES
  Location/Qualifiers
    1..18
      /organism="unknown"
BASE COUNT
  1 a 4 c 9 g 4 t
Query Match
  Score 13.8; DB 1; Length 18;
  Best Local Similarity 88.2%; Pred. No. 4.3e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 880 CCGGACGACGGGCCA 896
  |||||
Db 17 CCGGACGACGGGCCA 1
  |||||
RESULT 263
LOCUS
  AR284966 18 bp DNA linear PAT 10-APR-2003
DEFINITION
  Sequence 44 from patent US 6528261.
ACCESSION
  AR284966
VERSION
  AR284966.1 GI:29721872
KEYWORDS
  Unknown.
SOURCE
  Unknown.
ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 18)
AUTHORS
  De Canck, I., Mersch, G. and Rossau, R.
TITLE
  Method for typing of HLA alleles
JOURNAL
  Patent: US 6528261-A 44 04-MAR-2003;
FEATURES
  Location/Qualifiers
    1..18
      /organism="unknown"
BASE COUNT
  3 a 5 c 7 g 3 t
Query Match
  Score 13.8; DB 1; Length 18;
  Best Local Similarity 88.2%; Pred. No. 4.3e+02;
  Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 798 AGGACCTGAGCCCGGG 814
  |||||
Db 2 AGGACCTGAGCTCTGG 18
  |||||
RESULT 264
LOCUS
  AX003659 18 bp DNA linear PAT 24-AUG-2000
DEFINITION
  Sequence 17 from Patent WO9927092.
ACCESSION
  AX003659
VERSION
  AX003659.1 GI:9927448
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
ORGANISM
  Homo sapiens
REFERENCE
  1
AUTHORS
  Liu, N. and Mueller, R.
TITLE
  Purified transcription factor cdf-1 and its use
JOURNAL
  Patent: WO 9927092-A 17 03-JUN-1999;
  LIU NINGSHU (DE); MUELLER ROLF (DE)
FEATURES
  Location/Qualifiers
    1..18
      /organism="unknown"

```

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
4 a 1 c 9 g 4 t
BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 327 GCGGAGGTTGAAGG 343
Db 2 GCGGAGGTTGAAGG 18

RESULT 265
LOCUS AX003663 18 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 21 from Patent WO9927092.
ACCESSION AX003663
VERSION AX003663.1 GI:9927452
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Liu, N. and Mueller, R.
TITLE Purified transcription factor cdf-1 and its use
JOURNAL Patent: WO 9927092-A 21 03-JUN-1999;
LIU NINGSHU (DE); MUELLER ROLF (DE)
FEATURES
Location/Qualifiers
1..18
source
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Mutant construct"
3 t
BASE COUNT 4 a 1 c 10 g
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 327 GCGGAGGTTGAAGG 343
Db 2 GCGGAGGTTGAAGG 18

RESULT 266
AX012542 18 bp DNA linear PAT 06-SEP-2000
LOCUS AX012542
DEFINITION Sequence 44 from Patent WO9954496.
ACCESSION AX012542
VERSION AX012542.1 GI:9998537
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS De Cancke, I., Rossau, R. and Mersch, G.
TITLE Method for typing of hla alleles
JOURNAL Patent: WO 9954496-A 44 28-OCT-1999;
CANCK ILSE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE); MERSCH GUY (BE)
FEATURES
Location/Qualifiers
1..18
source
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
3 a 5 c 7 g 3 t
BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Oligonucleotide"
2 a 5 c 9 g
BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 950 ACCGCCGGCAGCTGCT 966
Db 18 ACCGCCGGCAGCTGCT 2

RESULT 268
AX286197 18 bp DNA linear PAT 20-NOV-2001
LOCUS AX286197
DEFINITION Sequence 6 from Patent WO0179273.
ACCESSION AX286197
VERSION AX286197.1 GI:17046061
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kawaoka, Y.
TITLE Viruses comprising mutation ion channel protein
JOURNAL Patent: WO 0179273-A 6 25-OCT-2001;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US); Kawaoka, Yoshihiro (US)
FEATURES
Location/Qualifiers
1..18
source
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="A primer"
5 a 7 c 3 g 3 t
BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1447 CCACTGGTACTCGCAGC 1483
Db 2 CCAATGATACCTCGCAGC 18

RESULT 269

```



```
source
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
4 t
BASE COUNT 3 a 7 c 4 g
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 120 ACAGCTCGGAAGTCATC 136
|||
Db 1 ACCGCTCGGAAGTCCTC 17

RESULT 273
E06465 E06465 18 bp DNA linear PAT 29-SEP-1997
LOCUS
DEFINITION
ACCESSION E06465
VERSION E06465.1 GI:2174652
KEYWORDS JP 199400086-A/109.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Seki,M., Honda,Y., Takahashi,K., Murakami,T., Teranishi,Y. and
Hayashi,N.
TITLE GENE FOR DNA FRAGMENT DERIVED FROM HEPATITIS C VIRUS, POLYPEPTIDE
CODED BY THE SAME AND ITS PRODUCTION
JOURNAL Patent: JP 199400086-A 109 11-JAN-1994;
COMMENT MITSUBISHI KASEI CORP
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 199400086-A/109
PD 11-JAN-1994
PF 07-OCT-1992 JP 1992293734
PR 07-OCT-1991 JP 91P 287008, 16-DEC-1991 JP 91P 332329, PR
20-APR-1992 JP 92P 99957
PI SEKI MAKOTO, HONDA YOSHIKAZU, TAKAHASHI KAZUNOSU, PI
MURAKAMI TOMOKO,
TERANISHI YUTAKA, HAYASHI NORIO
PC C12N15/51,C07K7/08,C07K7/10,C07K13/00,C12N5/10, PC
C12N15/11,
PC C12N15/85,C12P21/02//A61K39/29,(C12P21/02,C12R1:91),C07K99:00;
CC strandedness: Single;
topology: Linear.
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
4 t
BASE COUNT 3 a 7 c 4 g
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 120 ACAGCTCGGAAGTCATC 136
|||
Db 1 ACCGCTCGGAAGTCCTC 17

RESULT 274
I21664/I21664/c
LOCUS
DEFINITION
ACCESSION I21664
VERSION I21664.1 GI:1602018
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Lupski,J.R., Koeuth,T. and Versalovic,J.
TITLE Fingerprinting bacterial strains using repetitive DNA sequence
amplification
JOURNAL Patent: US 5523217-A 56 04-JUN-1996;
FEATURES
source
1. .18
Location/Qualifiers
1. .18
/organism="unknown"
2 a 8 c 5 g 3 t
BASE COUNT 2 a 8 c 5 g 3 t
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 111 CGCAGCGGGACAGCTCG 127
|||
Db 17 CGGACTGGGACAGCTCG 1

RESULT 275
I21665
LOCUS
DEFINITION
ACCESSION I21665
VERSION I21665.1 GI:1602019
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lupski,J.R., Koeuth,T. and Versalovic,J.
TITLE Fingerprinting bacterial strains using repetitive DNA sequence
amplification
JOURNAL Patent: US 5523217-A 57 04-JUN-1996;
FEATURES
source
1. .18
Location/Qualifiers
1. .18
/organism="unknown"
3 a 5 c 8 g 2 t
BASE COUNT 3 a 5 c 8 g 2 t
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 111 CGCAGCGGGACAGCTCG 127
|||
Db 2 CGGACTGGGACAGCTCG 18

RESULT 276
I76077/I76077/c
LOCUS
DEFINITION
ACCESSION I76077
VERSION I76077.1 GI:3012231
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lupski,J.R., Versalovic,J. and Koeuth,T.
TITLE Fingerprinting bacterial strains using repetitive DNA sequence
amplification
JOURNAL Patent: US 5691136-A 56 25-NOV-1997;
FEATURES
source
1. .18
Location/Qualifiers
1. .18
/organism="unknown"
2 a 8 c 5 g 3 t
BASE COUNT 2 a 8 c 5 g 3 t
Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 111 CGCAGCGGGACAGCTCG 127
```

```

Db      17 CGGACTGGGACAGCTCG 1
|||||
RESULT 277
LOCUS      I76078              18 bp      DNA      linear      PAT 03-APR-1998
DEFINITION Sequence 57 from patent US 5691136.
ACCESSION  I76078
VERSION     I76078.1 GI:3012232
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Lupski,J.R., Versalovic,J. and Koeuth,T.
TITLE      Fingerprinting bacterial strains using repetitive DNA sequence
JOURNAL    Patent: US 5691136-A 57 25-NOV-1997;
FEATURES    Location/Qualifiers
             source
             1..18
             /organism="unknown"
BASE COUNT  3 a      5 c      8 g      2 t
Query Match      0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      111 CGCAGGGGACAGCTCG 127
|||||
Db      2 CGGACTGGGACAGCTCG 18
|||||

RESULT 278
LOCUS      A33509/c            19 bp      DNA      linear      PAT 19-JUL-1996
DEFINITION Synthetic IVS-1-6 GC clamp.
ACCESSION  A33509
VERSION     A33509.1 GI:1567949
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 19)
AUTHORS     .
TITLE      PROCESS AND DEVICE FOR SEPARATING AND DETECTING CONSTITUENTS OF A
JOURNAL    MIXTURE OF SUBSTANCES BY TEMPERATURE GRADIENT GEL ELECTROPHORESIS
FEATURES    Patent: WO 9102815-A 3 07-MAR-1991;
             Location/Qualifiers
             source
             1..19
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
BASE COUNT  0 a      14 c      5 g      0 t
Query Match      0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1367 CGCGGGGGCGGGCGCG 1383
|||||
Db      17 CGCGGGGGCGGGCGCG 1
|||||

RESULT 279
LOCUS      AR020487/c          19 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5789168.
ACCESSION  AR020487
VERSION     AR020487.1 GI:3975102
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.

```

```

REFERENCE 1 (bases 1 to 19)
AUTHORS   Leushner,J., Hui,M., Dunn,J.M. and Larson,M.T.
TITLE     Method for amplification and sequencing of nucleic acid polymers
JOURNAL   Patent: US 5789168-A 6 04-AUG-1998;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
BASE COUNT  2 a      7 c      8 g      2 t
Query Match      0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      579 GCCGCGCAGTGGACATC 595
|||||
Db      18 GCCGCGCGGTGGACACC 2
|||||

RESULT 280
LOCUS      AR051219/c          19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5830657.
ACCESSION  AR051219
VERSION     AR051219.1 GI:5974583
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Leushner,J., Hui,M., Dunn,J.M. and Larson,M.T.
TITLE      Method for single-tube sequencing of nucleic acid polymers
JOURNAL    Patent: US 5830657-A 6 03-NOV-1998;
FEATURES    Location/Qualifiers
             source
             1..19
             /organism="unknown"
BASE COUNT  2 a      7 c      8 g      2 t
Query Match      0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      579 GCCGCGCAGTGGACATC 595
|||||
Db      18 GCCGCGCGGTGGACACC 2
|||||

RESULT 281
LOCUS      AR053210/c          19 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5834189.
ACCESSION  AR053210
VERSION     AR053210.1 GI:5978072
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Stevens,J.K., Dunn,J.M., Leushner,J. and Green,R.J.
TITLE      Method for evaluation of polymorphic genetic sequences, and the use
JOURNAL    thereof in identification of HLA types
FEATURES    Patent: US 5834189-A 6 10-NOV-1998;
             Location/Qualifiers
             source
             1..19
             /organism="unknown"
BASE COUNT  2 a      7 c      8 g      2 t
Query Match      0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      579 GCCGCGCAGTGGACATC 595
|||||

```


[illegible]

```

REFERENCE 1 (bases 1 to 19)
AUTHORS Hiroshi K. and Masahiro I.
TITLE Novel acidophilic serine protease
JOURNAL Patent: JP 1999032768-A 15 09-FEB-1999;
ONO PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 1999032768-A/15
PD 09-FEB-1999
PF 16-JUL-1997 JP 1997191319
PR HIROSHI KIDO, MASAHIRO INOUE
PI C12N15/09, A61K38/55, A61K39/395, A61K48/00, C07K7/00,
PC C07K16/40,
PC C12N9/64, C12N15/00, A61K37/64, A61K37/64
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..19
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
3 a 5 c 10 g 1 t

BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1166 GAGGAGCGCGGCGCGC 1182
Db |||||

RESULT 292
E30322 19 bp DNA linear PAT 18-JUN-2001
LOCUS Gene participating in flower formation of plant.
DEFINITION E30322
ACCESSION E30322.1 GI:13017068
VERSION JP 1999318462-A 9 24-NOV-1999;
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Shinichiro, S. and Kiyotaka, O.
TITLE Gene participating in flower formation of plant
JOURNAL Patent: JP 1999318462-A 9 24-NOV-1999;
MITSUI GIYOSAI SHOKUBUTSU BIO KENKYUSHO
COMMENT OS Unidentified
PN JP 1999318462-A/9
PD 24-NOV-1999
PF 15-MAY-1998 JP 1998134095
PR SHINICHIRO SAWA, KIYOTAKA OKADA
PI C12N15/09, A01H5/00, C07K14/415, C07K16/16, C12N1/21, C12N5/10, PC
C12P21/02,
PC C12P21/08, G01N33/53// (C12N1/21, C12R1/19), (C12N5/10, C12R1/91),
PC (C12P21/02, C12R1/91), C12N15/00, C12N5/00, (C12N5/00, C12R1/91) CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..19
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..19
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
8 a 5 c 2 g 4 t

BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 19;

```

```

Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 682 CAAGCACATATCAACT 698
Db |||||

RESULT 293
I88034/c 19 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 12 from patent US 5716846.
DEFINITION I88034
ACCESSION I88034
VERSION I88034.1 GI:3407974
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Brown, S. Joel., Dattagupta, N. and Naidu, Y. M.
TITLE Method for inhibiting cellular proliferation using antisense
oligonucleotides to interleukin-6 receptor mRNA
JOURNAL Patent: US 5716846-A 12 10-FEB-1998;
FEATURES Location/Qualifiers
source 1..19
/organism='unknown'
4 a 7 c 8 g 0 t

BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1303 CGCGCTCTGCTGCAC 1319
Db |||||

RESULT 294
I84406/c 33 bp DNA linear PAT 04-APR-1998
LOCUS Sequence 7 from patent US 5695933.
DEFINITION I84406
ACCESSION I84406
VERSION I84406.1 GI:3021926
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Schalling, M., Hudson, T. J. and Housman, D. E.
TITLE Direct detection of expanded nucleotide repeats in the human genome
JOURNAL Patent: US 5695933-A 7 09-DEC-1997;
FEATURES Location/Qualifiers
source 1..33
/organism='unknown'
0 a 11 c 22 g 0 t

BASE COUNT
Query Match 0.9%; Score 13.8; DB 1; Length 33;
Best Local Similarity 63.6%; Pred. No. 4.6e+02;
Matches 21; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1410 CTGCGGAGCTCCGGGTGCGGGGGCCACCGCGG 1442
Db |||||

RESULT 295
AXI46617 43 bp DNA linear PAT 31-MAY-2001
LOCUS Sequence 79 from Patent WO0134654.
DEFINITION AXI46617
ACCESSION AXI46617
VERSION AXI46617.1 GI:14285010
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)

```


ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Strauch, K.
TITLE	Hedgehog fusion proteins and uses
JOURNAL	Patent: WO 0134654-A 79 17-MAY-2001;
FEATURES	BIODEN, INC. (US) Location/Qualifiers
source	1. .43
BASE COUNT	8 a 10 c 14 g 11 t
Query Match	0.9%; Score 13.8; DB 1; Length 43;
Best Local Similarity	58.5%; Pred. No. 4.5e+02;
Matches	24; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY	124 CTCGGAGTTCATCAGTTCCTCCATGGCGGAGATGCTGCTGCTGG 164
Db	1 CTAGGCTCTTCGCCACATGGGAGAACTGCTTTAG 41
RESULT 296	
ARI139321/c	
LOCUS	ARI139321 20 bp DNA linear PAT 16-JUN-2001
DEFINITION	Sequence 29 from patent US 6207372.
ACCESSION	ARI139321
VERSION	ARI139321.1 GI:14481817
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Shuber, A.P.
TITLE	Universal primer sequence for multiplex DNA amplification
JOURNAL	Patent: US 6207372-A 29 27-MAR-2001;
FEATURES	Location/Qualifiers
source	1. .20
BASE COUNT	0 a 9 c 11 g 0 t
Query Match	0.9%; Score 13.6; DB 1; Length 20;
Best Local Similarity	80.0%; Pred. No. 4.6e+02;
Matches	16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	1351 CAGCGCGCGCGGCGGACCGCG 1370
Db	20 CCGCGCGCGCGGCGGCGCGCG 1
RESULT 297	
ARI146612/c	
LOCUS	ARI146612 45 bp DNA linear PAT 31-MAY-2001
DEFINITION	Sequence 74 from Patent WO0134654.
ACCESSION	ARI146612
VERSION	ARI146612.1 GI:14285005
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 Strauch, K.
TITLE	Hedgehog fusion proteins and uses
JOURNAL	Patent: WO 0134654-A 74 17-MAY-2001;
FEATURES	BIODEN, INC. (US) Location/Qualifiers
source	1. .45
BASE COUNT	0 a 9 c 11 g 0 t

```

RESULT 300
AR084532
LOCUS
DEFINITION Sequence 21 from patent US 5981185.
ACCESSION AR084532
VERSION AR084532.1 GI:10011303
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 21 09-NOV-1999;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"
BASE COUNT      0 a      5 c      10 g      0 t
Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1370 GGGCGCGCGCGCGC 1384
Db 1 GGC GCGCGCGCGCGC 15

RESULT 301
AR131624
LOCUS
DEFINITION Sequence 49 from patent US 6194150.
ACCESSION AR131624
VERSION AR131624.1 GI:14120527
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 49 27-FEB-2001;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"
BASE COUNT      2 a      3 c      5 g      5 t
Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 899 AAGCTCTTCTACGTG 913
Db 1 AGGCTCTTCTACGTG 15

RESULT 302
AR131626
LOCUS
DEFINITION Sequence 51 from patent US 6194150.
ACCESSION AR131626
VERSION AR131626.1 GI:14120529
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 51 27-FEB-2001;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"

RESULT 303
AR278935
LOCUS
DEFINITION Sequence 13 from patent US 6514693.
ACCESSION AR278935
VERSION AR278935.1 GI:29713578
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Lansdorp,P.
TITLE Method for detecting multiple copies of a repeat sequence in a nucleic acid molecule
JOURNAL Patent: US 6514693-A 13 04-FEB-2003;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="unknown"
BASE COUNT      0 a      5 c      10 g      0 t
Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1370 GGGCGCGCGCGCGC 1384
Db 1 GGC GCGCGCGCGCGC 15

RESULT 304
AX007909
LOCUS
DEFINITION Sequence 451 from Patent WO9967428.
ACCESSION AX007909
VERSION AX007909.1 GI:9995606
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Stuyver,L.
TITLE Method for detection of drug-selected mutations in the hiv protease gene
JOURNAL Patent: WO 9967428-A 451 29-DEC-1999;
FEATURES
    Location/Qualifiers
        source
            1..15
                /organism="Aids-associated retrovirus"
                /mol_type="genomic DNA"
                /db_xref="taxon:11966"
BASE COUNT      4 a      3 c      4 g      4 t
Query Match      0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 440 CTGATGACTCAGAGG 454
Db 1 CTGATGACTCAGATG 15

RESULT 305

```

```

AX328777
LOCUS AX328777 15 bp DNA linear PAT 08-JAN-2002
DEFINITION Sequence 274 from Patent EP1164203.
ACCESSION AX328777
VERSION AX328777.1 GI:18101976
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
AUTHORS Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
TITLE Dna diagnostics based on mass spectrometry
JOURNAL Patent: EP 1164203-A 274 19-DEC-2001;
SEQUENOM, INC. (US)
FEATURES
Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 3 a 6 c 3 g 3 t
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1480 CACCTGGCTCCTCGGA 1494
|||||
Db 1 CACCTGACTCCTCGGA 15

RESULT 306
LOCUS BD065658 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065658
VERSION BD065658.1 GI:22611261
KEYWORDS JP 2001511000-A/293.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS Schlingsiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 293 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
PN JP 2001511000-A/293
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
LOCATION/Qualifiers
source
1..15
/organism="Unknown".
FT
FT Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 0 a 3 c 11 g 1 t
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1370 GGGGGCGGGCGGCGC 1384
|||||
Db 1 GGGGGTGGGCGGCGC 15

```

```

RESULT 307
LOCUS BD132342 15 bp DNA linear PAT 18-SEP-2002
DEFINITION Dna diagnosis method based on mass spectrometry.
ACCESSION BD132342
VERSION BD132342.1 GI:23227287
KEYWORDS JP 2002507883-A/274.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 15)
AUTHORS Koester,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
Boom,D.V.D., Jurinke,C. and Rupert,A.
TITLE Dna diagnosis method based on mass spectrometry
JOURNAL Patent: JP 2002507883-A 274 12-MAR-2002;
SEQUENOM INC
COMMENT
PN JP 2002507883-A/274
PD 12-MAR-2002
PF 06-NOV-1997 JP 1998521832
PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR
06-NOV-1996 US 08/746055,06-NOV-1996 US 08/744590 PR
23-JAN-1998 US 08/786988,23-JAN-1997 US 08/787639 PR
19-SEP-1997 US 08/933792,08-OCT-1997 US 08/947801 PI HUBERT
KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI GUOSING
XIANG,
PI DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
C12Q1/68,C07H21/00,C07F9/24
CC Strandedness: Single;
CC Topology: Unknown;
PH Key Location/Qualifiers.
FEATURES
source
1..15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3 a 6 c 3 g 3 t
Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1480 CACCTGGCTCCTCGGA 1494
|||||
Db 1 CACCTGACTCCTCGGA 15

RESULT 308
LOCUS AR050989 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 58 from patent US 5830644.
ACCESSION AR050989
VERSION AR050989.1 GI:5974353
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J. and Wright,W.E.
TITLE Method for screening for agents which increase telomerase activity
JOURNAL Patent: US 5830644-A 58 03-NOV-1998;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
BASE COUNT 0 a 0 c 9 g 7 t
Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 72 CACACGCACACACCC 86
|||||
Db 16 CACACGCACACACCC 2

```

```

RESULT 309
LOCUS AR204607/c 16 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 57 from patent US 6368789.
ACCESSION AR204607
VERSION AR204607.1 GI:21501976
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W. and Blackburn,E.H.
TITLE Screening methods to identify inhibitors of telomerase activity
JOURNAL Patent: US 6368789-A 57 09-APR-2002;
FEATURES
source
BASE COUNT 0 a 0 c 9 g 7 t
Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 72 CACAGGCACACCCC 86
Db 16 CACACACACACCCC 2
RESULT 310
LOCUS AR307317/c 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 80 from patent US 6551774.
ACCESSION AR307317
VERSION AR307317.1 GI:31697844
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 80 22-APR-2003;
FEATURES
source
BASE COUNT 0 a 0 c 9 g 7 t
Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 72 CACAGGCACACCCC 86
Db 16 CACACACACACCCC 2
RESULT 311
LOCUS AX696120/c 16 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 19 from Patent WO03008640.
ACCESSION AX696120
VERSION AX696120.1 GI:29419280
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Canarrhini; Hominidae; Homo.
Whittaker,P.A., Meyers,D.A., Postma,D.S. and Bleecker,E.R.

```

```

TITLE Asthma-associated gene
JOURNAL Patent: WO 03008640-A 19 30-JAN-2003;
Novartis AG (CH); Novartis Pharma GmbH (AT); Wake Forest
University Health Sciences (US); Rijksuniversiteit te Groningen
(NL)
FEATURES
source
BASE COUNT 4 a 7 c 3 g 2 t
Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 138 GTTCATGGCGGAGA 152
Db 15 GTTCATGGCGGGA 1
RESULT 312
LOCUS I51790 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 58 from patent US 5645986.
ACCESSION I51790
VERSION I51790.1 GI:2472991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Harley,C.B., Strahl,C.M., McEachern,M.J., Shay,J.,
Wright,W.E., Blackburn,E.H. and Vaziri,H.
TITLE Therapy and diagnosis of conditions related to telomere length
and/or telomerase activity
JOURNAL Patent: US 5645986-A 58 08-JUL-1997;
FEATURES
source
BASE COUNT 0 a 0 c 9 g 7 t
Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 72 CACAGGCACACCCC 86
Db 16 CACACACACACCCC 2
RESULT 313
LOCUS I84399 16 bp DNA linear PAT 04-APR-1998
DEFINITION Sequence 57 from patent US 5695932.
ACCESSION I84399
VERSION I84399.1 GI:3021919
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
TITLE Telomerase activity assays for diagnosing pathogenic infections
JOURNAL Patent: US 5695932-A 57 09-DEC-1997;
FEATURES
source
BASE COUNT 0 a 0 c 9 g 7 t
Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 72 CACACGACACACCC 86
Db 16 CACACACACACACCC 2

RESULT 314
AR112330/C
LOCUS AR112330 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 10 from patent US 6130047.
ACCESSION AR112330
VERSION AR112330.1 GI:14092230
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Nadeau,J.G., Hsieh,H.V., Pitner,J.Bruce. and Linn,C.Preston.
TITLE Detection of nucleic acids by fluorescence quenching
JOURNAL Patent: US 6130047-A 10 10-OCT-2000;
FEATURES
    source
        Location/Qualifiers
            1..17
                /organism="unknown"
BASE COUNT 0 a 11 c 2 g 4 t
    Query Match 0.9%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 4.8e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GAGCGAGCGGCGAG 37
Db 16 GAGCGAGCGGAGAG 2

RESULT 315
AR164080/C
LOCUS AR164080 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6271210.
ACCESSION AR164080
VERSION AR164080.1 GI:16235018
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sivaraman,V.S., Wang,H.-Y. and Malbon,C.C.
TITLE Antisense oligonucleotides for mitogen-activated protein kinases as
therapy for cancer
JOURNAL Patent: US 6271210-A 3 07-AUG-2001;
FEATURES
    source
        Location/Qualifiers
            1..17
                /organism="unknown"
BASE COUNT 1 a 10 c 5 g 1 t
    Query Match 0.9%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 4.8e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGCGGGCGGC 1384
Db 15 GGGGGCGGGCGGC 1

RESULT 316
AR164081/C
LOCUS AR164081 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 4 from patent US 6271210.
ACCESSION AR164081
VERSION AR164081.1 GI:16235020
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sivaraman,V.S., Wang,H.-Y. and Malbon,C.C.
TITLE Antisense oligonucleotides for mitogen-activated protein kinases as
therapy for cancer
JOURNAL Patent: US 6271210-A 4 07-AUG-2001;
FEATURES
    source
        Location/Qualifiers
            1..17
                /organism="unknown"
BASE COUNT 1 a 10 c 5 g 1 t
    Query Match 0.9%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 4.8e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGCGGGCGGC 1384
Db 15 GGGGGCGGGCGGC 1

RESULT 317
AR286066
LOCUS AR286066 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 438 from patent US 6528640.
ACCESSION AR286066
VERSION AR286066.1 GI:29723662
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 438 04-MAR-2003;
FEATURES
    source
        Location/Qualifiers
            1..17
                /organism="unknown"
BASE COUNT 2 a 5 c 6 g 4 t
    Query Match 0.9%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 4.8e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 759 CCACGGTGCACCTGG 773
Db 2 CCACGGTGCAGCTGG 16

RESULT 318
AX007921
LOCUS AX007921 17 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 463 from Patent WO9967428.
ACCESSION AX007921
VERSION AX007921.1 GI:9995618
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
REFERENCE 1
AUTHORS Viruses; Retroid viruses; Retroviridae.
TITLE Stuyver,L.
JOURNAL Method for detection of drug-selected mutations in the hiv protease
gene
PATENT: WO 9967428-A 463 29-DEC-1999;
INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES
    source
        Location/Qualifiers
            1..17
                /organism="Aids-associated retrovirus"
                /mol_type="genomic DNA"
                /db_xref="taxon:11966"
BASE COUNT 5 a 3 c 4 g 5 t
    Query Match 0.9%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 4.8e+02;

```

```

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 440 CTGATGACTCAGAGG 454
Db |||||
3 CTGATGACTCAGATG 17

RESULT 319
AX215376/c
LOCUS AX215376 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 818 from Patent WO0159103.
ACCESSION AX215376
VERSION AX215376.1 GI:15525419
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 818 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"
Location/Qualifiers
1..17
BASE COUNT 1 a 9 c 5 g 2 t

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1043 GCACTGGGCGCTCGG 1057
Db |||||
16 GCACTGGGCGCGGG 2

RESULT 320
AX215397/c
LOCUS AX215397 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 839 from Patent WO0159103.
ACCESSION AX215397
VERSION AX215397.1 GI:15525440
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 839 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"
Location/Qualifiers
1..17
BASE COUNT 0 a 10 c 6 g 1 t

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1371 GGGCGGCGCGGCGCA 1385
Db |||||
17 GGGCGGCGCGGCGCA 3

RESULT 321
AX216951/c
LOCUS AX216951 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2393 from Patent WO0159103.
ACCESSION AX216951
VERSION AX216951.1 GI:15527012
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
PATENT: WO 0159103-A 2393 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/notes="Nucleic Acid"
Location/Qualifiers
1..17
BASE COUNT 0 a 9 c 7 g 1 t

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1371 GGGCGGCGCGGCGCA 1385
Db |||||
16 GGGCGGCGCGGCGCA 2

RESULT 322
AX226812/c
LOCUS AX226812 17 bp mRNA linear PAT 10-SEP-2001
DEFINITION Sequence 184 from Patent WO0157206.
ACCESSION AX226812
VERSION AX226812.1 GI:15555953
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Fattaey, A.R., Jarvis, T., McSwiggen, J., Booher, R.N. and Holman, P.S.
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (chk
JOURNAL 1) enzyme
PATENT: WO 0157206-A 184 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
Location/Qualifiers
1..17
BASE COUNT 4 a 4 c 4 g 5 t

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 261 AAAAGCTGACCCCTT 275
Db |||||
16 AAAAGCTGATCCCTT 2

RESULT 323
AX227179/c
LOCUS AX227179 17 bp mRNA linear PAT 10-SEP-2001
DEFINITION Sequence 551 from Patent WO0157206.
ACCESSION AX227179

```

```

VERSION      AX227179.1  GI:15556320
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      Fattaey,A.R., Jarvis,T., Mcswiggen,J., Boher,R.N. and Holman,P.S.
TITLE        Method and reagent for the inhibition of checkpoint kinase-1 (chk
JOURNAL      Patent: WO 0157206-A 551 09-AUG-2001;
FEATURES     RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)
SOURCE       Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
BASE COUNT  4 a 4 c 4 g 5 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 261 AAAAGCTGACCCCTT 275
Db 15 AAAAGCTGATCCCTT 1
RESULT 324
AX273063/c
LOCUS       AX273063
DEFINITION Sequence 632 from Patent WO0162911.
ACCESSION  AX273063
VERSION     AX273063.1  GI:16545800
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
REFERENCE  1
AUTHORS    Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
           Ellis,J.H.
TITLE      Method and reagent for the inhibition of grid
JOURNAL    Patent: WO 0162911-A 632 30-AUG-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
SOURCE     1..17
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT  3 a 5 c 8 g 1 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1284 CGCCCTTCGCCTGG 1298
Db 16 CGCCCTTCGCCTGG 2
RESULT 325
AX398152/c
LOCUS       AX398152
DEFINITION Sequence 29 from Patent WO0220837.
ACCESSION  AX398152
VERSION     AX398152.1  GI:21260967
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Ronaghi,M., Ekstroem,B. and Pourmand,N.
TITLE      Method

```

```

JOURNAL      Patent: WO 0220837-A 29 14-MAR-2002;
           Pyrosequencing AB (SE) ; The Board of Trustees of The Leland
           Stanford Junior University (US)
FEATURES     Location/Qualifiers
SOURCE       1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Sequencing primer - A063FS"
BASE COUNT  1 a 7 c 4 g 5 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 768 ACCTGGAGCAGGCG 782
Db 17 ACCTGGAGCAGAGCG 3
RESULT 326
AX422879
LOCUS       AX422879
DEFINITION Sequence 1215 from Patent WO0188124.
ACCESSION  AX422879
VERSION     AX422879.1  GI:21526261
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
           Randi,A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 1215 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
SOURCE     1..17
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT  5 a 7 c 3 g 2 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 389 TACAACCCCGACATC 403
Db 3 TACAACCCCGACATC 17
RESULT 327
AX422915
LOCUS       AX422915
DEFINITION Sequence 1251 from Patent WO0188124.
ACCESSION  AX422915
VERSION     AX422915.1  GI:21526297
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
           Randi,A.M.
TITLE      Method and reagent for the inhibition of erg
JOURNAL    Patent: WO 0188124-A 1251 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
SOURCE     1..17
/mol_type="mRNA"
/db_xref="taxon:9606"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT      1 a      8 c      4 g      4 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 968 TTGTGGCGCGGCAC 982
Db 1 TTGTGGCGCGGCAC 15

RESULT 328
AX423599
LOCUS      17 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 1935 from Patent WO018124.
ACCESSION AX423599
VERSION AX423599.1 GI:21526981
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
TITLE Randi, A.M.
JOURNAL Method and reagent for the inhibition of erg
PATENT: WO 018124-A 1935 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT      3 a      6 c      4 g      4 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 967 CTTGTGGCGCGCA 981
Db 3 CTTGTGGCGGCCCA 17

RESULT 329
AX498855
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 162 from Patent EP1229046.
ACCESSION AX498855
VERSION AX498855.1 GI:23381148
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 162 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      2 a      7 c      6 g      2 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 GACTCGGCACCGGG 1000
Db 3 GACTCTGCCACCGGG 17

RESULT 330
AX498856
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 163 from Patent EP1229046.
ACCESSION AX498856
VERSION AX498856.1 GI:23381149
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 163 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      2 a      7 c      6 g      2 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 GACTCGGCACCGGG 1000
Db 2 GACTCTGCCACCGGG 16

RESULT 331
AX498857
LOCUS      17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 164 from Patent EP1229046.
ACCESSION AX498857
VERSION AX498857.1 GI:23381150
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 164 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      2 a      8 c      5 g      2 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 GACTCGGCACCGGG 1000
Db 1 GACTCTGCCACCGGG 15

RESULT 332
AX687669
LOCUS      17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 401 from Patent EP1281758.

```


ACCESSION AX687669
VERSION AX687669.1 GI:29410365
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FEATURES
source 1
1.17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 7 c 2 g 5 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 863 TTCTCCTCACTTCTCTG 877
Db 2 TTCTCCTCACTTCTCTG 16
RESULT 333
AX687670 17 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 402 from Patent EP1281758.
ACCESSION AX687670
VERSION AX687670.1 GI:29410366
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FEATURES
source 1
1.17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 8 c 1 g 6 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 863 TTCTCCTCACTTCTCTG 877
Db 1 TTCTCCTCACTTCTCTG 15
RESULT 334
AX687747 17 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 479 from Patent EP1281758.
ACCESSION AX687747
VERSION AX687747.1 GI:29410443
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FEATURES
source 1
1.17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 3 c 7 g 3 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 792 TGGTGAAGGACCTGA 806
Db 3 TGGTGAAGGACCTGA 17
RESULT 335
AX687748 17 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 480 from Patent EP1281758.
ACCESSION AX687748
VERSION AX687748.1 GI:29410444
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
FEATURES
source 1
1.17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 3 c 7 g 3 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 792 TGGTGAAGGACCTGA 806
Db 2 TGGTGAAGGACCTGA 16
RESULT 336
AX687749 17 bp DNA linear PAT 31-MAR-2003
LOCUS
DEFINITION Sequence 481 from Patent EP1281758.
ACCESSION AX687749
VERSION AX687749.1 GI:29410445
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
4 a 3 c 7 g 3 t
BASE COUNT      4 a 3 c 7 g 3 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 792 TGGTCAAGGACCTGA 806
|||||
Db 1 TGGTGGAGGACCTGA 15

RESULT 337
AX723430/C
LOCUS AX723430 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1117 from Patent WO03025176.
ACCESSION AX723430
VERSION AX723430.1 GI:30423931
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1117 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
4 a 5 c 3 g 5 t
BASE COUNT      4 a 5 c 3 g 5 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 700 CTCGGTGAAGCAGA 714
|||||
Db 17 CTCGGTGAAGCAGA 3

RESULT 338
AX728094
LOCUS AX728094 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5781 from Patent WO03025176.
ACCESSION AX728094
VERSION AX728094.1 GI:30507437
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5781 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
2 a 6 c 4 g 5 t
BASE COUNT      2 a 6 c 4 g 5 t

source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
4 a 3 c 7 g 3 t
BASE COUNT      4 a 3 c 7 g 3 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1445 ATCCACTGGTACTCG 1459
|||||
Db 2 ATCCCTGGTACTCG 16

RESULT 339
AX729048
LOCUS AX729048 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 682 from Patent WO03025175.
ACCESSION AX729048
VERSION AX729048.1 GI:30508391
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 682 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
5 a 6 c 2 g 4 t
BASE COUNT      5 a 6 c 2 g 4 t
Query Match      0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 346 GATCTCCAGAACTC 350
|||||
Db 1 GATCTCCAGAACTC 15

RESULT 340
BD058091/C
LOCUS BD058091 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Antisense oligonucleotides for mitogen-activated protein kinases as
therapy for breast cancer.
ACCESSION BD058091
VERSION BD058091.1 GI:22603697
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Sivaraman,V.S., Wang,H.Y. and Malbon,C.C.
TITLE Antisense oligonucleotides for mitogen-activated protein kinases as
therapy for breast cancer
JOURNAL Patent: JP 2001518881-A 3 16-OCT-2001;
THE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
COMMENT OS Homo sapiens (human)
PN JP 2001518881-A/3
PD 16-OCT-2001
PP 19-MAR-1998 JP 1998541700
PI VIMALA S SIVARAMAN,HSIEN YU WANG,CRAIG C MALBON PC
C12N15/11,A61K31/70,C12Q1/68//A61K48/00
CC The molecular type is mRNA which is antisense. FH Key
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"

```

```

PF 22-SEP-1998 JP 1998267492
PR 23-SEP-1997 US 08/933749
PI JAMES G NADEAU, HELEN V C, J BLUCE PITONA, C PRESTON RIN PC
C12Q1/68, C07H21/00, C12N15/09, G01N33/542, G01N33/566, PC
C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32830" 4 t
BASE COUNT 0 a 11 c 2 g 4 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 23 GAGCGAGCGGCGGAG 37
|||||
Db 16 GAGCGAGCGGCGGAG 2
|||||
RESULT 343
126645
LOCUS
DEFINITION Sequence 12 from patent US 5559009.
ACCESSION 126645
VERSION 126645.1 GI:1606515
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 17)
AUTHORS Chandy, K.G., Kalman, K., Chandy, G. and Gutman, G.A.
TITLE Voltage-gated potassium channel gene, KV1.7, vectors and host cells
comprising the same, and recombinant methods of making potassium
channel proteins
JOURNAL Patent: US 5559009-A 12 24-SEP-1996;
FEATURES
source
1..17
Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 0 a 3 c 12 g 1 t 1 others
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1368 GCGGGGCGGCGGCGG 1383
|||||
Db 2 GCTGGGCGGCGGNGG 17
|||||
RESULT 344
A87319/c
LOCUS
DEFINITION Sequence 44 from Patent WO9837211.
ACCESSION A87319
VERSION A87319.1 GI:6736084
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE
1 (bases 1 to 18)
AUTHORS Ruttner, B. and Betzner, A.S.
TITLE PROTEIN COMPLEMENTATION IN TRANSGENIC PLANTS
JOURNAL Patent: WO 9837211-A 44 27-AUG-1998;
GENE SHEARS PTY LTD (AU); HUTTNER ERIC (AU)
FEATURES
source
1..18
Location/Qualifiers
/organism="unidentified"

```

```

/mol_type="genomic RNA"
/db_xref="taxon:9606" 1 t
BASE COUNT 1 a 10 c 5 g 1 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1370 GGGGGCGGCGGCGGC 1384
|||||
Db 15 GCGGGCGGCGGCGGC 1
|||||
RESULT 341
BD058092/c
LOCUS
DEFINITION Antisense oligonucleotides for mitogen-activated protein kinases as
therapy for breast cancer.
ACCESSION BD058092
VERSION BD058092.1 GI:22603698
KEYWORDS JP 2001518881-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 17)
AUTHORS Sivaraman, V.S., Wang, H.Y. and Malbon, C.C.
TITLE Antisense oligonucleotides for mitogen-activated protein kinases as
therapy for breast cancer
JOURNAL Patent: JP 2001518881-A 4 16-OCT-2001;
THE RESEARCH FOUNDATION OF STATE UNIV OF NEW YORK
COMMENT OS Homo sapiens (human)
PN JP 2001518881-A/4
PD 16-OCT-2001
PI 19-MAR-1998 JP 1998541700
PF VIMALA S SIVARAMAN, HSIEH YU WANG, CRAIG C MALBON PC
C12N15/11, A61K31/70, C12Q1/68//A61K48/00
CC The molecular type is cDNA which is antisense. FH Key
Location/Qualifiers
1..17
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606" 1 t
BASE COUNT 1 a 10 c 5 g 1 t
Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1370 GGGGGCGGCGGCGGC 1384
|||||
Db 15 GCGGGCGGCGGCGGC 1
|||||
RESULT 342
E33640/c
LOCUS
DEFINITION Detection of nucleic acid by disappearance of fluorescence.
ACCESSION E33640
VERSION E33640.1 GI:13027035
KEYWORDS JP 1999155598-A/10.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 17)
AUTHORS James, G.N., Helen, V.C., J.B.P. and C.P.R.
TITLE Detection of nucleic acid by disappearance of fluorescence
JOURNAL Patent: JP 1999155598-A 10 15-JUN-1999;
BECTON DICKINSON & CO
COMMENT OS Artificial Sequence
PN JP 1999155598-A/10
PD 15-JUN-1999

```

```

/mol_type="genomic DNA"
/db_xref="taxon:32644"
3 t
BASE COUNT      2 a      9 c      4 s      3 t
Query Match      0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1348 GGACAGCGCGCGG 1362
|||||
Db 15 GGACAGCGCGGTGG 1

RESULT 345
AR096628/c
LOCUS      AR096628      18 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 12 from patent US 6008048.
ACCESSION AR096628
VERSION AR096628.1 GI:10025593
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowsett,L.M.
TITLE Antisense inhibition of EGR-1 expression
JOURNAL Patent: US 6008048-A 12 28-DEC-1999;
FEATURES
Location/Qualifiers
1. .18
/organism="unknown"
4 a      8 c      2 g      4 t
BASE COUNT      4 a      8 c      2 g      4 t
Query Match      0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 GAGATGCTGCTGCTG 163
|||||
Db 15 GAGATGATGCTGCTG 1

RESULT 346
AX003666
LOCUS      AX003666      18 bp      DNA      linear      PAT 24-AUG-2000
DEFINITION Sequence 24 from Patent WO9927092.
ACCESSION AX003666
VERSION AX003666.1 GI:9927455
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Liu,N. and Mueller,R.
TITLE Purified transcription factor cdf-1 and its use
JOURNAL Patent: WO 9927092-A 24 03-JUN-1999;
Liu NINGSHU (DE); MUELLER ROLF (DE)
FEATURES
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Mutant construct"
4 a      1 c      8 g      5 t
BASE COUNT      4 a      1 c      8 g      5 t
Query Match      0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 327 GCGGAGGTTGAAG 341
|||||
Db 2 GCGGAGGTTGAAG 16

/mol_type="synthetic construct"
/db_xref="taxon:32630"
/notes="based on Homo sapiens"
8 a      4 c      6 g      0 t
BASE COUNT      8 a      4 c      6 g      0 t
Query Match      0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GAAGGAAAGCGCAA 62
|||||
Db 1 GAAGGAAAGCGCAA 15

RESULT 349
AX598747/c
LOCUS      AX598747      18 bp      DNA      linear      PAT 14-FEB-2003
DEFINITION Sequence 87 from Patent WO02077272.
ACCESSION AX598747
VERSION AX598747.1 GI:28398885
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

RESULT 347
AX353569
LOCUS      AX353569      18 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 101 from Patent WO0204636.
ACCESSION AX353569
VERSION AX353569.1 GI:18618644
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Roy,F., Goossens,S., Janssens,B. and Vanpoucke,G.
TITLE Novel g(a) expressed in heart and testis
JOURNAL Patent: WO 0204636-A 101 17-JAN-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="primer MCB2044"
4 a      4 c      2 g      8 t
BASE COUNT      4 a      4 c      2 g      8 t
Query Match      0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 289 GTTTATCCCAATGT 303
|||||
Db 2 GTTTAACCCCAATGT 16

RESULT 348
AX412098
LOCUS      AX412098      18 bp      DNA      linear      PAT 14-JUN-2002
DEFINITION Sequence 198 from Patent WO0226968.
ACCESSION AX412098
VERSION AX412098.1 GI:21444563
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Korneuk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 198 04-APR-2002;
University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="based on Homo sapiens"
8 a      4 c      6 g      0 t
BASE COUNT      8 a      4 c      6 g      0 t
Query Match      0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 48 GAAGGAAAGCGCAA 62
|||||
Db 1 GAAGGAAAGCGCAA 15

RESULT 349
AX598747/c
LOCUS      AX598747      18 bp      DNA      linear      PAT 14-FEB-2003
DEFINITION Sequence 87 from Patent WO02077272.
ACCESSION AX598747
VERSION AX598747.1 GI:28398885
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

REFERENCE
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE        Berlin, K., Braun, A., Distler, J., Gueig, D., Howe, A., Mueller, J.,
              Olek, A., Piepenbrock, C., Adorjan, P., Grabs, G., Lesche, R., Leu, E.,
              Lewin, A., Lipscher, E., Maier, S., Model, F., Mueller, V., Otto, T.,
              Pellet, C. and Ziebarth, H.
              Methods and nucleic acids for the analysis of hematopoietic cell
              proliferative disorders
JOURNAL      Patent: WO 02077272-A 87 03-OCT-2002;
              Epigenomics AG (DE)
FEATURES     source
              1. .18
              Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT   0 a 12 c 4 g 2 t
Query Match   0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1351 CAGCGCGCGCGGGA 1365
DB 17 CGCGCGCGCGGGGA 3

RESULT 350
BD057397/c
LOCUS         18 bp DNA linear PAT 27-AUG-2002
DEFINITION   Protein complementation in transgenic plants.
ACCESSION    BD057397
VERSION      BD057397.1 GI:22603003
KEYWORDS     JP 2001512322-A/41.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Paul, W., Perez, P., Huttner, E. and Betzner, A.S.
TITLE        Protein complementation in transgenic plants
JOURNAL      Patent: JP 2001512322-A 41 21-AUG-2001;
              GENE SHEARS PTY LTD
COMMENT      PN JP 2001512322-A/41
              PD 21-AUG-2001
              PF 20-FEB-1998 JP 1998536400
              PR 21-FEB-1997 GB 9703681.8
              PI WYATT PAUL, PASCUAL PEREZ, ERIC HUTTNER, ANDREAS STEFAN BETZNER
              PC
              A01H5/00, C12N5/10, C12N9/22, C12N15/09//C12Q1/68, C12N15/00, C12N5/ PC
              CC Strandedness: Single;
              CC Topology: Linear;
              CC /note= 'Fig 3B, lane 3, RN 7'
              FH Key Location/Qualifiers.
FEATURES     source
              1. .18
              Location/Qualifiers
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
BASE COUNT   2 a 9 c 4 g 3 t
Query Match   0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1348 GGACAGCGCGCGG 1362
DB 15 GGACAGCGCGGTCG 1

RESULT 351
AR222933
LOCUS         19 bp DNA linear PAT 26-SEP-2002

```

```

DEFINITION   Sequence 43 from patent US 6432639.
ACCESSION    AR222933
VERSION      AR222933.1 GI:23330770
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Lichter, J.B. and Guida, M.
TITLE        Isolated CYP3A4 nucleic acid molecules and detection methods
JOURNAL      Patent: US 6432639-A 43 13-AUG-2002;
              Location/Qualifiers
FEATURES     source
              1. .19
              /organism="unknown"
BASE COUNT   8 a 3 c 8 g 0 t
Query Match   0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 AAGCGCAAGAGAGAG 69
DB 3 AAGCGCAAGAGAGAG 17

RESULT 352
AX007819
LOCUS         19 bp DNA linear PAT 06-SEP-2000
DEFINITION   Sequence 361 from Patent WO9967428.
ACCESSION    AX007819
VERSION      AX007819.1 GI:9995516
KEYWORDS     Aids-associated retrovirus
SOURCE       Aids-associated retrovirus
ORGANISM     Aids-associated retrovirus
              Viruses; Retroviridae.
REFERENCE    1
AUTHORS      Stuyver, L.
TITLE        Method for detection of drug-selected mutations in the hiv protease
              gene
JOURNAL      Patent: WO 9967428-A 361 29-DEC-1999;
              INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
              Location/Qualifiers
FEATURES     source
              1. .19
              /organism="Aids-associated retrovirus"
              /mol_type="genomic DNA"
              /db_xref="taxon:11966"
BASE COUNT   6 a 3 c 5 g 5 t
Query Match   0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 440 CTGATGACTCAGAG 454
DB 5 CTGTTGACTCAGAG 19

RESULT 353
AX300524
LOCUS         19 bp DNA linear PAT 30-NOV-2001
DEFINITION   Sequence 30 from Patent WO0185933.
ACCESSION    AX300524
VERSION      AX300524.1 GI:17381875
KEYWORDS     synthetic construct
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1
AUTHORS      van Roy, F., Bonne, S. and Vanlandschoot, A.
TITLE        Plakoglobin interacting proteins
JOURNAL      Patent: WO 0185933-A 30 15-NOV-2001;
              Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
              Location/Qualifiers
FEATURES

```

```

source
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer FVR1595F"
2 t
BASE COUNT      4 a      6 c      7 g      2 t

Query Match      0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1246 GGTATCGAGAGCA 1260
Db       4 GGTATCGAGAGCA 18

RESULT 354
AX421254
LOCUS      AX421254      19 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 2 from Patent WO0218641.
ACCESSION  AX421254
VERSION     AX421254.1 GI:21524662
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Risinger,C., Andersson,M.K., Lewander,T. and Olaiisson,E.
TITLE      Detection of cyp3a4 and cyp2c9 polymorphisms
JOURNAL    Patent: WO 0218641-A 2 07-MAR-2002;
           Gemini Genomics PLC (GB)
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
           /note="Oligonucleotide of CYP3A4 region"
BASE COUNT      8 a      3 c      8 g      0 t

Query Match      0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      55 AAGCGCAGAGAGAG 69
Db       3 AAGCGCAGAGAGAG 17

RESULT 355
AX643373/c
LOCUS      AX643373      19 bp      DNA      linear      PAT 24-FEB-2003
DEFINITION Sequence 239 from Patent WO02099099.
ACCESSION  AX643373
VERSION     AX643373.1 GI:28551017
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Penger,A., Sprenger,R. and Brinkmann,U.
TITLE      Polymorphisms in the human gene for cytochrome p450 polypeptide 2c8
           and their use in diagnostic and therapeutic applications
JOURNAL    Patent: WO 02099099-A 239 12-DEC-2002;
           Epidauros Biotechnologie AG (DE)
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"
           /note="r-g or a"
BASE COUNT      1 a      2 g      9 t      1 others      Length 19;

Query Match      0.9%; Score 13.4; DB 1; Length 19;

source
1..19
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="y-t or c"
2 c
BASE COUNT      9 a      2 c      6 g      1 t      1 others      Length 19;

Query Match      0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 4.9e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      419 GAAACACCGGAGCGGA 435
Db       2 GAAACAAVGGAGCAGA 18

RESULT 357
E63275/c
LOCUS      E63275      19 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Cell death inhibitory protein.
ACCESSION  E63275
VERSION     E63275.1 GI:22557574
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Morishima,N. and Shibata,T.
TITLE      Cell death inhibitory protein
JOURNAL    Patent: JP 2001231566-A 4 28-AUG-2001;
           THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT    OS Artificial Sequence
           PN JP 2001231566-A//4
           PD 28-AUG-2001
           PF 18-FEB-2000 JP 2000041927
           PI NOBUHIRO MORISHIMA, TAKEHIKO SHIBATA
           PC C12N15/09,A61K38/55,A61P21/00,A61P25/28,A61P37/02,A61P43/00,
           PC C07K14/47,
           PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12N15/00,A61K37/ PC
           64,C12N5/00
CC Description of Artificial Sequence:synthetic DNA FH Key
FEATURES   Location/Qualifiers
           source
           1..19
           /organism="synthetic construct"
           /mol_type="genomic DNA"
           /db_xref="taxon:32630"

```

```

BASE COUNT      3 a      5 c      9 g      2 t
Query Match      0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1031 CCTTCGGGGCGCA 1045
|||||
Db 18 CCTTCGGGGCGCA 4

RESULT 358
188039
LOCUS      188039      19 bp      DNA      linear      PAT 10-AUG-1998
DEFINITION Sequence 17 from patent US 5716846.
ACCESSION 188039
VERSION 188039.1 GI:3407979
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Brown,S,Joel., Datta Gupta,N. and Naidu,Y.M.
TITLE Method for inhibiting cellular proliferation using antisense oligonucleotides to interleukin-6 receptor mRNA
JOURNAL Patent: US 5716846-A 17 10-FEB-1998;
FEATURES
Location/Qualifiers
source 1..19
/organism="unknown"

BASE COUNT      6 a      3 c      8 g      2 t
Query Match      0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 431 GCGGACAGGCTGATG 445
|||||
Db 1 GCGGACAGGCTGATG 15

RESULT 359
A18145
LOCUS      A18145      18 bp      DNA      linear      PAT 22-APR-1994
DEFINITION Probe specific for HLA-B27 group seq ID No:11.
ACCESSION A18145
VERSION A18145.1 GI:513200
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE PROCESS FOR AMPLIFYING NUCLEIC ACID
JOURNAL Patent: WO 9207956-A 13 14-MAY-1992;
FEATURES
Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT      6 a      6 c      5 g      1 t
Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 673 CTACAGTCCAGGCACA 690
|||||
Db 1 CTGACAGGCCAAGGCACA 18

RESULT 360
A34806/c
LOCUS      A34806      18 bp      DNA      linear      PAT 16-JUL-1996
DEFINITION Sequence 7 from patent US 5750376.
ACCESSION AR007264
VERSION AR007264.1 GI:3966748
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

```

```

DEFINITION HSV probe.
ACCESSION A34806
VERSION A34806.1 GI:1568287
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Renard,A. and Thiry,M.
TITLE Recombinant polypeptides of the haemorrhagic septicaemia virus in fish
JOURNAL Patent: EP 0377349-A 24 11-JUL-1990;
FEATURES
Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

BASE COUNT      5 a      4 c      6 g      3 t
Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 889 CGCGCCCAAGAGGCTCTT 906
|||||
Db 18 CGCCTCCAGATGCTCTT 1

RESULT 361
A63132
LOCUS      A63132      18 bp      DNA      linear      PAT 12-MAR-1998
DEFINITION Sequence 7 from Patent WO9720058.
ACCESSION A63132
VERSION A63132.1 GI:3716996
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Kapros,T., Dudits,D., Gyorgyey,J., Mai,A. and Kelenen,Z.
TITLE PLANT GENE EXPRESSION VECTOR FAMILY BASED ON THE REGULATORY DNA SEQUENCES OF AN ALPFA H3 HISTON GENE VARIANT (Msh3g1)
JOURNAL Patent: WO 9720058-A 7 05-JUN-1997;
COMMENT BAY ZOLTAN ALKALMAZOTT KUTATAS (HU)
Other publication HU 76355 19970828
Other publication AU 7705296 19970619.
FEATURES
Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT      1 a      5 c      11 g      1 t
Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1430 GGGGCCACCGGGGCATC 1447
|||||
Db 1 GGGGCCCGCGGGGCATC 18

RESULT 362
AR007264/c
LOCUS      AR007264      18 bp      DNA      linear      PAT 04-DEC-1998
DEFINITION Sequence 7 from patent US 5750376.
ACCESSION AR007264
VERSION AR007264.1 GI:3966748
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

```

```

REFERENCE 1 (bases 1 to 18)
AUTHORS Weiss S., Reynolds B., Hamman, J.P. and Baetge, E. Edward.
TITLE In vitro growth and proliferation of genetically modified
JOURNAL Patent: US 5750376-A 7 12-MAY-1998;
FEATURES Location/Qualifiers
    source 1..18
BASE COUNT 3 a 8 c 2 t
    Query Match 0.8%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTGCTGCTGGC 165
    ||||| ||||| ||||| |||||
Db 18 CGAGGTGATGCGCTGGC 1

RESULT 363
LOCUS AR007265 18 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 8 from patent US 5750376.
ACCESSION AR007265
VERSION AR007265.1 GI:3966749
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Weiss S., Reynolds B., Hamman, J.P. and Baetge, E. Edward.
TITLE In vitro growth and proliferation of genetically modified
JOURNAL Patent: US 5750376-A 8 12-MAY-1998;
FEATURES Location/Qualifiers
    source 1..18
BASE COUNT 2 a 5 c 8 g 3 t
    Query Match 0.8%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTGCTGCTGGC 165
    ||||| ||||| ||||| |||||
Db 1 CGAGGTGATGCGCTGGC 18

RESULT 364
LOCUS AR034870 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5869642.
ACCESSION AR034870
VERSION AR034870.1 GI:5950475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sakamoto, K.
TITLE Detection of the genus pectinatus
JOURNAL Patent: US 5869642-A 1 09-FEB-1999;
FEATURES Location/Qualifiers
    source 1..18
BASE COUNT 5 a 4 c 7 g 2 t
    Query Match 0.8%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 436 CAGGCTGATGACTCAGAG 453
    ||||| ||||| ||||| |||||

```

```

Db 1 CAGGCGGATGACTAAGCG 18

RESULT 365
LOCUS AR034880/1 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5869642.
ACCESSION AR034880
VERSION AR034880.1 GI:5950485
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sakamoto, K.
TITLE Detection of the genus pectinatus
JOURNAL Patent: US 5869642-A 11 09-FEB-1999;
FEATURES Location/Qualifiers
    source 1..18
BASE COUNT 2 a 7 c 4 g 5 t
    Query Match 0.8%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 436 CAGGCTGATGACTCAGAG 453
    ||||| ||||| ||||| |||||
Db 18 CAGGCGGATGACTAAGCG 1

RESULT 366
LOCUS AR034902/1 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 24 from patent US 5869643.
ACCESSION AR034902
VERSION AR034902.1 GI:5950507
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelet, F. and Kumarev, V.
TITLE Process for preparing polynucleotides on a solid support in a
JOURNAL Patent: US 5869643-A 24 09-FEB-1999;
FEATURES Location/Qualifiers
    source 1..18
BASE COUNT 0 a 18 c 0 g 0 t
    Query Match 0.8%; Score 13.2; DB 1; Length 18;
    Best Local Similarity 83.3%; Pred. No. 5.2e+02;
    Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1545 GGGGGCGCGGGGAGGGG 1562
    ||||| ||||| ||||| |||||
Db 18 GGGGGCGGGGGGGGGGGG 1

RESULT 367
LOCUS AR049396 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5824515.
ACCESSION AR049396
VERSION AR049396.1 GI:6005435
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hill, A. Vivian. Sinton.
TITLE Process for amplifying nucleic acid

```



```

JOURNAL Patent: US 5824515-A 11 20-OCT-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 6 a 6 c 5 g 1 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 673 CTACGAGTCCAGGCACA 690
Db 1 CTGCAAGGCCAGGCACA 18

RESULT 368
AR067397/c
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 745 from patent US 5851760.
ACCESSION AR067397
VERSION AR067397.1 GI:5998619
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Evans,G.A. and Smith,M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 745 22-DEC-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 2 a 7 c 4 g 5 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 CAGCGAGGCGAGGCGCA 28
Db 18 CAGCGAGTCAGTGAGCGCA 1

RESULT 369
AR067989/c
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5851832.
ACCESSION AR067989
VERSION AR067989.1 GI:5999211
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
TITLE In vitro growth and proliferation of multipotent neural stem cells
JOURNAL Patent: US 5851832-A 7 22-DEC-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 3 a 8 c 5 g 2 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTCTGCTGGC 165
Db 18 CGAGGTGATCCGCTGGC 1

RESULT 370
AR067990
LOCUS 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 8 from patent US 5851832.
ACCESSION AR067990
VERSION AR067990.1 GI:5999212
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Weiss,S., Reynolds,B., Hammang,J.P. and Baetge,E.Edward.
TITLE In vitro growth and proliferation of multipotent neural stem cells
JOURNAL Patent: US 5851832-A 8 22-DEC-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 2 a 5 c 8 g 3 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTCTGCTGGC 165
Db 1 CGAGGTGATCCGCTGGC 18

RESULT 371
AR069478
LOCUS 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 15 from patent US 5891666.
ACCESSION AR069478
VERSION AR069478.1 GI:7220366
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Matsuyama,T. and Grossman,A.
TITLE Genes encoding LSIRF polypeptides
JOURNAL Patent: US 5891666-A 15 06-APR-1999;
FEATURES Location/Qualifiers
source
BASE COUNT 7 a 2 c 6 g 3 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 502 GCCAGGAGTGAACTGCG 519
Db 1 GCTAGAGTGAACTGAG 18

RESULT 372
AR071801
LOCUS 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 30 from patent US 5912147.
ACCESSION AR071801
VERSION AR071801.1 GI:7222689
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Stoler,D., Basik,M. and Anderson,G.
TITLE Rapid means of quantitating genomic instability
JOURNAL Patent: US 5912147-A 30 15-JUN-1999;
FEATURES Location/Qualifiers
source
BASE COUNT 1. .18
/organism="unknown"

```

BASE COUNT 8 a 10 c 0 g 0 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 72 CACACGACACACCGCC 89
|||||
Db 1 CACACACACACACACC 18

RESULT 373
AR084251/c
LOCUS AR084251 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 7 from patent US 5980885.
ACCESSION AR084251
VERSION AR084251.1 GI:10011022
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Weiss, S. and Reynolds, B.
TITLE Growth factor-induced proliferation of neural precursor cells in vivo
JOURNAL Patent: US 5980885-A 7 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 3 a 8 c 5 g 2 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGC 165
|||||
Db 18 CGAGGTGATCGCTGCTGC 1

RESULT 374
AR084252
LOCUS AR084252 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 8 from patent US 5980885.
ACCESSION AR084252
VERSION AR084252.1 GI:10011023
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Weiss, S. and Reynolds, B.
TITLE Growth factor-induced proliferation of neural precursor cells in vivo
JOURNAL Patent: US 5980885-A 8 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 2 a 5 c 8 g 3 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGC 165
|||||
Db 1 CGAGGTGATCGCTGCTGC 18

RESULT 375
AR085578
LOCUS AR085578 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 14 from patent US 5981732.

BASE COUNT 4 a 6 c 8 g 0 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 603 CTGACCGCGACCGCAGCA 620
|||||
Db 1 CGGACCGCGACCGCAGCA 18

RESULT 376
AR096650/c
LOCUS AR096650 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 34 from patent US 6008048.
ACCESSION AR096650
VERSION AR096650.1 GI:10025636
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia, B.P. and Cowse, L.M.
TITLE Antisense inhibition of EGR-1 expression
JOURNAL Patent: US 6008048-A 34 28-DEC-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 2 a 5 c 8 g 3 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1194 TCACGCGCCGACGACCA 1211
|||||
Db 18 TCCGCGCCGACGACCA 1

RESULT 377
AR097623/c
LOCUS AR097623 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6071889.
ACCESSION AR097623
VERSION AR097623.1 GI:12806353
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Weiss, S., Reynolds, B., Hamang, J.P. and Baetge, E. Edward.
TITLE In vivo genetic modification of growth factor-responsive neural precursor cells
JOURNAL Patent: US 6071889-A 7 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

BASE COUNT 3 a 8 c 5 g 2 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGGC 165
|||||
Db 18 CGAGGTGATGCGCTGGC 1

RESULT 378
LOCUS AR097624 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6071889.
ACCESSION AR097624
VERSION AR097624.1 GI:12806354
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Weis, S., Reynolds, B., Hammang, J.P. and Baetge, E. Edward.
TITLE In vivo genetic modification of growth factor-responsive neural precursor cells
JOURNAL Patent: US 6071889-A 8 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 2 a 5 c 8 g 3 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGGC 165
|||||
Db 1 CGAGGTGATGCGCTGGC 18

RESULT 379
LOCUS AR098789 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 44 from patent US 6077672.
ACCESSION AR098789
VERSION AR098789.1 GI:12808555
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia, B.P. and Cowse, L.M.
TITLE Antisense modulation of TRADD expression
JOURNAL Patent: US 6077672-A 44 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 1 a 6 c 9 g 2 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGGCGCGCGGCA 1385
|||||
Db 1 GCGGCGCGCGCGGCTTCA 18

RESULT 380
LOCUS AR153937/c 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6238670.
ACCESSION AR153937
VERSION AR153937.1 GI:15121990
KEYWORDS
SOURCE

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Fearon, D.T. and Dempsey, P.W.
TITLE Compositions and methods employing a ligand for CD21 or CD19 for modulating the immune response to an antigen
JOURNAL Patent: US 6238670-A 11 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 3 c 5 g 5 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 124 CTCGGAAGTCATCAGTTC 141
|||||
Db 18 CTCGAAGTCTTCAGATC 1

RESULT 381
LOCUS AR162795 18 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 15 from patent US 6258935.
ACCESSION AR162795
VERSION AR162795.1 GI:16230136
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Matsuyama, T., Grossman, A. and Richardson, C. Donald.
TITLE LSIRF polypeptides
JOURNAL Patent: US 6258935-A 15 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 7 a 2 c 6 g 3 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 502 GCCAGGAGTGAAGTGGG 519
|||||
Db 1 GCTAGAAGTGAAGTGGAG 18

RESULT 382
LOCUS AR165009 18 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 10 from patent US 6274348.
ACCESSION AR165009
VERSION AR165009.1 GI:16238329
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Grinna, L.
TITLE Methods for the preparation of positively charged proteins
JOURNAL Patent: US 6274348-A 10 14-AUG-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 3 a 8 c 4 g 3 t
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 GCGCCTGCTGCTCACC 954

Binding assay using binding agents with tail groups

BASE COUNT	2 a	5 c	8 g	3 t
Query Match	0.8%;	Score 13.2;	DB 1;	Length 18;
Best Local Similarity	83.3%;	Pred. No. 5.2e+02;		
Matches	15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	148	CGAGATGCTGCTGCTGCC	165	
Db	1	CGAGGTGATGCCGCTGCC	18	
RESULT 391				
AR262417/c				
LOCUS	AR262417	18 bp	DNA	linear
DEFINITION	Sequence 42 from patent US 6323185.			
ACCESSION	AR262417			
VERSION	AR262417.1	GI:28073848		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 18)			
AUTHORS	Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O. and Hogan,M.E.			
TITLE	Anti-viral guanosine-rich oligonucleotides and method of treating HIV			
JOURNAL	Patent: US 6323185-A 42 27-NOV-2001;			
FEATURES	Location/Qualifiers			
source	1..18			
BASE COUNT	0 a	18 c	0 g	0 t
Query Match	0.8%;	Score 13.2;	DB 1;	Length 18;
Best Local Similarity	83.3%;	Pred. No. 5.2e+02;		
Matches	15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	1545	GGGGGGCCGGGGAGGGG	1562	
Db	18	GGGGGGGGGGGGGGGGGG	1	
RESULT 392				
AR262418/c				
LOCUS	AR262418	18 bp	DNA	linear
DEFINITION	Sequence 43 from patent US 6323185.			
ACCESSION	AR262418			
VERSION	AR262418.1	GI:28073849		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 18)			
AUTHORS	Rando,R.F., Fennwald,S., Zendeui,J.G., Ojwang,J.O. and Hogan,M.E.			
TITLE	Anti-viral guanosine-rich oligonucleotides and method of treating HIV			
JOURNAL	Patent: US 6323185-A 43 27-NOV-2001;			
FEATURES	Location/Qualifiers			
source	1..18			
BASE COUNT	0 a	18 c	0 g	0 t
Query Match	0.8%;	Score 13.2;	DB 1;	Length 18;
Best Local Similarity	83.3%;	Pred. No. 5.2e+02;		
Matches	15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	1545	GGGGGGCCGGGGAGGGG	1562	
Db	18	GGGGGGGGGGGGGGGGGG	1	
RESULT 393				
AR262417/c				
LOCUS	AR262417	18 bp	mRNA	linear
DEFINITION	Sequence 7 from patent US 6497872.			
ACCESSION	AR262417			
VERSION	AR262417.1	GI:28073848		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 18)			
AUTHORS	Weiss,S. and Reynolds,B.			
TITLE	Multipotent neural stem cell cDNA libraries			
JOURNAL	Patent: US 6399369-A 8 04-JUN-2002;			
FEATURES	Location/Qualifiers			
source	1..18			
BASE COUNT	3 a	8 c	5 g	2 t
Query Match	0.8%;	Score 13.2;	DB 1;	Length 18;
Best Local Similarity	83.3%;	Pred. No. 5.2e+02;		
Matches	15;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
QY	148	CGAGATGCTGCTGCTGCC	165	
Db	18	CGAGGTGATGCCGCTGCC	1	
RESULT 390				
AR211764				
LOCUS	AR211764	18 bp	DNA	linear
DEFINITION	Sequence 8 from patent US 6399369.			
ACCESSION	AR211764			
VERSION	AR211764.1	GI:21515173		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 18)			
AUTHORS	Weiss,S. and Reynolds,B.			
TITLE	Multipotent neural stem cell cDNA libraries			
JOURNAL	Patent: US 6399369-A 8 04-JUN-2002;			
FEATURES	Location/Qualifiers			
source	1..18			
BASE COUNT	7 a	2 c	6 g	3 t
Query Match	0.8%;	Score 13.2;	DB 1;	Length 18;

[illegible]

[illegible]

```

ORGANISM    synthetic construct
REFERENCE    1
AUTHORS      Brower,A., Brow,M.A., Cracauer,R.F., Fors,L., Granske,R., de arruda
             Indig,M., Kurensky,D., Luedtke,C., Lukowiak,A.A., Lyamichev,V.,
             Neri,B.P., Reimer,N.D., Roeven,R.T., Skrzypczynski,Z., Ziarno,W.A.,
             Comerford,J., Stump,S. and Viegut,D.D.
TITLE        Systems and method for detection assay production and sale
JOURNAL      Patent: WO 0244994-A 634 06-JUN-2002;
             THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES     source
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
BASE COUNT   4 a 5 c 7 g 2 t
Query Match  0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 760 CACGGTGACCTGGAGCA 777
Db 1 CAGGGTCCAGCTGGAGCA 18

RESULT 403
LOCUS      AX718621 18 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 185 from Patent WO02103043.
ACCESSION  AX718621
VERSION     AX718621.1 GI:29891187
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1
AUTHORS      Beifohr,C. and Snaird,J.
TITLE        Method for the specific fast detection of bacteria which is harmful
             to beer
JOURNAL      Patent: WO 02103043-A 185 27-DEC-2002;
             Vermicon AG (DE)
FEATURES     source
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
             /note="Oligonukleotid"
BASE COUNT   1 a 4 c 11 g 2 t
Query Match  0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1366 CCGCGGGGCGCGCGGG 1383
Db 1 CAGCGGTGGCGGTGGCGG 18

RESULT 404
LOCUS      B0089302 18 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION  B0089302
VERSION     B0089302.1 GI:22634912
KEYWORDS   JP 2001321190-A/1546.
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 18)
AUTHORS      Soeda,E.
TITLE        A method of arraying genome clone
JOURNAL      Patent: JP 2001321190-A 1546 20-NOV-2001;

THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUENKAISHA
GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/1546
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EII CHI SOEDA
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA PH Key
FT source
FT 1..18
/organism="Artificial Sequence".
FEATURES     source
             1..18
             Location/Qualifiers
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
BASE COUNT   6 a 5 c 6 g 1 t
Query Match  0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1517 GCGATGGCGTCAAGTCC 1534
Db 1 GCGATGGCAGACAAGACC 18

RESULT 405
LOCUS      BD104066/c 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION  BD104066
VERSION     BD104066.1 GI:22649640
KEYWORDS   WO 0192572-A/170.
SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE    1 (bases 1 to 18)
AUTHORS      Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
             Nishida,M.
TITLE        Kit and method for determining HLA type
JOURNAL      Patent: WO 0192572-A 170 06-DEC-2001;
             NISSHINO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
             KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,NICHIO
             NISHIDA
COMMENT      OS Artificial Sequence
             PN WO 0192572-A/170
             PD 06-DEC-2001
             PF 01-JUN-2001 WO 2001JP004662
             PR 01-JUN-2000 JP 00P 164798
             PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
             MATSUMURA,
             SHOGO MORIYA,MICHIO NISHIDA
             PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
             CC Description of Artificial Sequence:capture
             FH Key
             FT source
             1..18
             Location/Qualifiers
             1..18
             /organism="Artificial Sequence".
FEATURES     source
             1..18
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"
BASE COUNT   2 a 4 c 8 g 4 t
Query Match  0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1498 CGAGGCCCTGCACCGCT 1515

```


DEFINITION Primer for amplifying Epstein-Barr virus and cytomegalovirus.
 ACCESSION E09963
 VERSION E09963.1 GI:22026587
 KEYWORDS JP 1995250899-A/9.
 SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Yamanishi, K., Mukai, T., Aono, T., Kondo, M. and Takarada, Y.
 TITLE METHOD FOR DISCRIMINATORY DETECTION OF HUMAN HERPES VIRUS AND REAGENT THEREFOR
 JOURNAL Patent: JP 1995250699-A 9 03-OCT-1995;
 COMMENT TOYOBO CO LTD
 OS None
 OC Artificial sequences.
 PN JP 1995250699-A/9
 PD 03-OCT-1995
 PP 11-MAR-1994 JP 1994041101
 PI YAMANISHI KOICHI, MUKAI TORU, AONO TOSHIYA, KONDO MOTOHIRO, PI TAKARADA YUTAKA
 PC C12Q1/68.C12N15/09.C12Q1/70;
 CC strandedness: Single;
 CC topology: Linear;
 CC hypothetical: No;
 PH Key Location/Qualifiers
 FT source 1..18
 FT Location/Qualifiers
 FT /organism='Artificial sequences'.
 FEATURES source 1..18
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 BASE COUNT 4 a 6 c 4 g 4 t
 Query Match 0.8%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 716 AACTCGTGGCGGCCAAA 733
 Db 18 ACCTGGTGGTGGCCAAA 1

RESULT 410
 I12014
 LOCUS I12014 18 bp DNA linear PAT 26-JUL-1995
 DEFINITION Sequence 6 from Patent US 5418150.
 ACCESSION I12014
 VERSION I12014.1 GI:909455
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Topal, M.D. and Conrad, M.J.
 TITLE Method of cleaving DNA
 JOURNAL Patent: US 5418150-A 6 23-MAY-1995;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 BASE COUNT 0 a 5 c 10 g 3 t
 Query Match 0.8%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 641 CTGGCGGTGGAGCCGCC 658
 Db 1 CTGGTGGTGGCGCCGCC 18

RESULT 411
 I12014
 LOCUS I12014 18 bp DNA linear PAT 26-JUL-1995
 DEFINITION Sequence 6 from Patent US 5418150.
 ACCESSION I12014
 VERSION I12014.1 GI:909455
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Topal, M.D. and Conrad, M.J.
 TITLE Method of cleaving DNA
 JOURNAL Patent: US 5418150-A 6 23-MAY-1995;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 BASE COUNT 0 a 5 c 10 g 3 t
 Query Match 0.8%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 641 CTGGCGGTGGAGCCGCC 658
 Db 1 CTGGTGGTGGCGCCGCC 18

I13566
 LOCUS I13566 18 bp DNA linear PAT 26-SEP-1995
 DEFINITION Sequence 10 from patent US 5439807.
 ACCESSION I13566
 VERSION I13566.1 GI:996633
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Grinna, L.S.
 TITLE Methods for the preparation of endotoxin-binding proteins
 JOURNAL Patent: US 5439807-A 10 08-AUG-1995;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 BASE COUNT 3 a 8 c 4 g 3 t
 Query Match 0.8%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 937 GCGCTGCTGCTCAGCGC 954
 Db 1 GCACCTGCTACTGACGC 18

RESULT 412
 I21930
 LOCUS I21930 18 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 11 from patent US 5525492.
 ACCESSION I21930
 VERSION I21930.1 GI:1602284
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Hill, A.V.S.
 TITLE Process for amplifying HLA sequences
 JOURNAL Patent: US 5525492-A 11 11-JUN-1996;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 BASE COUNT 6 a 6 c 5 g 1 t
 Query Match 0.8%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 673 CTACGAGTCCAGGCACA 690
 Db 1 CTGCAAGGCCAAGGCACA 18

RESULT 413
 I27810/c
 LOCUS I27810 18 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 42 from patent US 5567604.
 ACCESSION I27810
 VERSION I27810.1 GI:1818586
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Rando, R.F., Pennewald, S., Zendejui, J.G. and Ojwang, J.O.
 TITLE Anti-viral guanosine-rich oligonucleotides
 JOURNAL Patent: US 5567604-A 42 22-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..18
 /organism="unknown"
 BASE COUNT 0 a 18 c 0 g 0 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCCCGGGAGGGG 1562
|||||
Db 18 GGGGGGGGGGGGGGGG 1

RESULT 414
I27811/c 127811 18 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 43 from patent US 5567604.
DEFINITION I27811
ACCESSION I27811
VERSION I27811.1 GI:1818587
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Rando,R.F., Fennewald,S., Zendequi,J.G. and Ojwang,J.O.
TITLE Anti-viral guanosine-rich oligonucleotides
JOURNAL Patent: US 5567604-A 43 22-OCT-1996;
FEATURES Location/Qualifiers
source
BASE COUNT 0 a 18 c 0 g 0 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCCCGGGAGGGG 1562
|||||
Db 18 GGGGGGGGGGGGGGGG 1

RESULT 415
I30029 130029 18 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 5 from patent US 5578716.
DEFINITION I30029
ACCESSION I30029
VERSION I30029.1 GI:1820820
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Szyf,M. and von Hofe,B.
TITLE DNA methyltransferase antisense oligonucleotides
JOURNAL Patent: US 5578716-A 5 26-NOV-1996;
FEATURES Location/Qualifiers
source
BASE COUNT 3 a 2 c 11 g 2 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 212 GGAATGGCGTGGGACCG 229
|||||
Db 1 GGACTGGGTGAGGACCG 18

RESULT 416
I34952 134952 18 bp DNA linear PAT 13-MAY-1997
LOCUS Sequence 38 from patent US 5599704.
DEFINITION I34952
ACCESSION I34952
VERSION I34952.1 GI:2087920
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE ErBB2/neu targeted ribozymes
JOURNAL Patent: US 5599704-A 38 04-FEB-1997;
FEATURES Location/Qualifiers
source
BASE COUNT 3 a 6 c 7 g 2 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1503 CCCTGCACCCCTGGGCA 1520
|||||
Db 1 CCCTGCAAGGCTGGGCA 18

RESULT 417
150676 150676 18 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 10 from patent US 5643570.
DEFINITION I50676
ACCESSION I50676
VERSION I50676.1 GI:2472379
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Theofan,G., Grinna,L.S. and Horwitz,A.
TITLE BPI-immunoglobulin fusion proteins
JOURNAL Patent: US 5643570-A 10 01-JUL-1997;
FEATURES Location/Qualifiers
source
BASE COUNT 3 a 8 c 4 g 3 t

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 GCGCTCTCTCTCACC GC 954
|||||
Db 1 GCACCTGTACTGACGC 18

RESULT 418
AR024073 AR024073 13 bp DNA linear PAT 05-DEC-1998
LOCUS Sequence 23 from patent US 5795778.
DEFINITION AR024073
ACCESSION AR024073
VERSION AR024073.1 GI:3977367
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 5795778-A 23 18-AUG-1998;
FEATURES Location/Qualifiers
source
BASE COUNT 1 a 6 c 5 g 1 t

Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1293 GCCTGGCGCACGC 1305

82712 PR

```

14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882885,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882888,14-MAY-1992 US 07/882821 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/935886,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
15-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC A61K39/135, A61K39/135, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61P1/16,
PC A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/69, PC
PC C12N15/09, C12R1/93, C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
C12R1/93)
CC
FH Key Location/Qualifiers
FT source 1. .13
FT Location/Qualifiers
FEATURES
source 1. .13
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
BASE COUNT 1 a 6 c 5 g 1 t
Query Match 0.8%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1293 GCGTGGCGACGC 1305
Db 1 GCGTGGCGACGC 13
RESULT 423
AX007863
LOCUS AX007863 15 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 405 from Patent WO9967428.
ACCESSION AX007863
VERSION AX007863.1 GI:9995560
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
VIRUSES; Retrovirdae.
REFERENCE
1 Stuyver, L.
AUTHORS Stuyver, L.
TITLE Method for detection of drug-selected mutations in the hiv protease
gene
JOURNAL
FEATURES
source 1. .15
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"
BASE COUNT 4 a 3 c 3 g 5 t
Query Match 0.8%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 440 CTGATGACTCAGA 452
Db 1 CTGATGACTCAGA 13

```

```

RESULT 424
AX007920
LOCUS AX007920 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 462 from Patent WO9967428.
ACCESSION AX007920
VERSION AX007920.1 GI:9995617
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
VIRUSES; Retrovirdae.
REFERENCE
1 Stuyver, L.
AUTHORS Stuyver, L.
TITLE Method for detection of drug-selected mutations in the hiv protease
gene
JOURNAL
FEATURES
source 1. .16
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"
BASE COUNT 6 a 3 c 3 g 4 t
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 440 CTGATGACTCAGA 452
Db 4 CTGATGACTCAGA 16
RESULT 425
AX007923
LOCUS AX007923 16 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 465 from Patent WO9967428.
ACCESSION AX007923
VERSION AX007923.1 GI:9995620
KEYWORDS
SOURCE Aids-associated retrovirus
ORGANISM Aids-associated retrovirus
VIRUSES; Retrovirdae.
REFERENCE
1 Stuyver, L.
AUTHORS Stuyver, L.
TITLE Method for detection of drug-selected mutations in the hiv protease
gene
JOURNAL
FEATURES
source 1. .16
/organism="Aids-associated retrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:11966"
BASE COUNT 4 a 3 c 4 g 5 t
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 440 CTGATGACTCAGA 452
Db 1 CTGATGACTCAGA 13
RESULT 426
AX139231
LOCUS AX139231 16 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 79 from Patent EP1076099.
ACCESSION AX139231
VERSION AX139231.1 GI:14274904
KEYWORDS

```

SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.

REFERENCE 1
AUTHORS Suzuki, Y., Nishida, M. and Takenishi, S.
TITLE Kit for diagnosis of tubercle bacilli
JOURNAL Patent: EP 1076099-A 79 14-FEB-2001;
NISSHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
(JP)

FEATURES source
1. .16
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"
/note="capture"
BASE COUNT 3 a 4 c 6 g 3 t
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 GGTGAAGGACCTG 805
|||||
Db 1 GGTGAAGGACCTG 13

RESULT 427
BD013515
LOCUS BD013515 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Diagnosis kit of tubercle bacillus.
ACCESSION BD013515
VERSION BD013515.1 GI:22553829
KEYWORDS JP 2001103981-A/79.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.

REFERENCE 1 (bases 1 to 16)
AUTHORS Suzuki, S., Nishida, M. and Takenishi, S.
TITLE Diagnosis kit of tubercle bacillus
JOURNAL Patent: JP 2001103981-A 79 17-APR-2001;
NISSHINBO IND INC.SYSTEM RESEARCH CO LTD
OS Mycobacterium tuberculosis
PN JP 2001103981-A/79
PD 17-APR-2001
PI 26-JUL-2000 JP 2000225985
PT SADAHIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/00, C12M1/00, C12Q1/68, C12R1:32), PC
(C12Q1/68, C12R1:325), (C12Q1/68, C12R1:33), C12N15/00, C12N15/00 CC
capture
FH Key Location/Qualifiers
FT source 1. .16
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"
BASE COUNT 3 a 4 c 6 g 3 t
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 GGTGAAGGACCTG 805
|||||
Db 1 GGTGAAGGACCTG 13

RESULT 428
BD013515
LOCUS BD013515 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Diagnosis kit of tubercle bacillus.
ACCESSION BD013515
VERSION BD013515.1 GI:22553829
KEYWORDS JP 2001103981-A/79.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.

REFERENCE 1 (bases 1 to 16)
AUTHORS Suzuki, S., Nishida, M. and Takenishi, S.
TITLE Diagnosis kit of tubercle bacillus
JOURNAL Patent: JP 2001103981-A 79 17-APR-2001;
NISSHINBO IND INC.SYSTEM RESEARCH CO LTD
OS Mycobacterium tuberculosis
PN JP 2001103981-A/79
PD 17-APR-2001
PI 26-JUL-2000 JP 2000225985
PT SADAHIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/00, C12M1/00, C12Q1/68, C12R1:32), PC
(C12Q1/68, C12R1:325), (C12Q1/68, C12R1:33), C12N15/00, C12N15/00 CC
capture
FH Key Location/Qualifiers
FT source 1. .16
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"
BASE COUNT 3 a 4 c 6 g 3 t
Query Match 0.8%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 793 GGTGAAGGACCTG 805
|||||
Db 1 GGTGAAGGACCTG 13

RESULT 429
AX215364
LOCUS AX215364 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 806 from Patent WO0159103.
ACCESSION AX215364
VERSION AX215364.1 GI:15525407
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., Meswigen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 806 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC.(US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES source
1. .17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 4 a 4 c 9 g 0 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1011 CGTCCTCGGCTC 1023
|||||
Db 17 CGTCCTCGGCTC 5

RESULT 430
AX215365
LOCUS AX215365 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 807 from Patent WO0159103.
ACCESSION AX215365
VERSION AX215365.1 GI:15525408
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 807 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 5 a 4 c 8 g 0 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1011 CGTCCTCGGGCTC 1023
|||||
Db 16 CGTCCTCGGGCTC 4
AX216111
Sequence 1553 from Patent WO0159103.
ACCESSION AX216111
VERSION AX216111.1 GI:15526154
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1553 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 4 a 4 c 9 g 0 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1011 CGTCCTCGGGCTC 1023
|||||
Db 15 CGTCCTCGGGCTC 3
AX216346
Sequence 1788 from Patent WO0159103.
ACCESSION AX216346
VERSION AX216346.1 GI:15526407
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 1788 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);

McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 1 a 8 c 8 g 0 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1373 GCGCGGGCGGCA 1385
|||||
Db 5 GCGCGGGCGGCA 17
AX216896
Sequence 2338 from Patent WO0159103.
ACCESSION AX216896
VERSION AX216896.1 GI:15526957
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2338 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 2 a 6 c 9 g 0 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1374 GCGCGGGCGGCA 1386
|||||
Db 1 GCGCGGGCGGCA 13
AX216909
Sequence 2351 from Patent WO0159103.
ACCESSION AX216909
VERSION AX216909.1 GI:15526970
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL Patent: WO 0159103-A 2351 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"

```
/db_xref="taxon:32630"
/notes="Nucleic Acid"
5 a 4 c 8 g 0 t
BASE COUNT
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1011 CGTCTCGGGCTC 1023
Db 13 CGTCTCGGGCTC 1
RESULT 435
AX532240/c
LOCUS AX532240 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1749 from Patent EP1239051.
ACCESSION AX532240
VERSION AX532240.1 GI:25256267
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1749 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
BASE COUNT 2 a 7 c 7 g 1 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 838 CCAGGCGGGCTG 850
Db 16 CCAGGCGGGCTG 4
RESULT 436
AX532241/c
LOCUS AX532241 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1750 from Patent EP1239051.
ACCESSION AX532241
VERSION AX532241.1 GI:25256269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1750 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
BASE COUNT 3 a 7 c 6 g 1 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 838 CCAGGCGGGCTG 850
Db 13 CCAGGCGGGCTG 1
RESULT 437
AX532242/c
LOCUS AX532242 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1751 from Patent EP1239051.
ACCESSION AX532242
VERSION AX532242.1 GI:25256270
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1751 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
BASE COUNT 3 a 7 c 6 g 1 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 838 CCAGGCGGGCTG 850
Db 14 CCAGGCGGGCTG 2
RESULT 438
AX532243/c
LOCUS AX532243 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1752 from Patent EP1239051.
ACCESSION AX532243
VERSION AX532243.1 GI:25256271
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1752 11-SEP-2002;
Aecomica, Inc. (US)
FEATURES
source
1..17
Location/Qualifiers
BASE COUNT 2 a 7 c 6 g 2 t
Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 838 CCAGGCGGGCTG 850
Db 13 CCAGGCGGGCTG 1
RESULT 439
AX724723
LOCUS AX724723 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2410 from Patent WO03025176.
ACCESSION AX724723
```



```

VERSION      AX724723.1  GI:30504066
KEYWORDS     Mus musculus (house mouse)
SOURCE       Mus musculus
ORGANISM     Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE    1
AUTHORS      Telerman, A., Amson, R. and Tuijinder, M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL      Patent: WO 03025177-A 2207 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     1. .17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              Location/Qualifiers
source       1. .17
BASE COUNT   3 a 5 c 7 g 2 t
              Query Match      0.8%; Score 13; DB 1; Length 17;
              Best Local Similarity 100.0%; Pred. No. 5.5e+02;
              Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           733 ATCGGAGGCTGC 745
Db           2 ATCGGAGGCTGC 14
              |||||
RESULT 440
LOCUS        AX735595 17 bp DNA linear PAT 08-MAY-2003
DEFINITION   Sequence 1185 from Patent WO03025177.
ACCESSION    AX735595
VERSION      AX735595.1 GI:30514872
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE    1
AUTHORS      Telerman, A., Amson, R. and Tuijinder, M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL      Patent: WO 03025177-A 1185 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     1. .17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              Location/Qualifiers
source       1. .17
BASE COUNT   1 a 6 c 5 g 5 t
              Query Match      0.8%; Score 13; DB 1; Length 17;
              Best Local Similarity 100.0%; Pred. No. 5.5e+02;
              Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           830 GCGGACGACGAG 842
Db           16 GCGGACGACGAG 4
              |||||
RESULT 441
LOCUS        AX736617 17 bp DNA linear PAT 08-MAY-2003
DEFINITION   Sequence 2207 from Patent WO03025177.
ACCESSION    AX736617
VERSION      AX736617.1 GI:30515905
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE    1
AUTHORS      Telerman, A., Amson, R. and Tuijinder, M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL      Patent: WO 03025177-A 2207 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     1. .17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              Location/Qualifiers
source       1. .17
BASE COUNT   5 a 3 c 4 g 5 t
              Query Match      0.8%; Score 13; DB 1; Length 17;
              Best Local Similarity 100.0%; Pred. No. 5.5e+02;
              Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           440 CTGATGACTCAGA 452
Db           4 CTGATGACTCAGA 16
              |||||
RESULT 442
LOCUS        AR085575 18 bp DNA linear PAT 01-SEP-2000
DEFINITION   Sequence 11 from patent US 5981732.
ACCESSION    AR085575
VERSION      AR085575.1 GI:10012342
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.

REFERENCE    1 (bases 1 to 18)
AUTHORS      Cowsett, L.M.
TITLE        Antisense modulation of G-alpha-13 expression
JOURNAL      Patent: US 5981732-A 11 09-NOV-1999;
              Location/Qualifiers
FEATURES     1. .18
              /organism="unknown"
              Location/Qualifiers
source       1. .18
BASE COUNT   1 a 10 c 4 g 3 t
              Query Match      0.8%; Score 13; DB 1; Length 18;
              Best Local Similarity 100.0%; Pred. No. 5.5e+02;
              Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1373 GCGCGCGCGCGCA 1385
Db           18 GCGCGCGCGCGCA 6
              |||||
RESULT 443
LOCUS        AR293763 18 bp DNA linear PAT 12-JUN-2003
DEFINITION   Sequence 5498 from patent US 6537751.
ACCESSION    AR293763
VERSION      AR293763.1 GI:31681047
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.

REFERENCE    1 (bases 1 to 18)
AUTHORS      Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE        Biallelic markers for use in constructing a high density
              disequilibrium map of the human genome
JOURNAL      Patent: US 6537751-A 5498 25-MAR-2003;
              Location/Qualifiers
FEATURES     1. .18
              /organism="unknown"
              Location/Qualifiers
source       1. .18
BASE COUNT   5 a 2 c 9 g 2 t
              Query Match      0.8%; Score 13; DB 1; Length 18;

```

Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1246	GGTCATCGAGGAG 1258			
Db	6	GGTCATCGAGGAG 18			
RESULT 444					
A01419					
LOCUS	A01419	Malaria parasitic epitope (T-cell).	31 bp	DNA	linear
DEFINITION	A01419				
ACCESSION	A01419				
VERSION	A01419.1	GI:344347			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1	(bases 1 to 31)			
AUTHORS					
JOURNAL					
FEATURES					
source					
Location/Qualifiers					
1..31		/organism="synthetic construct"			
/mol_type="genomic DNA"					
/db_xref="taxon:32630"					
BASE COUNT	0 a	20 c	10 g	0 t	1 others
Query Match		0.8%; Score 13; DB 1; Length 31;			
Best Local Similarity		65.5%; Pred. No. 5.7e+02;			
Matches	19; Conservative	0; Mismatches 10; Indels			0; Gaps 0;
QY	1412	GCGGAGCTCCGGTGCGGGGCCACC GC 1440			
Db	1	GCGGAGCTCCGGTGCGGGGCCACC GC 29			
RESULT 445					
A08144					
LOCUS	A08144		16 bp	DNA	linear
DEFINITION	A08144	Sequence 292 from Patent WO9833904.			PAT 22-JAN-2000
ACCESSION	A08144				
VERSION	A08144.1	GI:6736714			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1	(bases 1 to 16)			
AUTHORS		Brysch,W. and Schlingensiepen,K.			
TITLE		AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD			
JOURNAL		Patent: WO 9833904-A 292 06-AUG-1998;			
BIOSNOSTIK GES (DE); BRYSCH WOLFGANG (DE)					
FEATURES					
source					
Location/Qualifiers					
1..16		/organism="unidentified"			
/mol_type="genomic DNA"					
/db_xref="taxon:32644"					
BASE COUNT	0 a	3 c	12 g	1 t	
Query Match		0.8%; Score 12.8; DB 1; Length 16;			
Best Local Similarity		87.5%; Pred. No. 5.8e+02;			
Matches	14; Conservative	0; Mismatches 2; Indels			0; Gaps 0;
QY	1368	GCGGGCGCGCGCGG 1383			
Db	1	GCGGTGCGCGCGCGG 16			
RESULT 446					
A09111					
LOCUS	A09111		16 bp	DNA	linear
DEFINITION	A09111	Sequence 292 from Patent EP0856579.			PAT 22-JAN-2000
ACCESSION	A09111				
VERSION	A09111				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS					
TITLE					
JOURNAL					
BIOSNOSTIK GES (DE); BRYSCH WOLFGANG (DE)					
FEATURES					
source					
Location/Qualifiers					
1..16		/organism="unidentified"			
/mol_type="genomic DNA"					
/db_xref="taxon:32644"					
BASE COUNT	0 a	3 c	12 g	1 t	
Query Match		0.8%; Score 12.8; DB 1; Length 16;			
Best Local Similarity		87.5%; Pred. No. 5.8e+02;			
Matches	14; Conservative	0; Mismatches 2; Indels			0; Gaps 0;
QY	1368	GCGGGCGCGCGCGG 1383			
Db	1	GCGGTGCGCGCGCGG 16			
RESULT 447					
A0909040					
LOCUS	A0909040		16 bp	DNA	linear
DEFINITION	A0909040	Sequence 73 from Patent WO9963975.			PAT 06-SEP-2000
ACCESSION	A0909040				
VERSION	A0909040.1	GI:9996414			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS		Homo sapiens (human)			
TITLE					
JOURNAL					
BIOSNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)					
FEATURES					
source					
Location/Qualifiers					
1..16		/organism="Homo sapiens"			
/mol_type="genomic DNA"					
/db_xref="taxon:9606"					
BASE COUNT	0 a	3 c	13 g	0 t	
Query Match		0.8%; Score 12.8; DB 1; Length 16;			
Best Local Similarity		87.5%; Pred. No. 5.8e+02;			
Matches	14; Conservative				

```

JOURNAL Patent: WO 03031625-A 27 17-APR-2003;
Degussa AG (DE) ; Schwab, Helmut (AT)
FEATURES
  source
    1..16
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
    /note="Primer"
BASE COUNT      3 a      6 c      3 g      4 t
Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 481 CATCTCGGTGATGAAC 496
    ||||| ||||| |||||
Db 16 CATCTCGGTGAGGAAC 1

RESULT 449
BD065657
LOCUS          BD065657          16 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    An antisense oligonucleotide preparation method.
ACCESSION     BD065657
VERSION       BD065657.1 GI:22611260
KEYWORDS      JP 2001511000-A/292.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 16)
AUTHORS      Schlengensiepen,K.H. and Brysch,W.
TITLE         An antisense oligonucleotide preparation method
JOURNAL       Patent: JP 2001511000-A 292 07-AUG-2001;
              BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT       OS Unknown
              PN JP 2001511000-A/292
              PD 07-AUG-2001
              PF 30-JAN-1998 JP 1998532533
              PR 31-JAN-1997 EP 97101531.8
              PI KARL HERMANN SCHLENGENSIEPEN,WOLFGANG BRYSCH
              PC C12N15/11,C07H21/04,A61K31/70
              CC An antisense oligonucleotide preparation method FH Key
              Location/Qualifiers
              FT source
              FT 1..16
              /organism='Unknown'.
FEATURES
  source
    1..16
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
BASE COUNT      0 a      3 c      12 g      1 t
Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGCGGCGG 1383
    ||||| ||||| |||||
Db 1 GCGGTGGCGGCGGCGG 16

RESULT 450
BD088650
LOCUS          BD088650          16 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    A method of arraying genome clone.
ACCESSION     BD088650
VERSION       BD088650.1 GI:22634260
KEYWORDS      JP 2001321190-A/894.
SOURCE        synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE     1 (bases 1 to 16)
AUTHORS      Soeda,E.

TITLE         A method of arraying genome clone
JOURNAL       Patent: JP 2001321190-A 894 20-NOV-2001;
              THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
              GENOTECHS
COMMENT       OS Artificial Sequence
              PN JP 2001321190-A/894
              PD 20-NOV-2001
              PF 12-MAR-2001 JP 2001068285
              PI EIICHI SOEDA
              PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00.
              CC Description of Artificial Sequence:Synthetic DNA FH Key
              Location/Qualifiers
              FT source
              FT 1..16
              /organism='Artificial Sequence'.
FEATURES
  source
    1..16
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
BASE COUNT      3 a      7 c      3 g      3 t
Query Match      0.8%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 544 TGGCCCACTCAGAG 559
    ||||| ||||| |||||
Db 1 TGGCCCCCACTCATAG 16

RESULT 451
AB069179
LOCUS          AB069179          16 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION    Synthetic construct DNA, reverse primer for human STS sts-W37905 at
              1p36.
ACCESSION     AB069179
VERSION       AB069179.1 GI:15129983
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE     1
AUTHORS      Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
              Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
              Morohashi,A., Chira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
              and Soeda,E.
              A BAC-based STS-content map spanning a 35-Mb region of human
              chromosome 1p35-p36
              Genomics 74 (1), 55-70 (2001)
              21269192
              MEDLINE
              PUBMED
              11374902
REFERENCE     2 (bases 1 to 16)
AUTHORS      Horii,A.
TITLE         Direct Submission
JOURNAL       Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
              Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
              Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
              Tel:81-22-717-8042, Fax:81-22-717-8047)
              Location/Qualifiers
              FT source
              FT 1..16
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
              1..16
              /notes="reverse primer for human STS sts-W37905 at 1p36
              sts-W37905 obtained from clones B272H12, B51C6, B288N8,
              B191P23, B191O23, B43N9, B43P7, B304H10, Human BAC
              library RPCI-11"
BASE COUNT      3 a      7 c      3 g      3 t
Query Match      0.8%; Score 12.8; DB 1; Length 16;

```

```

Best Local Similarity 87.5%; Pred. No. 5.8e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 544 TGGCCACCACTCAG 559
Db 1 TGGCCCCCACTCATAG 16

RESULT 452
A26883/c
LOCUS 17 bp DNA linear PAT 24-JUL-1996
DEFINITION Primer no.2.
ACCESSION A26883
VERSION A26883.1 GI:1566920
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Macadam,A.J., Minor,P.D., Stone,D.M. and Almond,J.W.
TITLE Attenuated poliovirus and vaccines thereof
JOURNAL Patent: EP 0508783-A 2 14-OCT-1992;
BRITISH TECHNOLOGY GROUP LTD
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
4 t
BASE COUNT 6 a 4 c 3 g 4 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 468 TGAACGCTTGGGCAT 483
Db 17 TGAATGCTATGGCAT 2

RESULT 453
A27314/c
LOCUS 17 bp DNA linear PAT 26-SEP-1995
DEFINITION Synthetic betaGlc linker 2.
ACCESSION A27314
VERSION A27314.1 GI:1248430
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Seemann,G., Bosslet,K., Czech,J., Kolar,C., Hoffmann,D. and Sedlacek,H.H.
TITLE Fusion proteins with monoclonal antibody, Linker and beta Glucuronidase for prodrug activation; preparation and use thereof
JOURNAL Patent: EP 0501215-A 6 02-SEP-1992;
BEHRINGERWERKE Aktiengesellschaft
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
5 g 1 t
BASE COUNT 1 a 10 c 5 g 1 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 CGCGGGCGCGCGCG 1383
Db 16 GCAGCGGGCGGGCGG 1

RESULT 454
A89622
LOCUS 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 6 from Patent WO9833901.
ACCESSION A89622
VERSION A89622.1 GI:6738192
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Collins,J. and Roettgen,P.
TITLE GENERATION OF DIVERSITY IN COMBINATORIAL LIBRARIES
JOURNAL Patent: WO 9833901-A 6 06-AUG-1998;
COLLINS JOHN (DE); ROETTGEN PETER (DE)
FEATURES
source
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
3 a 4 c 7 g 3 t
BASE COUNT 3 a 4 c 7 g 3 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAGCA 777
Db 2 CGGGTACCTGGAGCA 17

RESULT 455
AR039947
LOCUS 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 795 from patent US 5807743.
ACCESSION AR039947
VERSION AR039947.1 GI:5959310
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 795 15-SEP-1998;
FEATURES
source
1..17
/organism="unknown"
1 a 5 c 7 g 4 t
BASE COUNT 1 a 5 c 7 g 4 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1016 TCGGGCTCGGGCGCG 1031
Db 2 TCGGGTTCGGAGCCGC 17

RESULT 456
AR053045/c
LOCUS 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5834181.
ACCESSION AR053045
VERSION AR053045.1 GI:5977907
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
JOURNAL Patent: US 5834181-A 15 10-NOV-1998;

```

FEATURES source Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 3 a 5 c 7 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 CTGGGCATGGCGGTCA 1529
Db 17 CTGGGCATGGCGGTCA 2
RESULT 457
LOCUS AR053062 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 32 from patent US 5834181.
ACCESSION AR053062
VERSION AR053062.1 GI:5977924
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
JOURNAL Patent: US 5834181-A 32 10-NOV-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 3 a 5 c 6 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 CTGGGCATGGCGGTCA 1529
Db 17 CTGCACATGGCGGTCA 2
RESULT 458
LOCUS AR065006 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5849483.
ACCESSION AR065006
VERSION AR065006.1 GI:5995222
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
JOURNAL Patent: US 5849483-A 15 15-DEC-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 3 a 5 c 7 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 CTGGGCATGGCGGTCA 1529
Db 17 CTGCACATGGCGGTCA 2
RESULT 459
LOCUS AR065023 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 32 from patent US 5849483.
ACCESSION AR065023
VERSION AR065023.1 GI:5995239
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
JOURNAL Patent: US 5849483-A 32 15-DEC-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 3 a 5 c 6 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 CTGGGCATGGCGGTCA 1529
Db 17 CTGCACATGGCGGTCA 2
RESULT 460
LOCUS AR159843 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 54 from patent US 6251632.
ACCESSION AR159843
VERSION AR159843.1 GI:16222661
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Lillicrap,D.; Cameron,C.; Nottley,C., Hoyle Horrocks,L.Suzanne. and Hough,C.
TITLE Canine factor VIII gene, protein and methods of use
JOURNAL Patent: US 6251632-A 54 26-JUN-2001;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 1 a 10 c 4 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1287 CCTTCGCGCTGGCGCA 1302
Db 1 CCTTCGCGCGCGCA 16
RESULT 461
LOCUS AR176117 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6310191.
ACCESSION AR176117
VERSION AR176117.1 GI:17917416
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Collins,J. and Rottgen,P.
TITLE Generation of diversity in combinatorial libraries
JOURNAL Patent: US 6310191-A 6 30-OCT-2001;
FEATURES Location/Qualifiers
1..17
source

AR065023/c
LOCUS AR065023 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 32 from patent US 5849483.
ACCESSION AR065023
VERSION AR065023.1 GI:5995239
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High throughput screening method for sequences or genetic alterations in nucleic acids
JOURNAL Patent: US 5849483-A 32 15-DEC-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 3 a 5 c 6 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1514 CTGGGCATGGCGGTCA 1529
Db 17 CTGCACATGGCGGTCA 2
RESULT 460
LOCUS AR159843 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 54 from patent US 6251632.
ACCESSION AR159843
VERSION AR159843.1 GI:16222661
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Lillicrap,D.; Cameron,C.; Nottley,C., Hoyle Horrocks,L.Suzanne. and Hough,C.
TITLE Canine factor VIII gene, protein and methods of use
JOURNAL Patent: US 6251632-A 54 26-JUN-2001;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 1 a 10 c 4 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1287 CCTTCGCGCTGGCGCA 1302
Db 1 CCTTCGCGCGCGCA 16
RESULT 461
LOCUS AR176117 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 6 from patent US 6310191.
ACCESSION AR176117
VERSION AR176117.1 GI:17917416
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Collins,J. and Rottgen,P.
TITLE Generation of diversity in combinatorial libraries
JOURNAL Patent: US 6310191-A 6 30-OCT-2001;
FEATURES Location/Qualifiers
1..17
source

```

BASE COUNT      3 a      4 c      7 g      3 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAGCA 777
|||||
Db 2 CGGGTACTGGAGCA 17
|||||

RESULT 462
ARI85974/c
LOCUS      ARI85974      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 1462 from patent US 6346398.
ACCESSION  ARI85974
VERSION     ARI85974.1 GI:20231939
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 1462 12-FEB-2002;
FEATURES     Location/Qualifiers
              source
              1. .17
              /organism="unknown"

BASE COUNT      1 a      6 c      8 g      2 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 805 GAGCCCGGAGCCGC 820
|||||
Db 17 GAGCCCGGAGCCGC 2
|||||

RESULT 463
ARI86641/c
LOCUS      ARI86641      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 2129 from patent US 6346398.
ACCESSION  ARI86641
VERSION     ARI86641.1 GI:20232606
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 2129 12-FEB-2002;
FEATURES     Location/Qualifiers
              source
              1. .17
              /organism="unknown"

BASE COUNT      0 a      10 c      4 g      3 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 942 TGCTGCTCCAGCCGC 957
|||||
Db 2 TGCTGCTCCAGCCGC 17
|||||

RESULT 464
ARI88483/c
LOCUS      ARI88483      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 3971 from patent US 6346398.
ACCESSION  ARI88483.1 GI:20234448
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 3971 12-FEB-2002;
FEATURES     Location/Qualifiers
              source
              1. .17
              /organism="unknown"

BASE COUNT      3 a      4 c      5 g      5 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1447 CCACTGGTACTGCGAC 1462
|||||
Db 1 CCACTGGTATTGGCAG 16
|||||

RESULT 465
ARI92381/c
LOCUS      ARI92381      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 7869 from patent US 6346398.
ACCESSION  ARI92381
VERSION     ARI92381.1 GI:20238346
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 7869 12-FEB-2002;
FEATURES     Location/Qualifiers
              source
              1. .17
              /organism="unknown"

BASE COUNT      1 a      8 c      2 g      6 t
Query Match      0.8%; Score 12.6; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 499 GTGGCCAGGAGTGAAA 514
|||||
Db 17 GAGCCAGGAGTGAGA 2
|||||

RESULT 466
ARI224417/c
LOCUS      ARI224417      17 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6440726.
ACCESSION  ARI224417
VERSION     ARI224417.1 GI:23333196
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Resnick,N.
TITLE        Expression vectors comprising multiple shear stress responsive
              elements (SSRE) and methods of use for treating disorders related
              to vasculogenesis and/or angiogenesis in a shear stress environment
JOURNAL      Patent: US 6440726-A 1 27-AUG-2002;
FEATURES     Location/Qualifiers
              source
              1. .17
              /organism="unknown"

```

```

BASE COUNT      0 a      2 c      15 g      0 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1547 GGGGCGGGGGGAGGGG 1562
|||||
Db 1 GGGGCGGGGGGCGGGG 16

RESULT 467
AR242714/c
LOCUS      AR242714
DEFINITION Sequence 2 from patent US 6475486.
ACCESSION AR242714
VERSION    AR242714.1 GI:27289218
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS    Kolar,C., Czech,J., Bosslet,K., Seemann,G., Sedlacek,H.-H. and Hoffman,D.
TITLE      Glycosyl-etosipside prodrugs, a process for preparation thereof and the use thereof in combination with functionalized tumor-specific enzyme conjugates
JOURNAL    Patent: US 6475486-A 2 05-NOV-2002;
FEATURES   Location/Qualifiers
source     1..17
            /organism="unknown"
BASE COUNT 1 a      10 c      5 g      1 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGGCGGGCGG 1383
|||||
Db 16 GCAGCGGGCGGGCGGG 1

RESULT 468
AR286220/c
LOCUS      AR286220
DEFINITION Sequence 592 from patent US 6528640.
ACCESSION AR286220
VERSION    AR286220.1 GI:29723816
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS    Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE      Synthetic ribonucleic acids with RNase activity
JOURNAL    Patent: US 6528640-A 592 04-MAR-2003;
FEATURES   Location/Qualifiers
source     1..17
            /organism="unknown"
BASE COUNT 3 a      4 c      8 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1502 GCCTCCACCCGCTGG 1517
|||||
Db 17 GCCTCCACCTCTCTGG 2

RESULT 469
AR286443
LOCUS      AR286443
DEFINITION Sequence 815 from patent US 6528640.
ACCESSION AR286443
VERSION    AR286443.1 GI:29724039
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS    Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE      Synthetic ribonucleic acids with RNase activity
JOURNAL    Patent: US 6528640-A 815 04-MAR-2003;
FEATURES   Location/Qualifiers
source     1..17
            /organism="unknown"
BASE COUNT 2 a      3 c      10 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1352 AGCGGGCGGGCGGACC 1367
|||||
Db 2 AGTGGCGGTGGGACC 17

RESULT 470
AX139196
LOCUS      AX139196
DEFINITION Sequence 44 from Patent EP1076099.
ACCESSION AX139196
VERSION    AX139196.1 GI:14274869
KEYWORDS
SOURCE
ORGANISM   Mycobacterium tuberculosis
            Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE 1
AUTHORS    Suzuki,Y., Nishida,M. and Takenishi,S.
TITLE      Kit for diagnosis of tubercle bacilli
JOURNAL    Patent: EP 1076099-A 44 14-FEB-2001;
            NISSHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
            (JP)
FEATURES   Location/Qualifiers
source     1..17
            /organism="Mycobacterium tuberculosis"
            /mol_type="genomic DNA"
            /db_xref="taxon:1773"
            /note="capture"
BASE COUNT 1 a      6 c      9 g      1 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1370 GGGGCGGGCGGGCGGCA 1385
|||||
Db 1 GGGCGCGGGCGGGCGGCA 16

RESULT 471
AX214605/c
LOCUS      AX214605
DEFINITION Sequence 47 from Patent WO0159103.
ACCESSION AX214605
VERSION    AX214605.1 GI:15524648
KEYWORDS
SOURCE
ORGANISM   synthetic construct
            synthetic construct
            artificial sequences.

```

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 13 c 2 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1549 GCGCGGGGAGGGCG 1564
Db 17 GCGCGGGGAGGAGG 2
RESULT 472
AX215323/c
LOCUS AX215323 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 765 from Patent WO0159103.
ACCESSION AX215323
VERSION AX215323.1 GI:15525366
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 2 a 6 c 8 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1404 CAGGTGCTGCGGCGC 1419
Db 16 CAGGTGCTGCGGCGC 1
RESULT 473
AX215324/c
LOCUS AX215324 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 766 from Patent WO0159103.
ACCESSION AX215324
VERSION AX215324.1 GI:15525367
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 3 a 6 c 7 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1400 GCTCAGTGTGCGC 1415
Db 17 GCTCAGTGTGCGC 2
RESULT 474
AX215378/c
LOCUS AX215378 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 820 from Patent WO0159103.
ACCESSION AX215378
VERSION AX215378.1 GI:15525421
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 2 a 9 c 5 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1041 GCGCACTGGGCGCTCG 1056
Db 16 GCGCACTGGGCGCGC 1
RESULT 475
AX215389/c
LOCUS AX215389 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 831 from Patent WO0159103.
ACCESSION AX215389
VERSION AX215389.1 GI:15525432
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1. .17
Location/Qualifiers
/organism="synthetic construct"


```

/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
10 c 6 g 1 t
BASE COUNT 0 a 10 c 6 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1371 GGGCGCGCGCGGCAG 1386
Db 17 GCGCGCGCGCGGCAG 2

RESULT 476
AX215398 17 bp mRNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 840 from Patent WO0159103.
ACCESSION AX215398
VERSION AX215398.1 GI:15525441
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 840 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
1 a 8 c 8 g 0 t
BASE COUNT 1 a 8 c 8 g 0 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 802 CCGCGCGCGCGGCAG 817
Db 2 CCGCGCGCGCGGCAG 17

RESULT 477
AX215400 17 bp mRNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 842 from Patent WO0159103.
ACCESSION AX215400
VERSION AX215400.1 GI:15525443
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 842 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
1 a 9 c 7 g 0 t
BASE COUNT 1 a 9 c 7 g 0 t

/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
10 c 6 g 1 t
BASE COUNT 0 a 10 c 6 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 803 CTGAGCCCGCGGCAC 818
Db 1 CGCGCGCGCGGCAC 16

RESULT 478
AX215460 17 bp mRNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 902 from Patent WO0159103.
ACCESSION AX215460
VERSION AX215460.1 GI:15525503
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 902 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
1 a 12 c 2 g 2 t
BASE COUNT 1 a 12 c 2 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1549 GCGCGCGCGCGGCAG 1564
Db 16 GCGCGCGCGCGGCAG 1

RESULT 479
AX215727 17 bp mRNA linear PAT 07-SEP-2001
LOCUS
DEFINITION Sequence 1169 from Patent WO0159103.
ACCESSION AX215727
VERSION AX215727.1 GI:15525770
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 1169 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
2 a 6 c 2 g 7 t
BASE COUNT 2 a 6 c 2 g 7 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 786 CCAAGCTGTGAAGGA 801

```

```

Db      16 CAAACTGGTGAAGG 1
|||||
RESULT 480
AX216350/c
LOCUS      17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 1792 from Patent WO0159103.
ACCESSION AX216350
VERSION    AX216350.1 GI:15526411
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL    nogo gene expression
PATENT: WO 0159103-A 1792 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   Location/Qualifiers
source     1..17
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"
BASE COUNT  4 a 6 c 6 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1400 GCTCCAGGCTGCTCCG 1415
|||||
Db      16 GCTGCAGCTGCTCCG 1

RESULT 481
AX216369/c
LOCUS      17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 1811 from Patent WO0159103.
ACCESSION AX216369
VERSION    AX216369.1 GI:15526430
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL    nogo gene expression
PATENT: WO 0159103-A 1811 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   Location/Qualifiers
source     1..17
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"
BASE COUNT  1 a 7 c 6 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1044 CACTGGGGCTCTCGGC 1059
|||||
Db      17 CACTGGGGCGCGGCAC 2

RESULT 482
AX216370/c
LOCUS      17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 1812 from Patent WO0159103.
ACCESSION AX216370
VERSION    AX216370.1 GI:15526431
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL    nogo gene expression
PATENT: WO 0159103-A 1812 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   Location/Qualifiers
source     1..17
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"
BASE COUNT  2 a 10 c 4 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1038 GGGCGCGCACTGGGGCC 1053
|||||
Db      17 GGTGGGCACTGGGGCC 2

RESULT 483
AX216371/c
LOCUS      17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 1813 from Patent WO0159103.
ACCESSION AX216371
VERSION    AX216371.1 GI:15526432
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL    nogo gene expression
PATENT: WO 0159103-A 1813 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   Location/Qualifiers
source     1..17
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"
BASE COUNT  0 a 10 c 6 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1370 GGGCGCGCGCGCGGCA 1385
|||||
Db      16 GGGCGCGCGCGCGGCA 1

RESULT 484
AX216894
LOCUS      17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2336 from Patent WO0159103.
ACCESSION AX216894
VERSION    AX216894.1 GI:15526955

```

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 8 c 9 g 0 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1366 CCGCGGGGGCGCGCGC 1381
DB 2 CCGCGGGGGCGCGCGC 17
|||||

RESULT 485
LOCUS AX216952 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2394 from Patent WO0159103.
ACCESSION AX216952
VERSION AX216952.1 GI:15527013
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 1 a 9 c 7 g 0 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 805 GAGCCCCGGGACCGC 820
DB 2 GCGCCCCGGGACCGC 17
|||||

RESULT 486
LOCUS AX216953 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2395 from Patent WO0159103.
ACCESSION AX216953
VERSION AX216953.1 GI:15527014
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1

AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 1 a 9 c 6 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 805 GAGCCCCGGGACCGC 820
DB 1 GCGCCCCGGGACCGC 16
|||||

RESULT 487
LOCUS AX218005 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 3447 from Patent WO0159103.
ACCESSION AX218005
VERSION AX218005.1 GI:15528066
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 10 a 0 c 3 g 4 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 408 TTAAGGATGAGAGAAA 423
DB 1 TTAAGGATGAGAGAAA 16
|||||

RESULT 488
LOCUS AX218198 17 bp mRNA linear PAT 08-SEP-2001
DEFINITION Sequence 3640 from Patent WO0159103.
ACCESSION AX218198
VERSION AX218198.1 GI:15528259
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;

McSwiggen, James (US) ; Chowrira, Bharat M. (US)

Location/Qualifiers

1. .17

/organism="synthetic construct"

/mol_type="mRNA"

/db_xref="taxon:32630"

/note="Nucleic Acid"

BASE COUNT 8 a 0 c 3 g 6 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 5.9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 407 TTTAAGGATGAGAAA 422

Db 2 TTTAAGGATGATAAA 17

RESULT 489

AX239680

LOCUS AX239680 17 bp DNA linear PAT 26-SEP-2001

DEFINITION Sequence 20 from Patent WO0164948.

ACCESSION AX239680

VERSION AX239680.1 GI:15797345

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS van Haeringen, W.A. and van Haeringen, H.

TITLE Universal variable fragments

JOURNAL Patent: WO 0164948-A 20 07-SEP-2001;

Dr. van Haeringen/Laboratorium B.V. (NL)

FEATURES

Location/Qualifiers

1. .17

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="primer"

BASE COUNT 8 a 8 c 1 g 0 t

Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 GGCACACGACACAC 84

Db 1 GCACACACACACAC 16

RESULT 490

AX272860/c

LOCUS AX272860 17 bp mRNA linear PAT 29-OCT-2001

DEFINITION Sequence 429 from Patent WO0162911.

ACCESSION AX272860

VERSION AX272860.1 GI:16545597

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and

Ellis, J.H.

TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 429 30-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES

Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

BASE COUNT 3 a 4 c 9 g 1 t

Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1282 CGCGCCCTCCGCTG 1297

Db 16 CTCGCCCTCGCGCTG 1

RESULT 491

AX273062/c

LOCUS AX273062 17 bp mRNA linear PAT 29-OCT-2001

DEFINITION Sequence 631 from Patent WO0162911.

ACCESSION AX273062

VERSION AX273062.1 GI:16545799

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and

Ellis, J.H.

TITLE Method and reagent for the inhibition of grid

JOURNAL Patent: WO 0162911-A 631 30-AUG-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES

Location/Qualifiers

1. .17

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

BASE COUNT 3 a 5 c 8 g 1 t

Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1286 CCCTTCGCGCTGGGC 1301

Db 17 CCCTGCGCGCTGGAGC 2

RESULT 492

AX325861/c

LOCUS AX325861 17 bp DNA linear PAT 02-SEP-2002

DEFINITION Sequence 1999 from Patent WO0192512.

ACCESSION AX325861

VERSION AX325861.1 GI:18096620

KEYWORDS

SOURCE Oryza glaberrima (African rice)

ORGANISM Oryza glaberrima

REFERENCE 1

AUTHORS Kmeic, B.B., Camper, H.B., Rice, M.C. and Kim, J.

TITLE Targeted chromosomal genomic alterations in plants using modified

JOURNAL single stranded oligonucleotides

Patent: WO 0192512-A 1999 06-DEC-2001;

UNIVERSITY OF DELAWARE (US)

FEATURES

Location/Qualifiers

1. .17

/organism="Oryza glaberrima"

/mol_type="genomic DNA"

/db_xref="taxon:4538"

BASE COUNT 1 a 6 c 7 g 3 t

Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 17;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 880 CGCGACGACGCGGCC 895

```

Db      16 CAGCGACTACGGCGCC 1
|||||
RESULT 493
AX325862
LOCUS      17 bp      DNA      linear      PAT 02-SEP-2002
DEFINITION Sequence 2000 from Patent WO0192512.
ACCESSION AX325862
VERSION    AX325862.1 GI:18096621
KEYWORDS
SOURCE     Oryza glaberrima (African rice)
ORGANISM   Oryza glaberrima
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1
AUTHORS    Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE      Targeted chromosomal genomic alterations in plants using modified
           single stranded oligonucleotides
JOURNAL    Patent: WO 0192512-A 2000 06-DEC-2001;
           UNIVERSITY OF DELAWARE (US)
FEATURES   Location/Qualifiers
           source
           1..17
           /organism="Oryza glaberrima"
           /mol_type="genomic DNA"
           /db_xref="taxon:4530"
BASE COUNT      3 a      6 g      1 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      880 CCGCGACGACGGCGCC 895
|||||
Db      2 CAGCGACTACGGCGCC 17

RESULT 494
AX325861/c
LOCUS      17 bp      DNA      linear      PAT 02-SEP-2002
DEFINITION Sequence 2019 from Patent WO0192512.
ACCESSION AX325861
VERSION    AX325861.1 GI:18096640
KEYWORDS
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1
AUTHORS    Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE      Targeted chromosomal genomic alterations in plants using modified
           single stranded oligonucleotides
JOURNAL    Patent: WO 0192512-A 2019 06-DEC-2001;
           UNIVERSITY OF DELAWARE (US)
FEATURES   Location/Qualifiers
           source
           1..17
           /organism="Oryza sativa"
           /mol_type="genomic DNA"
           /db_xref="taxon:4530"
BASE COUNT      1 a      6 c      7 g      3 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      880 CCGCGACGACGGCGCC 895
|||||
Db      16 CAGCGACTACGGCGCC 1

RESULT 495
AX325882
LOCUS      17 bp      DNA      linear      PAT 02-SEP-2002
DEFINITION Sequence 2020 from Patent WO0192512.
ACCESSION AX325882
VERSION    AX325882.1 GI:18096641
KEYWORDS
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1
AUTHORS    Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE      Targeted chromosomal genomic alterations in plants using modified
           single stranded oligonucleotides
JOURNAL    Patent: WO 0192512-A 2020 06-DEC-2001;
           UNIVERSITY OF DELAWARE (US)
FEATURES   Location/Qualifiers
           source
           1..17
           /organism="Oryza sativa"
           /mol_type="genomic DNA"
           /db_xref="taxon:4530"
BASE COUNT      3 a      7 c      6 g      1 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      880 CCGCGACGACGGCGCC 895
|||||
Db      2 CAGCGACTACGGCGCC 17

RESULT 496
AX421845
LOCUS      17 bp      mRNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 181 from Patent WO0188124.
ACCESSION AX421845
VERSION    AX421845.1 GI:21525227
KEYWORDS
SOURCE     Homo sapiens (human)
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
           Randi, A.M.
TITLE      Method and reagent for the inhibition of erg
           Patents: WO 0188124-A 181 22-NOV-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES   Location/Qualifiers
           source
           1..17
           /organism="Homo sapiens"
           /mol_type="mRNA"
           /db_xref="taxon:9606"
BASE COUNT      3 a      4 c      5 g      5 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      963 TGCCTCTTTGTGGCGCC 978
|||||
Db      2 TGAACCTTTGTGGCGCC 17

RESULT 497
AX422332
LOCUS      17 bp      mRNA      linear      PAT 18-JUN-2002
DEFINITION Sequence 668 from Patent WO0188124.
ACCESSION AX422332
VERSION    AX422332.1 GI:21525714
KEYWORDS

```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
AUTHORS
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 668 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 9 c 2 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 377 CTCACCCCAATTACA 392 17 bp mRNA linear PAT 18-JUN-2002
LOCUS AX422748/c
DEFINITION Sequence 1084 from Patent WO0188124.
ACCESSION AX422748
VERSION AX422748.1 GI:21526130
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
AUTHORS
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1084 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 4 c 6 g 5 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 893 GCCAAGAGGCTCTCT 908 17 bp mRNA linear PAT 18-JUN-2002
LOCUS AX422749/c
DEFINITION Sequence 1085 from Patent WO0188124.
ACCESSION AX422749
VERSION AX422749.1 GI:21526131
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
AUTHORS

TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1085 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 4 c 5 g 6 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 893 GCCAAGAGGCTCTCT 908 17 bp mRNA linear PAT 18-JUN-2002
LOCUS AX422880
DEFINITION Sequence 1216 from Patent WO0188124.
ACCESSION AX422880
VERSION AX422880.1 GI:21526262
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
AUTHORS
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1216 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 7 c 2 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 390 ACAACCCCGACATCAT 405 17 bp mRNA linear PAT 18-JUN-2002
LOCUS AX422914
DEFINITION Sequence 1250 from Patent WO0188124.
ACCESSION AX422914
VERSION AX422914.1 GI:21526296
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
AUTHORS
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1250 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"

```

BASE COUNT      2 a      5 c      5 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 963 TGCTCTTTGGCGCC 978
DB 1 TGAACCTTTGTGGCGCC 16

RESULT 502
AX423093      17 bp mRNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 1429 from Patent WO0188124.
ACCESSION AX423093
VERSION AX423093.1 GI:21526475
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
JOURNAL Randi, A.M.
METHOD Method and reagent for the inhibition of erg
RIBOZYME Patent: WO 0188124-A 1429 22-NOV-2001; GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT      5 a      9 c      2 g      1 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 379 CACCCCAATTACAC 394
DB 1 CACCCCAAGCTACAC 16

RESULT 503
AX499046      17 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 353 from Patent EP1229046.
ACCESSION AX499046
VERSION AX499046.1 GI:23381339
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Zhan, J.
JOURNAL Human testis expressed patched like protein
PATENT: EP 1229046-A 353 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      1 a      5 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 636 CCCGCTGGCGTGA 651

```

```

BASE COUNT      2 a      5 c      5 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 963 TGCTCTTTGGCGCC 978
DB 1 TGAACCTTTGTGGCGCC 16

RESULT 502
AX423093      17 bp mRNA linear PAT 18-JUN-2002
LOCUS
DEFINITION Sequence 1429 from Patent WO0188124.
ACCESSION AX423093
VERSION AX423093.1 GI:21526475
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
JOURNAL Randi, A.M.
METHOD Method and reagent for the inhibition of erg
RIBOZYME Patent: WO 0188124-A 1429 22-NOV-2001; GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT      5 a      9 c      2 g      1 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 379 CACCCCAATTACAC 394
DB 1 CACCCCAAGCTACAC 16

RESULT 503
AX499046      17 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 353 from Patent EP1229046.
ACCESSION AX499046
VERSION AX499046.1 GI:23381339
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Zhan, J.
JOURNAL Human testis expressed patched like protein
PATENT: EP 1229046-A 353 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      1 a      5 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 636 CCCGCTGGCGTGA 651

```

```

DB 2 CCCGCTGGCGTGA 17

RESULT 504
AX499048      17 bp DNA linear PAT 27-SEP-2002
LOCUS
DEFINITION Sequence 355 from Patent EP1229046.
ACCESSION AX499048
VERSION AX499048.1 GI:23381341
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Zhan, J.
JOURNAL Human testis expressed patched like protein
PATENT: EP 1229046-A 355 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      1 a      8 c      6 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 637 CCGCCTGGCGTGAG 652
DB 1 CCGCCTGGCGTGAG 16

RESULT 505
AX530991      17 bp DNA linear PAT 22-NOV-2002
LOCUS
DEFINITION Sequence 500 from Patent EP1239051.
ACCESSION AX530991
VERSION AX530991.1 GI:25253769
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shannon, M.
JOURNAL Human posh-like protein 1
PATENT: EP 1239051-A 500 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      3 a      3 c      10 g      1 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1418 GCTCCGGGTGGGGG 1433
DB 2 GCTCCGGGTGGGGG 17

RESULT 506
AX530993      17 bp DNA linear PAT 22-NOV-2002
LOCUS
DEFINITION Sequence 502 from Patent EP1239051.
ACCESSION AX530993

```

[illegible]


```
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGCGCGCGG 1383
Db      |||||
16 GCGGGGCGCGCTGGG 1

RESULT 511
AX531619/c
LOCUS      AX531619      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1128 from Patent EP1239051.
ACCESSION  AX531619
VERSION     AX531619.1 GI:25255028
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1128 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source          1..17
            +-----+
            |         |
            +-----+
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      2 c      9 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1480 CACCTGGCTCCTGGAC 1495
Db      |||||
17 CACCTTCCTCCTGGAC 2

RESULT 512
AX531623/c
LOCUS      AX531623      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1132 from Patent EP1239051.
ACCESSION  AX531623
VERSION     AX531623.1 GI:25255035
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1132 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source          1..17
            +-----+
            |         |
            +-----+
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      3 c      8 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1477 AGGCACCTGCTCTG 1492
Db      |||||
16 AGGCACCTCCTCTG 1

RESULT 513
AX531926/c
LOCUS      AX531926      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1435 from Patent EP1239051.
ACCESSION  AX531926
VERSION     AX531926.1 GI:25255622
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1435 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source          1..17
            +-----+
            |         |
            +-----+
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      6 c      5 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 133 CATCATGTCATGGGC 148
Db      |||||
17 CATCGGCTCCATGGGC 2

RESULT 514
AX531928/c
LOCUS      AX531928      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1437 from Patent EP1239051.
ACCESSION  AX531928
VERSION     AX531928.1 GI:25255626
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1437 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            source          1..17
            +-----+
            |         |
            +-----+
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      6 c      5 g      2 t

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 132 TCATCAGTTCATGGG 147
Db      |||||
16 TCATCGGCTCCATGGG 1

RESULT 515
AX532238/c
LOCUS      AX532238      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1747 from Patent EP1239051.
ACCESSION  AX532238
VERSION     AX532238.1 GI:25256263
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Shannon,M.
 Human posh-like protein 1
 Patent: EP 1239051-A 1747 11-SEP-2002;
 Aeomica, Inc. (US)
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 4 a 7 c 5 g 1 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 839 CAGGGCCGGCTGCTCT 854
 |||||
 Db 17 CAGGGCCGGCTGCTCT 2
 RESULT 516
 AX578660
 LOCUS AX578660 17 bp mRNA linear PAT 10-JAN-2003
 DEFINITION Sequence 498 from Patent WO0211674.
 ACCESSION AX578660
 VERSION AX578660.1 GI:27647862
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
 and Grupe,A.
 Method and reagent for the inhibition of calcium activated chloride
 channel-1 (cica-1)
 Patent: WO 0211674-A 498 14-FEB-2002;
 RIBOZYNE PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
 Thompson, James (US)
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 0 a 7 c 3 g 7 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e-02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 171 GTCTGCTCTAGTCTCT 186
 |||||
 Db 2 GTCTGCTCTCTTGTCT 17
 RESULT 517
 AX579335
 LOCUS AX579335 17 bp mRNA linear PAT 10-JAN-2003
 DEFINITION Sequence 1173 from Patent WO0211674.
 ACCESSION AX579335
 VERSION AX579335.1 GI:27648537
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
 and Grupe,A.
 Method and reagent for the inhibition of calcium activated chloride

Channel-1 (cica-1)
 Patent: WO 0211674-A 1173 14-FEB-2002;
 RIBOZYNE PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
 Thompson, James (US)
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 1 a 6 c 3 g 7 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 171 GTCTGCTCTAGTCTCT 186
 |||||
 Db 1 GTCTGCTCTTGTCTCT 16
 RESULT 518
 AX648902/c
 LOCUS AX648902 17 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 742 from Patent EP1273660.
 ACCESSION AX648902
 VERSION AX648902.1 GI:29151720
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Gu, Y.
 Human sodium-hydrogen exchanger like protein 1
 Patent: EP 1273660-A 742 08-JAN-2003;
 Aeomica, Inc. (US)
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 2 a 5 c 4 g 6 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e-02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 539 GAAGATGGCCACCACT 554
 |||||
 Db 17 GAAATGGCCACCACT 2
 RESULT 519
 AX648903/c
 LOCUS AX648903 17 bp DNA linear PAT 22-MAR-2003
 DEFINITION Sequence 743 from Patent EP1273660.
 ACCESSION AX648903
 VERSION AX648903.1 GI:29151721
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Gu, Y.
 Human sodium-hydrogen exchanger like protein 1
 Patent: EP 1273660-A 743 08-JAN-2003;
 Aeomica, Inc. (US)
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

```

BASE COUNT      2 a      5 c      4 g      6 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 539 GAAGATGGCCACCACT 554
Db 16 GAAATGGCCAGCACT 1

RESULT 520
AX672061/1/c      17 bp      DNA      linear      PAT 27-MAR-2003
LOCUS      Sequence 506 from Patent WO03004526.
DEFINITION      AX672061
ACCESSION      AX672061
VERSION      AX672061.1 GI:29330409
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL      Patent: WO 03004526-A 506 16-JAN-2003;
            Molecular Engines Laboratories (FR)
FEATURES      source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT      4 a      6 c      5 g      2 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 147 GCGAGTGTCTGCTGCT 162
Db 17 GCGAGTGTCTGCTGAT 2

RESULT 521
AX687648      17 bp      DNA      linear      PAT 31-MAR-2003
LOCUS      Sequence 380 from Patent EP1281758.
DEFINITION      AX687648
ACCESSION      AX687648
VERSION      AX687648.1 GI:29410344
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 380 05-FEB-2003;
            Aecomica, Inc. (US)
FEATURES      source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT      1 a      3 c      9 g      4 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 ACTTCCTCACCTTCCT 876
Db 2 AGTTCTCCTCATCCT 17

RESULT 524
AX688672/c

```

```

QY 149 GAGATGCTGCTGCTGG 164
Db 2 GAGCTGCTGCTGCTGG 17

RESULT 522
AX687649      17 bp      DNA      linear      PAT 31-MAR-2003
LOCUS      Sequence 381 from Patent EP1281758.
DEFINITION      AX687649
ACCESSION      AX687649
VERSION      AX687649.1 GI:29410345
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 381 05-FEB-2003;
            Aecomica, Inc. (US)
FEATURES      source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT      2 a      3 c      8 g      4 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 149 GAGATGCTGCTGCTGG 164
Db 1 GAGCTGCTGCTGCTGG 16

RESULT 523
AX687667      17 bp      DNA      linear      PAT 31-MAR-2003
LOCUS      Sequence 399 from Patent EP1281758.
DEFINITION      AX687667
ACCESSION      AX687667
VERSION      AX687667.1 GI:29410363
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 399 05-FEB-2003;
            Aecomica, Inc. (US)
FEATURES      source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT      3 a      7 c      1 g      6 t
Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 ACTTCCTCACCTTCCT 876
Db 2 AGTTCTCCTCATCCT 17

RESULT 524
AX688672/c

```

LOCUS AX688672 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1404 from Patent EP1281758.
 ACCESSION AX688672
 VERSION AX688672.1 GI:29411374
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Shannon, M., Gu, Y. and Nguyen, C.T.
 Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 Patent: EP 1281758-A 1404 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 6 a 4 c 6 g 1 t
 BASE COUNT 6 a 4 c 6 g 1 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 291 TTATCCCCCAATGTGGC 306
 ||| ||||| |||||
 Db 17 TTCTCCCCAGTGTGGC 2
 RESULT 525
 LOCUS AX688673/c 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1405 from Patent EP1281758.
 ACCESSION AX688673
 VERSION AX688673.1 GI:29411375
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Shannon, M., Gu, Y. and Nguyen, C.T.
 Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 Patent: EP 1281758-A 1405 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 5 a 4 c 7 g 1 t
 BASE COUNT 5 a 4 c 7 g 1 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 291 TTATCCCCCAATGTGGC 306
 ||| ||||| |||||
 Db 16 TTCTCCCCAGTGTGGC 1
 RESULT 526
 LOCUS AX690655 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 3387 from Patent EP1281758.
 ACCESSION AX690655
 VERSION AX690655.1 GI:29413536
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Shannon, M., Gu, Y. and Nguyen, C.T.
 Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 Patent: EP 1281758-A 3387 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 2 a 3 c 8 g 4 t
 BASE COUNT 2 a 3 c 8 g 4 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 149 GAGATGCTGCTGCTGG 164
 ||| ||||| |||||
 Db 2 GAGCTGCTGCTGCTGG 17
 RESULT 527
 LOCUS AX690656 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 3388 from Patent EP1281758.
 ACCESSION AX690656
 VERSION AX690656.1 GI:29413537
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Shannon, M., Gu, Y. and Nguyen, C.T.
 Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 Patent: EP 1281758-A 3388 05-FEB-2003;
 Aeomica, Inc. (US)
 LOCATION/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 2 a 3 c 8 g 4 t
 BASE COUNT 2 a 3 c 8 g 4 t
 Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 149 GAGATGCTGCTGCTGG 164
 ||| ||||| |||||
 Db 1 GAGCTGCTGCTGCTGG 16
 RESULT 528
 LOCUS AX724644/c 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 2331 from Patent WO03025176.
 ACCESSION AX724644
 VERSION AX724644.1 GI:30503987
 KEYWORDS Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Teitelman, A., Amson, R. and Tuijinder, M.
 Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines

```

JOURNAL Patent: WO 03025176-A 2331 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 4 a 4 c 7 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 155 CTGCTGCTGCGAGAT 170
Db 17 CTGCTGCTGCGAGAT 2

RESULT 529
AX725179 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 2866 from Patent WO03025176.
DEFINITION AX725179
ACCESSION AX725179.1 GI:30504522
VERSION
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Telerman, A., Anson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 2866 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 5 a 8 c 2 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 346 GATCTCCAGAACTCC 361
Db 1 GATCTCCAGAACTCC 16

RESULT 530
AX725846/c 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3533 from Patent WO03025176.
DEFINITION AX725846
ACCESSION AX725846
VERSION AX725846.1 GI:30505189
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Telerman, A., Anson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3533 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
/organism="Mus musculus"

JOURNAL Patent: WO 03025176-A 2331 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 4 a 5 c 5 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 155 CTGCTGCTGCGAGAT 170
Db 17 CTGCTGCTGCGAGAT 2

RESULT 531
AX729300 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 934 from Patent WO03025175.
DEFINITION AX729300
ACCESSION AX729300
VERSION AX729300.1 GI:30508643
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
TITLE Telerman, A., Anson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 934 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 6 a 5 c 1 g 5 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 346 GATCTCCAGAACTCC 361
Db 1 GATCTCCAGAACTCC 16

RESULT 532
AX738076/c 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3666 from Patent WO03025177.
DEFINITION AX738076
ACCESSION AX738076
VERSION AX738076.1 GI:30517364
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
TITLE Telerman, A., Anson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3666 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 6 a 6 c 4 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;

```

```

Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 477 TGGCATCTCGGTGAT 492
Db 17 TGGCTGTCTCGGTGAT 2

RESULT 533
BD013480
LOCUS BD013480 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Diagnosis kit of tubercle bacillus.
ACCESSION BD013480
VERSION BD013480.1 GI:22553794
KEYWORDS JP 2001103981-A/44.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
REFERENCE 1 (bases 1 to 17)
AUTHORS Suzuki, S., Nishida, M. and Takenishi, S.
TITLE Diagnosis kit of tubercle bacillus
JOURNAL Patent: JP 2001103981-A 44 17-APR-2001;
NISHINEO IND INC, SYSTEM RESEARCH CO LTD
COMMENT OS Mycobacterium tuberculosis
PN JP 2001103981-A/44
PD 17-APR-2001
PF 26-JUL-2000 JP 200225985
PI SADAIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/00, C12Q1/68//C12Q1/68, C12R1.32, PC
(C12Q1/68, C12R1.325), (C12Q1/68, C12R1.33), C12N15/00, C12N15/00 CC
capture
FH Key Location/Qualifiers
FT source 1..17
/organism="Mycobacterium tuberculosis"
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"

BASE COUNT 1 a 6 c 9 g 1 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1370 GGGCGCGCGCGCGCA 1385
Db 1 GGGCGCGCGCGCGCA 16

RESULT 534
BD056833
LOCUS BD056833 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Generation of diversity in combinatorial libraries.
ACCESSION BD056833
VERSION BD056833.1 GI:22602439
KEYWORDS JP 2001509672-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Collins, J. and Rottgen, P.
TITLE Generation of diversity in combinatorial libraries
JOURNAL Patent: JP 2001509672-A 6 24-JUL-2001;
COSMIX MOLECULAR BIOLOGICALS GMBH
COMMENT PN JP 2001509672-A/6
PD 24-JUL-2001
PF 02-FEB-1998 JP 1998532545
PR 31-JAN-1997 EP 97101539.1
PI JOHN COLLINS, PETER ROTTGEN
C12N15/09, C07K2/00, C12N15/00

```

```

CC Strandedness: Single;
CC Topology: Linear;
CC /desc="DNA oligomer"
FH Key Location/Qualifiers
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3 a 4 c 7 g 3 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAGCA 777
Db 2 CGGGTACTGGAGCA 17

RESULT 535
BD103923
LOCUS BD103923 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD103923
VERSION BD103923.1 GI:22649497
KEYWORDS WO 0192572-A/27.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and
Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 27 06-DEC-2001;
NISHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TAEKO
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/27
PD 06-DEC-2001
PF 01-JUN-2000 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
MATSUMURA,
PI SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH Key Location/Qualifiers
FT source 1..17
/organism="Artificial Sequence"
FEATURES
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 2 a 4 c 8 g 3 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 635 GCCCGCTGGCGGTGG 650
Db 2 GACTGCTGGCGGTGG 17

RESULT 536
BD105164
LOCUS BD105164 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD105164
VERSION BD105164.1 GI:22650738

```

KEYWORDS WO 0192572-A/1268.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1268 06-DEC-2001.
NISHINOBO INDUSTRIES INC. SYSTEM RESEARCH INC. HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1268
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP OOP 164798
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
PI SHOGO MORIYA, MICHIO NISHIDA
PC C12Q/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH Key Location/Qualifiers
FT source 1..17
PTA /organism=Artificial Sequence
FEATURES
source Location/Qualifiers
1..17 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3 a 6 c 7 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;
QY 1336 GGACCGCGCGGAC 1351
Db 2 GGACCGCGCGGAC 17
RESULT 537
BD105171/c 17 bp DNA linear PAT 27-AUG-2002
LOCUS BD105171
DEFINITION Kit and method for determining HLA type.
ACCESSION BD105171.1 GI:22650745
VERSION WO 0192572-A/1275.
KEYWORDS synthetic construct
SOURCE artificial construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1275 06-DEC-2001.
NISHINOBO INDUSTRIES INC. SYSTEM RESEARCH INC. HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1275
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP OOP 164798
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
PI SHOGO MORIYA, MICHIO NISHIDA
PC C12Q/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH Key Location/Qualifiers
FT source 1..17
PTA /organism=Artificial Sequence
FEATURES
source Location/Qualifiers
1..17 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 3 a 6 c 7 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;
QY 1336 GGACCGCGCGGAC 1351
Db 2 GGACCGCGCGGAC 17

source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 4 a 5 c 7 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1134 TGCCCGCGCGTGTGCA 1149
Db 16 TGCCCGCGCGTGTCCA 1
RESULT 538
I26684
LOCUS I26684
DEFINITION Sequence 14 from patent US 5559028.
ACCESSION I26684
VERSION I26684.1 GI:1606554
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hoshino,Y., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Methods of enhancing br antigen presentation to T cells inhibiting
JOURNAL Patent: US 5559028-A 14 24-SEP-1997
FEATURES
source Location/Qualifiers
1..17 /organism="unknown"
BASE COUNT 3 a 4 c 6 g 4 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1306 GTCCTGCGTGTGCACTG 1321
Db 2 GTCCTGCGTGTGCAATG 17
RESULT 539
I32551/c 17 bp DNA linear PAT 06-FEB-1997
LOCUS I32551
DEFINITION Sequence 15 from patent US 5589330.
ACCESSION I32551
VERSION I32551.1 GI:1623342
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber,A.P.
TITLE High-throughput screening method for sequence or genetic alterations in nucleic acids using elution and sequencing of complementary oligonucleotides
JOURNAL Patent: US 5589330-A 15 31-DEC-1996;
FEATURES
source Location/Qualifiers
1..17 /organism="unknown"
BASE COUNT 3 a 5 c 7 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1134 TGCCCGCGCGTGTGCA 1149
Db 16 TGCCCGCGCGTGTCCA 1

RESULT 540
132568/c
LOCUS 132568 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 32 from patent US 5589330
ACCESSION 132568
VERSION 132568.1 GI:1823359
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Shuber, A.P.
TITLE High-throughput screening method for sequence or genetic alterations in nucleic acids using elution and sequencing of complementary oligonucleotides
JOURNAL Patent: US 5589330-A 32 31-DEC-1996;
FEATURES Location/Qualifiers
1..17 /organism="unknown"
3 a 5 c 6 g 3 t
BASE COUNT
Query Match 0.8% Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1514 CTGGCATGGCGGTCA 1529
Db 17 CTGCACATGGCGGTCA 2
RESULT 541
146480/c
LOCUS 146480 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 459 from patent US 5639612.
ACCESSION 146480
VERSION 146480.1 GI:2470445
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsushashi, M. and Cohen, J.
TITLE Method for selecting polynucleotides with immobilized polynucleotide probes identified based on a sub-
JOURNAL Patent: US 5639612-A 459 17-OCT-1997
FEATURES Location/Qualifiers
1..17 /organism="unknown"
3 a 8 c 4 g 2 t
BASE COUNT
Query Match 0.8% Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 642 TGGCGGTGGAGCGCG 657
Db 16 TGGCGGTGGAGCGCCAG 1
RESULT 542
188026/c
LOCUS 188026 17 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 4 from patent US 5716846.
ACCESSION 188026
VERSION 188026.1 GI:3407566
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brown, S. Joel, Dattagupta, N. and Naidu, Y. M.
TITLE Method for inhibiting cellular proliferation using antisense oligonucleotides to interleukin-6 receptor mRNA

JOURNAL Patent: US 5716846-A 4 10-FEB-1998;
FEATURES Location/Qualifiers
1..17 /organism="unknown"
3 a 7 c 4 g 1 t
BASE COUNT
Query Match 0.8% Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 574 CGAGCGCGCGCGCATGTG 589
Db 17 CGAGCGACTCGCATGTG 2
RESULT 543
AL2313
LOCUS AL2313 18 bp DNA linear PAT 06-DEC-1993
DEFINITION oligonucleotide 195K repeat.
ACCESSION AL2313
VERSION AL2313.1 GI:491325
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS HYBRID PROTEINS OR POLYPEPTIDES
TITLE Patent: WO 8802757-A 14 21-APR-1988;
JOURNAL Location/Qualifiers
1..18 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
3 a 7 g 0 t
BASE COUNT
Query Match 0.8% Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 336 GACCGCGCGCGCGCG 341
Db 3 CGAGCGCGCGCGCGCG 18
RESULT 544
AL9460
LOCUS AL9460 18 bp DNA linear PAT 08-JUN-1994
DEFINITION oligonucleotide.
ACCESSION AL9460
VERSION AL9460.1 GI:583200
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS MODIFIED SEED STORAGE PROTEINS
TITLE Patent: WO 9104270-A 5 04-APR-1991;
JOURNAL Location/Qualifiers
1..18 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
3 a 4 c 5 g 5 t
BASE COUNT
Query Match 0.8% Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 891 GGCCCAAGAGGTCTT 906
Db 2 GGCCCATGATGCTCTT 17


```

RESULT 545
LOCUS A87987 18 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 135 from Patent WO9833904.
ACCESSION A87987
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 3 a 5 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 785 ACCAGCTGCTGACGG 800
DB 17 ACCAGCTGCTGACGG 2

RESULT 546
LOCUS A63131 18 bp DNA linear PAT 12-MAR-1998
DEFINITION Sequence 6 from Patent WO9720058.
ACCESSION A63131
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Kapros,T., Dudits,D., Gyoertgyey,J., Mai,A. and Kelemen,Z.
TITLE PLANT GENE EXPRESSION VECTOR FAMILY BASED ON THE REGULATORY DNA
SEQUENCES OF AN ALFALFA H3 HISTON GENE VARIANT (MSH3g1)
JOURNAL Patent: WO 9720058-A 6 05-JUN-1997;
COMMENT BAY ZOLTAN ALKALMAZOTT KUTATAS (HU)
Other publication HU 76355 19970828
Other publication AU 7705296 19970619.
FEATURES
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 1 a 11 c 5 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGCGCGG 1383
DB 17 GCTGGGGCGGCGCGCGG 2

RESULT 547
LOCUS A87987 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 135 from Patent WO9833904.
ACCESSION A87987
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 1 a 5 c 10 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 GGTGCGGGGGCGGCGG 1439
DB 2 GGTGCGGGGGCGGCGG 17

RESULT 548
LOCUS A89954 18 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 135 from Patent EP0856579.
ACCESSION A89954
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Brysch,W.D. and Schlengersiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A.135 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
Location/Qualifiers
1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 1 a 5 c 10 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 GGTGCGGGGGCGGCGG 1439
DB 2 GGTGCGGGGGCGGCGG 17

RESULT 549
LOCUS AR003675 18 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 9 from patent US 5744353.
ACCESSION AR003675
VERSION 1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 18)
AUTHORS Herman,J., Coulie,P., Boon-Palleur,T., van der Bruggen,P. and

```

Luescher, I.
Cytolytic T cell lines which bind to complexes of tumor rejection
antigens and HLA-B44 molecules
JOURNAL Patent: US 5744353-A 9 28-APR-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 4 a 6 c 6 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1013 TCCTCGGCTCGGGC 1028
Db 17 TCCTCGGACTCGTGGC 2
RESULT 550
AR003677/c
LOCUS 18 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 11 from patent US 5744353.
ACCESSION AR003677
VERSION AR003677.1 GI:3964936
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Herman, J., Coulie, P., Boon-Falleur, T., van der Bruggen, P. and
Luescher, I.
TITLE Cytolytic T cell lines which bind to complexes of tumor rejection
antigens and HLA-B44 molecules
JOURNAL Patent: US 5744353-A 11 28-APR-1998;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 6 c 6 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1013 TCCTCGGCTCGGGC 1028
Db 17 TCCTCGGACTCGTGGC 2
RESULT 551
AR069474
LOCUS 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 11 from patent US 5891666.
ACCESSION AR069474
VERSION AR069474.1 GI:7220362
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matsuyama, T. and Grossman, A.
TITLE Genes encoding LSIIRF polypeptides
JOURNAL Patent: US 5891666-A 11 06-APR-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 7 a 2 c 6 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 504 CAGGAGTCAAACTGAG 519
|||||

Db 3 CAGGAGTCAAACTGAG 18
RESULT 552
AR070852/c
LOCUS 18 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 23 from patent US 5908827.
ACCESSION AR070852
VERSION AR070852.1 GI:7221740
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sirna, A.
TITLE Protein from urine named component B
JOURNAL Patent: US 5908827-A 23 01-JUN-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 3 a 7 c 5 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 785 ACCAAGCTGGTGAAGG 800
Db 17 ACCACGCTGGTGACGG 2
RESULT 553
AR083621/c
LOCUS 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 9 from patent US 5977300.
ACCESSION AR083621
VERSION AR083621.1 GI:10010392
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Herman, J., Coulie, P., van der Bruggen, P. and Boon-Falleur, T.
TITLE Isolated nonapeptide which bind to HLA-B44 molecules and the uses
thereof
JOURNAL Patent: US 5977300-A 9 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 4 a 6 c 6 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1013 TCCTCGGCTCGGGC 1028
Db 17 TCCTCGGACTCGTGGC 2
RESULT 554
AR083623/c
LOCUS 18 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 11 from patent US 5977300.
ACCESSION AR083623
VERSION AR083623.1 GI:10010394
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Herman, J., Coulie, P., van der Bruggen, P. and Boon-Falleur, T.
TITLE Isolated nonapeptide which bind to HLA-B44 molecules and the uses

```

thereof
JOURNAL Patent: US 5977300-A 11 02-NOV-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 6 c 6 g 1 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1013 TCCTCGGCTCGGGC 1028
Db 17 TCCTCGGACTCGTGC 2

RESULT 555
AR096629/c
LOCUS 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 13 from patent US 6008048.
ACCESSION AR096629
VERSION AR096629.1 GI:10025595
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowsett,L.M.
TITLE Antisense inhibition of EGR-1 expression
JOURNAL Patent: US 6008048-A 13 28-DEC-1999;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 1 a 13 c 3 g 1 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1368 CGGGGGCGGGCGG 1383
Db 18 GCGGTGGAGCGCGG 3

RESULT 556
AR098791/c
LOCUS 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 46 from patent US 6077672.
ACCESSION AR098791
VERSION AR098791.1 GI:12808557
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowsett,L.M.
TITLE Antisense modulation of TRADD expression
JOURNAL Patent: US 6077672-A 46 20-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 1 a 4 c 12 g 1 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1123 CGCGCGCTCTCGCC 1138
Db 16 CGCGCGCCACCTGCC 1

RESULT 557
AR100282
LOCUS 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6080580.
ACCESSION AR100282
VERSION AR100282.1 GI:12810730
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F., Bennett C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
TITLE Antisense oligonucleotide modulation of tumor necrosis
factor-.alpha. (TNF-.alpha.) expression
JOURNAL Patent: US 6080580-A 13 27-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 2 c 7 g 4 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 236 GGGTTCGGAAGGGA 251
Db 1 GGGTTCGAGAGATGA 16

RESULT 558
AR105370/c
LOCUS 18 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 8 from patent US 6096543.
ACCESSION AR105370
VERSION AR105370.1 GI:12818967
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Monia,B.P. and Cowsett,L.M.
TITLE Antisense inhibition of human mekl expression
JOURNAL Patent: US 6096543-A 8 01-AUG-2000;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 0 a 9 c 2 g 7 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 CGAGCGGAGAGCGAG 29
Db 17 CGAGCGGAGGAGCGAG 2

RESULT 559
AR117923
LOCUS 18 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 62 from patent US 6140466.
ACCESSION AR117923
VERSION AR117923.1 GI:14098829
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Barbas,C.F. III, Gottesfeld,J.M. and Wright,P.E.
TITLE Zinc finger protein derivatives and methods therefor
JOURNAL Patent: US 6140466-A 62 31-OCT-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"

```

```
BASE COUNT      0 a      3 c      14 g      1 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGGCGGG 1383
|||||
Db 1 GCGTGGCGGGGGCGG 16

RESULT 560
ARI20115
LOCUS      ARI20115      18 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 15 from patent US 6153737.
ACCESSION  ARI20115
VERSION     ARI20115.1 GI:14102814
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Manoharan,M., Cook,P.Dan. and Bennett,C.Frank.
TITLE      Derivatized oligonucleotides having improved uptake and other
            properties
JOURNAL     Patent: US 6153737-A 15 28-NOV-2000;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"

BASE COUNT      3 a      4 c      9 g      2 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 GCGAGCGCGAGCGAGG 48
|||||
Db 2 GGGAGCGCTAGCGAGG 17

RESULT 561
ARI21115/c
LOCUS      ARI21115      18 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6159697.
ACCESSION  ARI21115
VERSION     ARI21115.1 GI:14104691
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Monia,B.P. and Cowser,L.M.
TITLE      Antisense modulation of Smad7 expression
JOURNAL     Patent: US 6159697-A 11 12-DEC-2000;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"

BASE COUNT      6 a      5 c      6 g      0 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGCGG 166
|||||
Db 16 GCTGCTGCTGCTGCTG 1

RESULT 562
ARI23810/c
LOCUS      ARI23810      18 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6171806.
ACCESSION  ARI23810
```

```
VERSION     ARI23810.1 GI:14109171
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Herman,J., Coulie,P., van der Bruggen,P. and Boon-Falleur,T.
TITLE      Isolated peptide defined by SEQ ID NO: 17 and uses thereof
JOURNAL     Patent: US 6171806-A 9 09-JAN-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"

BASE COUNT      4 a      6 c      6 g      2 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGCTCGGGC 1028
|||||
Db 17 TCCTCGGACTCGTGGC 2

RESULT 563
ARI23812/c
LOCUS      ARI23812      18 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 11 from patent US 6171806.
ACCESSION  ARI23812
VERSION     ARI23812.1 GI:14109173
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Herman,J., Coulie,P., van der Bruggen,P. and Boon-Falleur,T.
TITLE      Isolated peptide defined by SEQ ID NO: 17 and uses thereof
JOURNAL     Patent: US 6171806-A 11 09-JAN-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"

BASE COUNT      5 a      6 c      6 g      1 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGCTCGGGC 1028
|||||
Db 17 TCCTCGGACTCGTGGC 2

RESULT 564
ARI49937
LOCUS      ARI49937      18 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 13 from patent US 6228642.
ACCESSION  ARI49937
VERSION     ARI49937.1 GI:15114528
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS    Baker,B.F., Bennett,C.Frank., Butler,M.M. and Shanahan,W.R. Jr.
TITLE      Antisense oligonucleotide modulation of tumor necrosis
            factor-(alpha) (TNF- alpha) expression
JOURNAL     Patent: US 6228642-A 13 08-MAY-2001;
FEATURES    Location/Qualifiers
            source
            1..18
            /organism="unknown"

BASE COUNT      5 a      2 c      7 g      4 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 GGGTTCGGAGAGGA 251
Db 1 GGGTTCGAGAGATGA 16

RESULT 565
LOCUS AR157304 18 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 9 from patent US 6245333.
ACCESSION AR157304
VERSION AR157304.1 GI:16218235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Coulie,P. and Boon-Falleur,T.
TITLE Isolated protein processed to peptides which form complexes with HLA molecules
JOURNAL Patent: US 6245333-A 9 12-JUN-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 4 a 6 c 6 g 2 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGGTCGGGC 1028
Db 17 TCCTCGGACTCGTGC 2

RESULT 566
LOCUS AR157306 18 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6245333.
ACCESSION AR157306
VERSION AR157306.1 GI:16218237
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Coulie,P. and Boon-Falleur,T.
TITLE Isolated protein processed to peptides which form complexes with HLA molecules
JOURNAL Patent: US 6245333-A 11 12-JUN-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 5 a 6 c 6 g 1 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGGTCGGGC 1028
Db 17 TCCTCGGACTCGTGC 2

RESULT 567
LOCUS AR162791 18 bp DNA PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6258935.
ACCESSION AR162791
VERSION AR162791.1 GI:16230132
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matsuyama,T., Grossman,A. and Richardson,C.Donald.
TITLE LSIRF polypeptides
JOURNAL Patent: US 6258935-A 11 10-JUL-2001;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 7 a 2 c 6 g 3 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 504 CAGGAGTGAACCTGCG 519
Db 3 CAGAGTGAACTGAG 18

RESULT 568
LOCUS AR196090 18 bp DNA PAT 20-APR-2002
DEFINITION Sequence 555 from patent US 6350934.
ACCESSION AR196090
VERSION AR196090.1 GI:20245527
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens., Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 555 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 0 a 8 c 8 g 2 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1079 CGCCCGCGCGCGCG 1094
Db 16 CGCCCGCGCGCGCG 1

RESULT 569
LOCUS AR205718 18 bp DNA PAT 20-JUN-2002
DEFINITION Sequence 11 from patent US 6369202.
ACCESSION AR205718
VERSION AR205718.1 GI:21503372
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Matsuyama,T., Grossman,A. and Richardson,C.Donald.
TITLE Genes encoding LSIRF polypeptides
JOURNAL Patent: US 6369202-A 11 09-APR-2002;
FEATURES Location/Qualifiers
source 1..18
BASE COUNT 7 a 2 c 6 g 3 t

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 504 CAGGAGTGAACCTGCG 519


```

QY 1246 GGTCTCGAGGAGCC 1261
Db 18 GGTCTAGAGAGCC 3

RESULT 575
AX004745
LOCUS AX004745 18 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 4 from Patent WO9911817.
ACCESSION AX004745
VERSION AX004745.1 GI:9928162
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Matlashewski, G.J. and Storey, A.
TITLE Screening method for determining individuals at risk of developing
diseases associated with different polymorphic forms of wildtype
p53
JOURNAL Patent: WO 9911817-A 4 11-MAR-1999;
MATLASHESKI GREG J (CA); UNIV MCGILL (CA)
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Human p53"
BASE COUNT 2 a 6 c 8 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1422 CGGTGCGGGGCCAC 1437
Db 1 CTGGTGCAGGGCCAC 16

RESULT 576
AX047241/c
LOCUS AX047241 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 4 from Patent WO0068421.
ACCESSION AX047241
VERSION AX047241.1 GI:11876522
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Snaidr, J.
TITLE Method for detecting microorganisms in a sample
JOURNAL Patent: WO 0068421-A 4 16-NOV-2000;
Vermicon AG (DE)
FEATURES
source
1. .18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide sonde"
BASE COUNT 1 a 7 c 7 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1537 CTGAAGCCGGGGGCC 1552
Db 17 CCGAAGCCGGTGGCC 2

RESULT 577
AX081062/c
LOCUS AX081062 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 57 from Patent WO0109301.
ACCESSION AX081062
VERSION AX081062.1 GI:13169990
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
REFERENCE 1
AUTHORS Francis-Lang, H.L., Gillett, L.A., Margolis, J.S., Reddy, B.P., Winslow, J.W., Luo, Y., Gendreau, S.B., Jacobus, D.A., Tietjen, K., Nauen, R. and Jeschke, P.
TITLE Nucleic acids and polypeptides of invertebrate twik channels and methods of use
JOURNAL Patent: WO 0109301-A 57 08-FEB-2001;
Genoptera, LLC (US)
FEATURES
source
1. .18
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
BASE COUNT 4 a 6 c 3 g 5 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 142 CATGGCGAGATGCTG 157
Db 16 CATGGCGAGATGTTG 1

RESULT 578
AX082556/c
LOCUS AX082556 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 7 from Patent WO0111047.
ACCESSION AX082556
VERSION AX082556.1 GI:13184666
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Bowman, B.M. and Wang, K.
TITLE Dna sequences isolated from human colonic epithelial cells
JOURNAL Patent: WO 0111047-A 7 15-FEB-2001;
Bayer Corporation (US)
FEATURES
source
1. .18
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 5 c 9 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 CCAGGCGGCTGCTC 853
Db 18 CCAGGCTGGCTCCTC 3

RESULT 579
AX082560/c
LOCUS AX082560 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 11 from Patent WO0111047.
ACCESSION AX082560
VERSION AX082560.1 GI:13184670
KEYWORDS

```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE       Bowman,B.M. and Wang,K.
JOURNAL     Dna sequences isolated from human colonic epithelial cells
            Patent: WO 0111047-A 11 15-FEB-2001;
            Bayer Corporation (US)
FEATURES    Location/Qualifiers
            source
              1..18
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
            3 a 5 c 9 g 1 t
            BASE COUNT      3 a 5 c 9 g 1 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;
            Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      838 CCAGGCGCGGTGCTC 853
Db      18 CCAGGCGGTGCTCCTC 3

RESULT 580
LOCUS     AX082562
DEFINITION Sequence 13 from Patent WO0111047.
ACCESSION AX082562
VERSION   AX082562.1 GI:13184672
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
TITLE     Bowman,B.M. and Wang,K.
JOURNAL   Dna sequences isolated from human colonic epithelial cells
            Patent: WO 0111047-A 13 15-FEB-2001;
            Bayer Corporation (US)
FEATURES  Location/Qualifiers
            source
              1..18
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
            3 a 5 c 9 g 1 t
            BASE COUNT      3 a 5 c 9 g 1 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;
            Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      838 CCAGGCGCGGTGCTC 853
Db      18 CCAGGCGGTGCTCCTC 3

RESULT 581
LOCUS     AX118127
DEFINITION Sequence 3250 from Patent WO0129262.
ACCESSION AX118127
VERSION   AX118127.1 GI:14035078
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 Picoult-Newburg,L. and Pohl,M.
AUTHORS   Genotyping reagents, kits and methods of use thereof
            Patent: WO 0129262-A 3250 26-APR-2001;
            Orchid Biosciences, Inc. (US)
FEATURES  Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="Primer XPD exon 10 consensus"
            2 a 11 c 3 g 2 t
            BASE COUNT      2 a 11 c 3 g 2 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;

SOURCE      1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Primer"
            3 a 8 c 5 g 2 t
            BASE COUNT      3 a 8 c 5 g 2 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;
            Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      799 GGACCTGAGCCCGGG 814
Db      18 GGTCTGAGCCCGGG 3

RESULT 582
LOCUS     AX147718
DEFINITION Sequence 20 from Patent WO0136673.
ACCESSION AX147718
VERSION   AX147718.1 GI:14346763
KEYWORDS
SOURCE    Issatchenkia orientalis (anamorph: Candida krusei)
ORGANISM  Issatchenkia orientalis
REFERENCE 1 Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Issatchenkia.
AUTHORS   Apfel,H., Hesseann,J., Trebesius,K. and Autenrieth,I.
TITLE     Test for micro-organisms
            Patent: WO 0136673-A 20 25-MAY-2001;
            Creatogen Aktiengesellschaft (DE)
FEATURES  Location/Qualifiers
            source
              1..18
                /organism="Issatchenkia orientalis"
                /mol_type="genomic DNA"
                /db_xref="taxon:4909"
            2 a 6 c 6 g 4 t
            BASE COUNT      2 a 6 c 6 g 4 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;
            Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      297 CCAATGTGGCGCGAGAA 312
Db      18 CCAATGTGGCGCGAGAA 3

RESULT 583
LOCUS     AX229739
DEFINITION Sequence 9 from Patent WO0162964.
ACCESSION AX229739
VERSION   AX229739.1 GI:15591951
KEYWORDS
SOURCE    synthetic construct
ORGANISM  synthetic construct
REFERENCE 1 Winsey,S.U., Haldar,N., Wojnarowska,F.U. and Welsh,K.N.
AUTHORS   A genetic determinant for malignant melanoma
            Patent: WO 0162964-A 9 30-AUG-2001;
            Isis Innovation Limited (GB)
FEATURES  Location/Qualifiers
            source
              1..18
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                /note="Primer XPD exon 10 consensus"
            2 a 11 c 3 g 2 t
            BASE COUNT      2 a 11 c 3 g 2 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;

SOURCE      1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Primer"
            3 a 8 c 5 g 2 t
            BASE COUNT      3 a 8 c 5 g 2 t
            Query Match      0.8%; Score 12.8; DB 1; Length 18;
            Best Local Similarity 87.5%; Pred. No. 5.9e+02;

```



```

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1541 AGCGGGGGGGCGGGG 1556
Db 17 ATCTGGGGGGCGGGG 2

RESULT 584
AX278630/c
LOCUS AX278630 18 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 167 from Patent WO0177372.
ACCESSION AX278630
VERSION AX278630.1 GI:16606084
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Remacle,J., Hamels,S., Zammattéo,N., Lockman,L., Dufour,S.,
TITLE Identification of biological (micro) organisms by detection of the
JOURNAL ir homologous nucleotide sequences on arrays
JOURNAL Patent: WO 0177372-A 167 18-OCT-2001;
FACULTES Universitaires Notre-Dame de la Paix (BE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="HTR6 Capture Probe"
BASE COUNT 4 a 4 c 9 g 1 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1456 CTCGAGCTGCTCTAC 1471
Db 16 CTCGCGCTGCGCTAC 1

RESULT 585
AX284155
LOCUS AX284155 18 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 12 from Patent WO0178756.
ACCESSION AX284155
VERSION AX284155.1 GI:17044843
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wiederanders,B. and Maubach,G.
TITLE Agent for postoperative use after the removal of bone tumours
JOURNAL Patent: WO 0178756-A 12 25-OCT-2001;
JOURNAL Dupuy Biotech Jena GmbH (DE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Spacer molecule spacer between Cystatin C und BMP-2"
CDS
<1..>18
/notes="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAD12163.1"
/db_xref="GI:17044844"
/translation="SGGGGG"
BASE COUNT 1 a 3 c 11 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGCGCGG 1383
Db 2 GCGGTGGCGGTGGCGG 17

RESULT 586
AX323452/c
LOCUS AX323452 18 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 44 from Patent WO0192578.
ACCESSION AX323452
VERSION AX323452.1 GI:18094215
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Roninson,I.B., Dokmanovic,M. and Chang,B.D.
TITLE Reagents and methods for identifying and modulating expression of
JOURNAL genes regulated by retinoids
JOURNAL Patent: WO 0192578-A 44 06-DEC-2001;
FACULTES Board of Trustees of the University of Illinois (US)
FEATURES
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/notes="Antisense primer for beta-IG-H3 reporter gene
construction"
BASE COUNT 4 a 4 c 8 g 2 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 866 CTCACCTTCCTGGACC 881
Db 18 CTCACCTTCCTGGACC 3

RESULT 587
AX394481/c
LOCUS AX394481 18 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 26 from Patent WO0218638.
ACCESSION AX394481
VERSION AX394481.1 GI:21065619
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Risager,C., Andersson,M.K., Lewander,T. and Ollason,E.
TITLE Detection of cyp2d6 polymorphisms
JOURNAL Patent: WO 0218638-A 26 07-MAR-2002;
JOURNAL Gemini Genomics PLC (GB)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide"
BASE COUNT 1 a 9 c 2 g 6 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 GAAGGAAAGCGCAAG 63
Db 18 GTAGGAAAGCGCAAG 3

```

```

RESULT 588
AX556880 LOCUS 18 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 7 from Patent WO02058723.
ACCESSION AX556880
VERSION AX556880.1 GI:25989978
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1. Vicari, A.P., Caux, C. and Laface, D.
Chemokines as adjuvants of immune response
Patent: WO 02058723-A 7 01-AUG-2002;
Schering Corporation (US)
JOURNAL
FEATURES
LOCATION/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 0 a 5 c 5 g 8 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1306 GCTCTGGCTGCTGCTG 1321
Db 3 GCTCTGGCTGCTGCTG 18

RESULT 589
AX659153 LOCUS 18 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 8 from Patent WO02101002.
ACCESSION AX659153
VERSION AX659153.1 GI:29161387
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Escary, J.L.
New polynucleotides and polypeptides of the HGH-V gene
Patent: WO 02101002-A 8 19-DEC-2002;
GenOdyssée (FR)
JOURNAL
FEATURES
LOCATION/Qualifiers
source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 0 a 5 c 5 g 8 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1226 GTGCTGGCTGCTGCTGCT 1241
Db 1 GTGCTGGCTGCTGCTGCT 16

RESULT 590
AX705791 LOCUS 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 460 from Patent WO03014388.
ACCESSION AX705791
VERSION AX705791.1 GI:29562456
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1. Waschuetz, S., Schnakenberg, E. and Lustig, M.
Method and diagnostic kit for the molecular diagnosis of
pharmacologically relevant genes
Patent: WO 03018837-A 81 06-MAR-2003;
Adnagen AG (DE)
JOURNAL
FEATURES
LOCATION/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Detection oligonucleotide for TP53"
BASE COUNT 6 a 1 c 5 g 6 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 464 AAGTTGAACGCTTTGG 479
Db 1 AAGTTGAACGTTTAGG 16

RESULT 591
AX708559 LOCUS 18 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 10 from Patent WO02101089.
ACCESSION AX708559
VERSION AX708559.1 GI:29564326
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1. Snaldr, J. and Beimfohr, C.
Method for specific, fast detection of threadlike bacteria
Patent: WO 02101089-A 10 19-DEC-2002;
Vermicon AG (DE)
JOURNAL
FEATURES
LOCATION/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
BASE COUNT 1 a 7 c 7 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1537 CTGAAGCCGGGGGGCC 1552
Db 17 CCGAAGCCGGTGGCC 2

RESULT 592
AX713195 LOCUS 18 bp DNA linear PAT 11-APR-2003
DEFINITION Sequence 81 from Patent WO03016837.
ACCESSION AX713195
VERSION AX713195.1 GI:29823784
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1. Waschuetz, S., Schnakenberg, E. and Lustig, M.
Method and diagnostic kit for the molecular diagnosis of
pharmacologically relevant genes
Patent: WO 03018837-A 81 06-MAR-2003;
Adnagen AG (DE)
JOURNAL
FEATURES
LOCATION/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
BASE COUNT 1 a 7 c 7 g 3 t
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1537 CTGAAGCCGGGGGGCC 1552
Db 17 CCGAAGCCGGTGGCC 2

```

```

source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
4 a 3 c 9 g 2 t

BASE COUNT
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 515 CTGCGGGTGACCGAGG 530
Db 2 CAGTGGGTGACCGAGG 17

RESULT 593
AX718864/c
LOCUS AX718864 18 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 428 from Patent WO02103043.
ACCESSION AX718864
VERSION AX718864.1 GI:29891431
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Beinfuhr, C. and Snaidr, J.
TITLE Method for the specific fast detection of bacteria which is harmful
JOURNAL Patent: WO 02103043-A 428 27-DEC-2002;
Vermicon AG (DE)
FEATURES
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Oligonukleotid"
3 a 7 c 3 g 5 t

BASE COUNT
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 506 GGAGTCAAACTGGGG 521
Db 17 GGATTGAACCTGCGG 2

RESULT 594
AX719127
LOCUS AX719127 18 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 8 from Patent EP1295938.
ACCESSION AX719127
VERSION AX719127.1 GI:29891614
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Becary, J.L.
TITLE Corrected sequence of the hgh-v gene and an allelic variant
JOURNAL Patent: EP 1295938-A 8 26-MAR-2003;
GenOdysee (FR)
FEATURES
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
0 a 5 c 8 t

BASE COUNT
Query Match 0.8%; Score 12.8; DB 1; Length 18;

```

```

Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1226 GTGCTGGCTCGTCT 1241
Db 1 GTGTGGCTCTTGCT 16

RESULT 595
BD012743
LOCUS BD012743 18 bp DNA linear PAT 02-AUG-2002
DEFINITION A novel frizzled family gene, 584.
ACCESSION BD012743
VERSION BD012743.1 GI:22092932
KEYWORDS WO 0112808-A/16.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Seno, C. and Numata, M.
TITLE A novel frizzled family gene, 584
JOURNAL Patent: WO 0112808-A 16 22-FEB-2001;
CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE INC, CHIAKI SENO,
MARIKO NUMATA
COMMENT
OS Artificial Sequence
PN WO 0112808-A/16
PD 22-FEB-2001
PF 18-AUG-2000 WO 2000JP005552
PR 18-AUG-1999 JP 99F 232018
PI CHIAKI SENO, MARIKO NUMATA
PC C12N15/12, C12N5/10, C12N1/15, C12N1/19, C12N1/21, C12Q1/02, PC
C07K14/705
PC C07K16/28, C12P21/02
CC Description of Artificial Sequence: artificially synthesized
primer
CC sequence C07K14/705,
FH Key Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
4 a 7 c 7 g 0 t

BASE COUNT
Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1342 CGCGGGGACAGCGG 1357
Db 1 CGACGGGACAGCGG 16

RESULT 596
BD065500
LOCUS BD065500 18 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065500
VERSION BD065500.1 GI:22611103
KEYWORDS JP 2001511000-A/135.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 135 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/135
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533

```

```

PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCHE
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
   Location/Qualifiers
FT source 1..18
FT /organism='Unknown'.

FEATURES
    source
    1..18
    /organism='unidentified'
    /mol_type='genomic DNA'
    /db_xref='taxon:32644'
BASE COUNT 1 a 5 c 10 g 2 t
    Query Match 0.8%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 5.9e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1424 GGTGGGGGGCCACCG 1439
DB 2 GGTGAGGGGGCCCG 17

RESULT 597
BD074290
LOCUS 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Screening method for assaying individual having danger of onset of
KEYWORDS disease related to polymorphic morphology of different wild-type
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Matlashewski,G.J., Banks,L, and Storey,A.
TITLE Screening method for assaying individual having danger of onset of
    disease related to polymorphic morphology of different wild-type
JOURNAL
COMMENT Patent: JP 2001514860-A 4 18-SEP-2001;
    MCILL UNIVERSITY, IMPERIAL CANCER RESEARCH TECHNOLOGY,
    INTERNATIONAL CENTER FOR GENETIC ENGINEERING AND BIOTECHNOLOGY
OS Artificial Sequence
PN JP 2001514860-A/4
PD 18-SEP-2001
PF 31-AUG-1998 JP 2000508823
PR 02-SEP-1997 CA 2214461
PI GREG J MATLASHESKI,LAWRENCE BANKS,ALAN STOREY PC
C12Q1/68,C12N15/09,G01N33/15,G01N33/50,G01N33/569,G01N33/574, PC
C12N15/00
CC Human p53
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.

FEATURES
    source
    1..18
    /organism='synthetic construct'
    /mol_type='genomic DNA'
    /db_xref='taxon:32630'
BASE COUNT 2 a 6 c 8 g 2 t
    Query Match 0.8%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 5.9e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1422 CGGTGGGGGGCCAC 1437
DB 1 CCGGTGAGGGGGCCAC 16

RESULT 598
BD104198/c

```

```

BD104198
LOCUS 18 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104198
VERSION BD104198.1 GI:22649772
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
    Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 302 06-DEC-2001;
    NISSHINO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO
    KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO
    NISHIDA
COMMENT OS Artificial Sequence
    PN WO 0192572-A/302
    PD 06-DEC-2001
    PF 01-JUN-2001 WO 2001JP004562
    PR 01-JUN-2000 JP 00P 164798
    PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI PI
    MATSUMURA,
    PT SHOGO MORIYA,MICHIO NISHIDA
    PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
    CC Description of Artificial Sequence:capture
    FH Key Location/Qualifiers
    FT source 1..18
    FT /organism='Artificial Sequence'.

FEATURES
    source
    1..18
    /organism='synthetic construct'
    /mol_type='genomic DNA'
    /db_xref='taxon:32630'
BASE COUNT 2 a 9 g 1 t
    Query Match 0.8%; Score 12.8; DB 1; Length 18;
    Best Local Similarity 87.5%; Pred. No. 5.9e+02;
    Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 949 CACCGCGCGCACCTG 964
DB 17 CACCGCGCGCGCTG 2

RESULT 599
BD106627
LOCUS 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Zinc finger protein derivatives and methods therefor.
ACCESSION BD106627
VERSION BD106627.1 GI:23201445
KEYWORDS JP 2002502249-A/42.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Iii,C.F.B., Gottesfeld,J.M. and Wright,P.E.
TITLE Zinc finger protein derivatives and methods therefor
JOURNAL Patent: JP 2002502249-A 42 22-JAN-2002;
    THE SCRIPPS RESEARCH INSTITUTE
COMMENT PN JP 2002502249-A/42
    PD 22-JAN-2002
    PF 27-MAY-1998 JP 1999500870
    PR 27-MAY-1997 US 08/863813
    PI CARLOS F BARBAS III,JOEL M GOTTESFELD,PETER E WRIGHT PC
    C12N15/01,C12N15/11,C12N15/12,C12N15/33,C12N15/62,C12N15/70, PC
    C07K14/00,
    PC C07K14/005,C07K14/435,C07K19/00,A61K38/16,A61K38/17,C12Q1/02,
    PC C12Q1/68,
    PC C12Q1/70
    CC Strandedness: Single;
    CC Topology: Linear;
    FH Key Location/Qualifiers

```

```

FEATURES             FT    CDS             1..18.
source               Location/Qualifiers
                     1..18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT          0 a 3 c 14 g 1 t
Query Match          0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1368 GCGGGGGCGGGCGG 1383
DB 1 GCGTGGCGGGCGGG 15

RESULT 600
BD107307
LOCUS               18 bp DNA linear PAT 18-SEP-2002
DEFINITION          Reelin protein CR-50 epitope domain.
ACCESSION            BD107307
VERSION              BD107307.1 GI:23202125
KEYWORDS              JP 2002017361-A/10.
SOURCE               synthetic construct
ORGANISM              artificial sequences.
REFERENCE             1 (bases 1 to 18)
AUTHORS              Mikeshiba,K. and Tate,N.
TITLE                Reelin protein CR-50 epitope domain
JOURNAL              Patent: JP 2002017361-A 10 22-JAN-2002;
                     THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH
COMMENT              OS Artificial Sequence
                     PN JP 2002017361-A/10
                     PD 22-JAN-2002
                     PF 04-JUL-2000 JP 20020202801
                     PI KATSUHIKO MIKOSHIBA,NAOKO TATE
                     PC C12N15/09,A61K31/711,A61K48/00,A61P25/00,C07K14/47,
                     PC C12N1/15,
                     PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,G01N33/15,G01N33/50, PC
                     G01N33/50,
                     PC G01N33/53// (C12N15/09,C12R1:91), (C12N1/21,C12R1:19),C12N15/00,
                     PC A61K37/02,
                     PC C12N5/00, (C12N15/00,C12R1:91)
                     CC synthetic primer for PCR
                     FH Key Location/Qualifiers
                     FT source 1..18
                     /organism="Artificial Sequence".
FEATURES             source
                     1..18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
BASE COUNT          4 a 5 c 6 g 3 t
Query Match          0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 773 GAGCAGGGCGGCACCA 788
DB 1 GAGCAGTGTGGCACCA 16

RESULT 601
BD171754/c
LOCUS               18 bp DNA linear PAT 18-FEB-2003
DEFINITION          Method for detecting microorganisms, and primer set for detecting
                     microorganisms.
ACCESSION            BD171754
VERSION              BD171754.1 GI:28413048
KEYWORDS              JP 2002223766-A/12.
SOURCE               synthetic construct

```

```

ORGANISM              synthetic construct
                     artificial sequences.
REFERENCE             1 (bases 1 to 18)
AUTHORS              Ezaki,T.
TITLE                Method for detecting microorganisms, and primer set for detecting
                     microorganisms
JOURNAL              Patent: JP 200223766-A 12 13-AUG-2002;
                     RAKAN CO LTD,TAKAYUKI EZAKI,KATSUMI ENDO
COMMENT              OS Artificial Sequence
                     PN JP 200223766-A/12
                     PD 13-AUG-2002
                     PF 31-JAN-2001 JP 2001023742
                     PI TAKAYUKI EZAKI
                     PC
                     C12N15/09,C12O1/69// (C12N15/09,C12R1:01), (C12N15/09,C12R1:385), PC
                     (C12N15/09,C12R1:19), (C12N15/09,C12R1:325), (C12N15/09 PC
                     ,C12R1:645),C12N15/00,
                     PC
                     (C12N15/00,C12R1:01), (C12N15/00,C12R1:385), (C12N15/00,C12R1:19) PC
                     PC
                     (C12N15/00,C12R1:325), (C12N15/00,C12R1:645)
                     CC Description of Artificial Sequence:Synthesized Primer Sequence
                     CC
                     CC for
                     CC Acinetobacter spp
                     FH Key Location/Qualifiers
                     FT source 1..18
                     /organism="Artificial Sequence".
FEATURES             source
                     1..18
                     Location/Qualifiers
                     3 a 6 c 3 g 6 t
BASE COUNT          3 a 6 c 3 g 6 t
Query Match          0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1157 ACCCTAAGCGAGGAGG 1172
DB 17 ACTTTAAGCGAGGAGG 2

RESULT 602
E06267/c
LOCUS               E06267
DEFINITION          Primer.
ACCESSION            E06267
VERSION              E06267.1 GI:2174454
KEYWORDS              JP 1994000085-A/107.
SOURCE               synthetic construct
ORGANISM              artificial sequences.
REFERENCE             1 (bases 1 to 18)
AUTHORS              Seki,M., Honda,Y., Takahashi,K., Murakami,T., Teranishi,Y. and
                     Hayashi,N.
TITLE                GENE OR DNA FRAGMENT DERIVED FROM HEPATITIS C VIRUS, POLYPEPTIDE
                     CODED BY THE SAME AND ITS PRODUCTION
JOURNAL              Patent: JP 1994000085-A 107 11-JAN-1994;
                     MITSUBISHI KASEI CORP
COMMENT              OS Artificial gene
                     OC Artificial sequence; Genes.
                     PN JP 1994000085-A/107
                     PD 11-JAN-1994
                     PF 11-JUN-1992 JP 1992194497
                     PR 11-JUN-1991 JP 91P 139268, 12-JUL-1991 JP 91P 172794, PR
                     07-OCT-1991 JP 91P 287008, 16-DEC-1991 JP 91P 332329, PR
                     20-APR-1992 JP 92P 99957
                     PI SEKI MAKOTO, HONDA YOSHIKAZU, TAKAHASHI KAZUNOBU, PI
                     MURAKAMI TOMOKO,
                     PI TERANISHI YUTAKA, HAYASHI NORIO
                     PC C12N15/51,C07K7/06,C07K7/08,C07K7/10,C07K13/00,C07K15/12, PC

```

C12N1/21,C12N5/10,
 PC C12N15/11,C12N15/70,C12N15/85,C12P21/02//A61K39/00,A61K39/29,
 PC (C12N1/21,C12N15/10,C12R1:91),(C12P21/02,C12R1:19),(C12P21/02,
 PC C12R1:19),(C12N5/10,C12R1:91),(C12P21/02,C12R1:19),(C12P21/02,
 PC C12R1:91),
 PC C07K99:00;
 CC strandedness: Single;
 CC topology: Linear;
 CC Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630" 2 t
 5 a 4 c 7 g
 BASE COUNT
 Query Match 0.8%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 121 CAGCTCGGAGTCATC 136
 Db 18 CCGCTCGGAGTCCTTC 3

RESULT 603
 E06463/c
 LOCUS
 DEFINITION
 E06463
 E06463
 E06463.1 GI:2174650
 JP 1994000086-A/107.
 synthetic construct
 ORGANISM
 artificial sequences.
 1 (bases 1 to 18)
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 5 a 4 c 7 g
 BASE COUNT
 Query Match 0.8%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 121 CAGCTCGGAGTCATC 136
 Db 18 CCGCTCGGAGTCCTTC 3

RESULT 604
 E06463/c
 LOCUS
 DEFINITION
 E06463
 E06463
 E06463.1 GI:2174650
 JP 1994000086-A/107.
 synthetic construct
 ORGANISM
 artificial sequences.
 1 (bases 1 to 18)
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 5 a 4 c 7 g
 BASE COUNT
 Query Match 0.8%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 121 CAGCTCGGAGTCATC 136
 Db 18 CCGCTCGGAGTCCTTC 3

E32535/c
 LOCUS
 DEFINITION
 E32535
 E32535
 E32535.1 GI:13026782
 JP 1999123094-A/35.
 synthetic construct
 ORGANISM
 artificial sequences.
 1 (bases 1 to 18)
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 6 a 8 c 4 g 0 t
 BASE COUNT
 Query Match 0.8%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1225 GGTGCTGGCTCGTGC 1240
 Db 18 GGTGCTGGCTCGTTC 3

RESULT 605
 I34449
 LOCUS
 DEFINITION
 I34449
 I34449
 I34449.1 GI:1825240
 US 5597895-A 9 28-JAN-1997;
 Transdominant tat mutants and uses thereof
 Patent: US 5597895-A 9 28-JAN-1997;
 ORGANISM
 Unclassified.
 1 (bases 1 to 18)
 /organism="unknown"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 3 a 3 c 12 g 0 t
 BASE COUNT
 Query Match 0.8%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1545 GGGGGCGGGGAGG 1560
 Db 2 GGGAGCCGGGAGG 17

RESULT 606
 I73252
 LOCUS
 DEFINITION
 I73252
 I73252.1 GI:1825240
 US 5597895-A 9 28-JAN-1997;
 Transdominant tat mutants and uses thereof
 Patent: US 5597895-A 9 28-JAN-1997;
 ORGANISM
 Unclassified.
 1 (bases 1 to 18)
 /organism="unknown"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 3 a 3 c 12 g 0 t
 BASE COUNT
 Query Match 0.8%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 5.9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1545 GGGGGCGGGGAGG 1560
 Db 2 GGGAGCCGGGAGG 17

```

LOCUS       I73252               18 bp    DNA             linear      PAT 03-APR-1998
DEFINITION   Sequence 9 from patent US 5686264.
ACCESSION    I73252
VERSION      I73252.1   GI:3009391
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Gaynor,R.B., Garcia,J.A. and Harrich,D.
TITLE        Compositions and methods relating to transdominant Tat mutants
JOURNAL      Patent: US 5686264-A 9 11-NOV-1997;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
BASE COUNT   3 a    3 c    12 g    0 t
             0.8%; Score 12.8; DB 1; Length 18;
             Best Local Similarity 87.5%; Pred. No. 5.9e+02;
             Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1545 GGGGGCGCGGGGAGG 1560
      ||||| ||||| ||||| |||||
Db 2 GGGGAGCGCGGAGG 17

RESULT 607
ATH524348/c
LOCUS       ATH524348/c          18 bp    DNA             linear      PRI 21-SEP-2002
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence, left border, clone
              0.8%; Score 12.8; DB 1; Length 18;
              Best Local Similarity 87.5%; Pred. No. 5.9e+02;
              Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ACCESSION    AJ524348
VERSION      AJ524348.1   GI:26792584
KEYWORDS     left border; T-DNA flanking sequence.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE    1
AUTHORS      Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
              Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
              Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
              of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE      22363535
PUBMED       12446565
REFERENCE    2 (bases 1 to 18)
AUTHORS      Balzerque,S.
TITLE        Direct Submission
JOURNAL      Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
              Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="Arabidopsis thaliana"
               /mol_type="genomic DNA"
               /cultivar="Wassilewskija"
               /db_xref="taxon:3702"
               /clone="073E12"
               /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..18

```

```

LOCUS       I73252               18 bp    DNA             linear      PAT 03-APR-1998
DEFINITION   Sequence 9 from patent US 5686264.
ACCESSION    I73252
VERSION      I73252.1   GI:3009391
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 18)
AUTHORS      Gaynor,R.B., Garcia,J.A. and Harrich,D.
TITLE        Compositions and methods relating to transdominant Tat mutants
JOURNAL      Patent: US 5686264-A 9 11-NOV-1997;
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="unknown"
BASE COUNT   3 a    3 c    12 g    0 t
             0.8%; Score 12.8; DB 1; Length 18;
             Best Local Similarity 87.5%; Pred. No. 5.9e+02;
             Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1545 GGGGGCGCGGGGAGG 1560
      ||||| ||||| ||||| |||||
Db 2 GGGGAGCGCGGAGG 17

RESULT 608
D00269S13/c
LOCUS       D00269S13/c          18 bp    DNA             linear      PRI 21-SEP-2002
DEFINITION   Homo sapiens gene for tyrosine hydroxylase, exon 9, partial
              sequence.
ACCESSION    D00281
VERSION      D00281.1   GI:220111
KEYWORDS     13 of 24
SEGMENT      Homo sapiens (human)
SOURCE       Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
AUTHORS      O'Malley,K.L., Anhalt,M.J., Martin,B.M., Kelsae,J.R., Winfield,S.L.
              and Ginsu,B.I.
TITLE        Isolation and characterization of the human tyrosine hydroxylase
              gene: identification of 5' alternative splice sites responsible for
              multiple mRNAs
JOURNAL      Biochemistry 26 (22), 6910-6914 (1987)
MEDLINE      88107612
PUBMED       2892528
REFERENCE    2 (bases 1 to 18)
AUTHORS      Kobayashi,K., Kaneda,N., Ichinose,H., Kishi,F., Nakazawa,A.,
              Kurosawa,Y., Fujita,K. and Nagatsu,T.
TITLE        Structure of the human tyrosine hydroxylase gene: alternative
              splicing from a single gene accounts for generation of four mRNA
              types
JOURNAL      J. Biochem. 103 (6), 907-912 (1988)
MEDLINE      89008200
PUBMED       2902075
COMMENT      In [1], they determined the nucleotide sequences of all exons and
              their surrounding regions of human TH gene, and the exon/intron
              boundaries are shown. The boundaries were determined by comparing
              the genomic DNA sequence with the cDNA sequence. The human TH gene
              is split into 14 exons. In [1], they concluded that the four types
              of human TH mRNA are produced through alternative splicing from a
              single gene.
FEATURES     Location/Qualifiers
             source
               1..18
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /notes="120 bp after segment 12"
             exon
               <1..18
               /product="tyrosine hydroxylase"
               /notes="AA 355 at 1"
               /number=9
             intron
               9..>18
               /number=9
             conflict
               16
               /citation=[1]
               /replace="c"
BASE COUNT   2 a    5 c    8 g    3 t
             0.8%; Score 12.8; DB 1; Length 18;
             Best Local Similarity 87.5%; Pred. No. 5.9e+02;
             Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1190 CCGCTCACGGCCGAGG 1205

```

```

Db      16  CCACTCAGCGCTCAGG 1
|| ||||| |||||
Query Match      0.8%; Score 12.8; DB 1; Length 32;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

RESULT 609
AB069291
LOCUS      18 bp      DNA      linear      SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-R-48021R
at 1p36.
ACCESSION AB069291.1 GI:15130095
VERSION    1
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Matanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
and Soeda, E.
TITLE      A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL    Genomics 74 (1), 55-70 (2001)
MEDLINE    21269192
PUBMED     11374902
REFERENCE  2 (bases 1 to 18)
AUTHORS    Horii, A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES   Location/Qualifiers
            source
              1..18
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
            misc_feature
              1..18
              /note="reverse primer for human STS sts-R-48021R at 1p36
              sts-R-48021R obtained from clones B48021, B337E17, B83P11,
              Human BAC library RPCI-11"
BASE COUNT 4 a 7 c 5 g 2 t
Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1530 AGTCCAGCTGAAGCCG 1545
|| ||||| |||||
Db      2  AGGCCACCTGAAGCCG 17

RESULT 610
LOCUS      32 bp      DNA      linear      PAT 12-MAR-1998
DEFINITION Sequence 5 from Patent WO9720068.
ACCESSION  A62993
VERSION     A62993.1 GI:3716865
KEYWORDS    unidentified
SOURCE       unidentified
ORGANISM     unidentified.
REFERENCE  1
AUTHORS      Oerum, H. and Seeger, C.
TITLE        METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
JOURNAL      Patent: WO 9720068-A 5 05-JUN-1997;
BOEHRINGER MANNHEIM GMBH (DE)
FEATURES     Location/Qualifiers
              1..32
              /organism="unidentified"
              /mol_type="genomic DNA"
              /db_xref="taxon:32644"
BASE COUNT 0 a 30 c 2 g 0 t

Db      16  CCACTCAGCGCTCAGG 1
|| ||||| |||||
Query Match      0.8%; Score 12.8; DB 1; Length 32;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

RESULT 611
LOCUS      32 bp      DNA      linear      PAT 16-MAY-2002
DEFINITION Sequence 5 from patent US 6326143.
ACCESSION  ARI79068
VERSION     ARI79068.1 GI:20220623
KEYWORDS    Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE  1 (bases 1 to 32)
AUTHORS      Orum, H. and Seeger, C.
TITLE        Method for generating multiple double stranded nucleic acids
JOURNAL      Patent: US 6326143-A 5 04-DEC-2001;
FEATURES     Location/Qualifiers
              1..32
              /organism="unknown"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
BASE COUNT 0 a 30 c 2 g 0 t
Query Match      0.8%; Score 12.8; DB 1; Length 32;
Best Local Similarity 62.5%; Pred. No. 5.9e+02;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy      76  CGCACACACCGCGCGCGCGCTCGCGCCGG 107
|| ||||| |||||
Db      1  CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 32

RESULT 612
LOCUS      50 bp      DNA      linear      PAT 31-MAY-2001
DEFINITION Sequence 78 from Patent WO0134654.
ACCESSION  AX146616
VERSION     AX146616.1 GI:14285009
KEYWORDS    Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE  1
AUTHORS      Strauch, K.
TITLE        Hedgehog fusion proteins and uses
JOURNAL      Patent: WO 0134654-A 78 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES     Location/Qualifiers
              1..50
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT 6 a 19 c 15 g 10 t
Query Match      0.8%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1346 GGGGACAGCGCGCGCGCGCGCGCGCG 1369
|| ||||| |||||
Db      5  GGGGTACGCTGCTGGGGTGCTC 28

RESULT 613
BD016571/c
LOCUS      20 bp      DNA      linear      PAT 27-AUG-2002

```


DEFINITION Genes and proteins participating in the upstream of degradation
passage of aromatic polycyclic compound.
ACCESSION BD016571
VERSION BD016571.1 GI:22557747
KEYWORDS JP 2001245662-A/59.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Saito,A., Tamatsubo,K. and Adachi,K.
TITLE Genes and proteins participating in the upstream of degradation
JOURNAL Passage of aromatic polycyclic compound
COMMENT Patent: JP 2001245662-A 59 11-SEP-2001;
MARINE BIOTECHNOLOGY INST CO LTD
OS Artificial Sequence
PN JP 2001245662-A/59
PD 11-SEP-2001
PF 03-MAR-2000 JP 2000059523
PI ATSUSHI SAITO,KAZUAKI TAMATSUBO,KYOKO ADACHI
PC C12N15/09,C12N9/02,C12N15/00
CC Description of Artificial Sequence: Synthetic primer KP205. FH
Key Location/Qualifiers
FEATURES
Source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630" 1 t
BASE COUNT 5 a 5 c 9 g 1 t
Query Match 0.8%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 6.3e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 864 TCCTCACTTCCTGGACCG 882
Db 19 TCCTCGCTGCCAGTCCG 1
RESULT 614
AX146611/C
LOCUS AX146611 47 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 73 from Patent WO0134654.
ACCESSION AX146611
VERSION AX146611.1 GI:14285004
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Strauch,K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 73 17-MAY-2001;
BIOGEN, INC. (US)
FEATURES
Source 1..47
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606" 3 t
BASE COUNT 9 a 15 c 20 g
Query Match 0.8%; Score 12.6; DB 1; Length 47;
Best Local Similarity 55.8%; Pred. No. 5.6e+02;
Matches 24; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 959 CACCTGCTCTTTTGGCGGCACACGACTCGGCCACCGGG 1001
Db 44 CAGCTGCTGGGGTGCTCTCTTCCGAACCCCTGCCCGGG 2
RESULT 615
A87910
LOCUS A87910 14 bp DNA linear PAT 22-JAN-2000

DEFINITION Sequence 58 from Patent WO9833904.
ACCESSION A87910
VERSION A87910.1 GI:6736480
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 58 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Source 1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 3 t
BASE COUNT 1 a 6 c 4 g
Query Match 0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1400 GCTCCAGGTGCTGC 1413
Db 1 GCTCCAGGTGCTGC 14
RESULT 616
A89202/c
LOCUS A89202 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1350 from Patent WO9833904.
ACCESSION A89202
VERSION A89202.1 GI:6737772
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1350 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
Source 1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 0 t
BASE COUNT 5 a 6 c 3 g
Query Match 0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 153 TGCTGCTGCTGGCG 166
Db 14 TGCTGCTGCTGGTG 1
RESULT 617
A89877
LOCUS A89877 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 58 from Patent EP0856579.
ACCESSION A89877
VERSION A89877.1 GI:6738391
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 58 05-AUG-1998;

```

FEATURES
Source
  BIOGNOSTIK GES (DE)
  Location/Qualifiers
    1..14
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
  3 t
BASE COUNT
  1 a 6 c 4 g
Query Match
  0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1400 GCTCCAGGTCGTC 1413
Db 1 GCTCCAGGTCGTC 14

RESULT 618
AX007878
LOCUS
  AX007878
DEFINITION
  Sequence 420 from Patent WO9967428.
ACCESSION
  AX007878
VERSION
  AX007878.1 GI:9995575
KEYWORDS
  Aids-associated retrovirus
SOURCE
  Aids-associated retrovirus
  Viruses; Retroviral viruses; Retroviridae.
REFERENCE
  1
  Stuyver, L.
  Method for detection of drug-selected mutations in the hiv protease
  gene
  INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
  Patent: WO 9967428-A 420 29-DEC-1999;
  Location/Qualifiers
    1..14
    /organism="Aids-associated retrovirus"
    /mol_type="genomic DNA"
    /db_xref="taxon:11966"
  3 a 4 c 4 g 3 t
BASE COUNT
  3 a 4 c 4 g 3 t
Query Match
  0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 440 CTGATGACTCAGAG 453
Db 1 CTGATGACTCAGCG 14

RESULT 619
AX019396/c
LOCUS
  AX019396
DEFINITION
  Sequence 12 from Patent WO9940187.
ACCESSION
  AX019396
VERSION
  AX019396.1 GI:10043366
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
SOURCE
  1
  Abken, H.
  Nucleic acids provided for modulating cellular activation
  Patent: WO 9940187-A 12 12-AUG-1999;
  ABKEN HINRICH (DE)
  Location/Qualifiers
    1..14
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
    /note="synthetic"
  0 a 8 c 3 g 3 t
BASE COUNT
  0 a 8 c 3 g 3 t
Query Match
  0.8%; Score 12.4; DB 1; Length 14;

QY 1164 GCGAGGAGGCGCG 1177
Db 14 GCGAGGAGGCGCG 1

RESULT 620
AX028355/c
LOCUS
  AX028355
DEFINITION
  Sequence 174 from Patent WO036143.
ACCESSION
  AX028355
VERSION
  AX028355.1 GI:10189568
KEYWORDS
  Sus scrofa (pig)
SOURCE
  Sus scrofa
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  1
  Georges, M., Spincemalle, G. and Andersson, L.
  Selecting animals for parentally imprinted traits
  Patent: WO 0036143-A 174 22-JUN-2000;
  SEGHERSGENTEC N V (BE); GEORGES MICHEL (BE); UNIV LIEGE (BE);
  SPINCEMALLE GEERT (BE); MELICA HB (SE); ANDERSSON LEIF (SE)
  Location/Qualifiers
    1..14
    /organism="Sus scrofa"
    /mol_type="genomic DNA"
    /db_xref="taxon:9823"
    /note="Polymorphism in coding region"
  0 a 11 c 3 g 0 t
BASE COUNT
  0 a 11 c 3 g 0 t
Query Match
  0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1551 CCGGGGAGGCGCG 1564
Db 14 CCGGGGAGGCGCG 1

RESULT 621
AX419965
LOCUS
  AX419965
DEFINITION
  Sequence 302 from Patent WO0198537.
ACCESSION
  AX419965
VERSION
  AX419965.1 GI:21524332
KEYWORDS
  synthetic construct
  synthetic construct
  artificial sequences.
SOURCE
  1
  Lyamichev, V., Allawi, H., Dong, F., Neri, B.P. and Vener, I.T.
  Nucleic acid accessible hybridization sites
  Patent: WO 0198537-A 302 27-DEC-2001;
  THIRD WAVE TECHNOLOGIES, INC. (US)
  Location/Qualifiers
    1..14
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
  5 a 2 c 7 g 0 t
BASE COUNT
  5 a 2 c 7 g 0 t
Query Match
  0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CCAGCGGAGGAGAG 23
Db 1 CAAGCGGAGGAGAG 14
```

```

RESULT 622
BD065423          14 bp      DNA      linear      PAT 27-AUG-2002
LOCUS
DEFINITION      An antisense oligonucleotide preparation method.
ACCESSION      BD065423
VERSION        BD065423.1 GI:22611026
KEYWORDS       JP 2001511000-A/58.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS       Schlingensiepen,K.H. and Brysch,W.
TITLE         An antisense oligonucleotide preparation method
JOURNAL       Patent: JP 2001511000-A 58 07-AUG-2001;
              BIOGENSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT       OS Unknown
              PN JP 2001511000-A/58
              PD 07-AUG-2001
              PF 30-JAN-1998 JP 1998532533
              PR 31-JAN-1997 EP 97101331.8
              PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
              PC C12N15/11,C07H21/04,A61K31/70
              CC An antisense oligonucleotide preparation method FH Key
              Location/Qualifiers
              FT source 1..14
              FT Location/Qualifiers
              FT /organism='Unknown'
              FT 1..14
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'
              FT 1 a 6 c 4 g 3 t

BASE COUNT      1 a 6 c 4 g 3 t

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 GTCCACGTCGTCG 1413
Db 1 GTCCACGTCGTCG 14

RESULT 623
BD066715/C
LOCUS
DEFINITION      An antisense oligonucleotide preparation method.
ACCESSION      BD066715
VERSION        BD066715.1 GI:22612318
KEYWORDS       JP 2001511000-A/1350.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS       Schlingensiepen,K.H. and Brysch,W.
TITLE         An antisense oligonucleotide preparation method
JOURNAL       Patent: JP 2001511000-A 1350 07-AUG-2001;
              BIOGENSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT       OS Unknown
              PN JP 2001511000-A/1350
              PD 07-AUG-2001
              PF 30-JAN-1998 JP 1998532533
              PR 31-JAN-1997 EP 97101331.8
              PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
              PC C12N15/11,C07H21/04,A61K31/70
              CC An antisense oligonucleotide preparation method FH Key
              Location/Qualifiers
              FT source 1..14
              FT Location/Qualifiers
              FT /organism='Unknown'
              FT 1..14
              FT /organism='unidentified'
              FT /mol_type='genomic DNA'
              FT /db_xref='taxon:32644'
              FT 1 a 6 c 4 g 3 t

BASE COUNT      1 a 6 c 4 g 3 t

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1400 GTCCACGTCGTCG 1413
Db 1 GTCCACGTCGTCG 14

RESULT 624
BD068930
LOCUS
DEFINITION      Enzymatic nucleic acid treatment of diseases or conditions related
              to levels of epidermal growth factor receptors.
ACCESSION      BD068930
VERSION        BD068930.1 GI:22614533
KEYWORDS       JP 2001511003-A/1770.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS       Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE         Enzymatic nucleic acid treatment of diseases or conditions related
              to levels of epidermal growth factor receptors
JOURNAL       Patent: JP 2001511003-A 1770 07-AUG-2001;
              RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT       OS Unidentified
              PN JP 2001511003-A/1770
              PD 07-AUG-2001
              PF 14-JAN-1998 JP 1998532913
              PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
              PI SAGHR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
              C12N9/00,C07K14/71
              CC Strandedness: Single;
              CC Topology: Linear;
              CC Enzymatic nucleic acid treatment of diseases or conditions CC
              related to
              CC levels of epidermal growth factor receptors
              FH Key
              FT source 1..14
              FT Location/Qualifiers
              FT /organism='Unidentified'
              FT 1..14
              FT Location/Qualifiers
              FT /organism='unidentified'
              FT /mol_type='genomic RNA'
              FT /db_xref='taxon:32644'
              FT 0 a 5 c 6 g 3 t

BASE COUNT      0 a 5 c 6 g 3 t

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1304 GCGCTCCTGCTGCTG 1317
Db 1 GCGCTCCTGCTGCTG 14

RESULT 625
A87986
LOCUS
DEFINITION      Sequence 134 from Patent WO9833904.
ACCESSION      A87986
VERSION        A87986.1 GI:6736556
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Brysch,W. and Schlingensiepen,K.
TITLE         AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL       Patent: WO 9833904-A 134 06-AUG-1998;

```

```

BASE COUNT      5 a 6 c 3 g 0 t

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 153 TGCTGCTGCTGCTG 166
Db 14 TGCTGCTGCTGCTG 1

RESULT 624
BD068930
LOCUS
DEFINITION      Enzymatic nucleic acid treatment of diseases or conditions related
              to levels of epidermal growth factor receptors.
ACCESSION      BD068930
VERSION        BD068930.1 GI:22614533
KEYWORDS       JP 2001511003-A/1770.
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 14)
AUTHORS       Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE         Enzymatic nucleic acid treatment of diseases or conditions related
              to levels of epidermal growth factor receptors
JOURNAL       Patent: JP 2001511003-A 1770 07-AUG-2001;
              RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT       OS Unidentified
              PN JP 2001511003-A/1770
              PD 07-AUG-2001
              PF 14-JAN-1998 JP 1998532913
              PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
              PI SAGHR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
              C12N9/00,C07K14/71
              CC Strandedness: Single;
              CC Topology: Linear;
              CC Enzymatic nucleic acid treatment of diseases or conditions CC
              related to
              CC levels of epidermal growth factor receptors
              FH Key
              FT source 1..14
              FT Location/Qualifiers
              FT /organism='Unidentified'
              FT 1..14
              FT Location/Qualifiers
              FT /organism='unidentified'
              FT /mol_type='genomic RNA'
              FT /db_xref='taxon:32644'
              FT 0 a 5 c 6 g 3 t

BASE COUNT      0 a 5 c 6 g 3 t

Query Match      0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1304 GCGCTCCTGCTGCTG 1317
Db 1 GCGCTCCTGCTGCTG 14

RESULT 625
A87986
LOCUS
DEFINITION      Sequence 134 from Patent WO9833904.
ACCESSION      A87986
VERSION        A87986.1 GI:6736556
KEYWORDS       .
SOURCE         unidentified
ORGANISM       unclassified.
REFERENCE      1 (bases 1 to 15)
AUTHORS       Brysch,W. and Schlingensiepen,K.
TITLE         AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL       Patent: WO 9833904-A 134 06-AUG-1998;

```

Db 15 GGGGTTCCGAGAAGA 2

FEATURES
source
Location/Qualifiers
1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 2 a 4 c 8 g 1 t

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1424 GTGCGGGGCCAC 1437
1 GGTGCAGGGGCCAC 14

Db

RESULT 626
LOCUS A89953
DEFINITION Sequence 134 from Patent EP0856579.
ACCESSION A89953
VERSION A89953.1 GI:6738467
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 134 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES Location/Qualifiers
source
1. .15
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 2 a 4 c 8 g 1 t

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1424 GTGCGGGGCCAC 1437
1 GGTGCAGGGGCCAC 14

Db

RESULT 627
LOCUS AR041268/c
DEFINITION Sequence 58 from patent US 5811300.
ACCESSION AR041268
VERSION AR041268.1 GI:5961764
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TITLE TNF- α ribozymes
JOURNAL Patent: US 5811300-A 58 22-SEP-1998;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"

BASE COUNT 3 a 7 c 1 g 4 t

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 GGGGTTCCGAGAAGA 248
1 GGTGCAGGGGCCAC 14

Db

RESULT 628
LOCUS AR050983/c
DEFINITION Sequence 52 from patent US 5830644.
ACCESSION AR050983
VERSION AR050983.1 GI:5974347
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS West,M.D., Shay,J. and Wright,W.E.
TITLE Method for screening for agents which increase telomerase activity in a cell
JOURNAL Patent: US 5830644-A 52 03-NOV-1998;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"

BASE COUNT 0 a 0 c 8 g 7 t

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACACC 85
15 CACACACACACACC 2

Db

RESULT 629
LOCUS AR131623
DEFINITION Sequence 48 from patent US 6194150.
ACCESSION AR131623
VERSION AR131623.1 GI:14120526
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 48 27-FEB-2001;
FEATURES Location/Qualifiers
source
1. .15
/organism="unknown"

BASE COUNT 2 a 3 c 6 g 4 t

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 898 GAAGGTCCTTCTACG 911
2 GAGGGTCCTTCTACG 15

Db

RESULT 630
LOCUS AR180559/c
DEFINITION Sequence 627 from patent US 6333152.
ACCESSION AR180559
VERSION AR180559.1 GI:20222592
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells

RESULT 633					
AX003643 15 bp DNA linear PAT 24-AUG-2000					
LOCUS					
DEFINITION Sequence 1 from Patent WO927092.					
ACCESSION AX003643					
VERSION AX003643.1 GI:9927432					
KEYWORDS Homo sapiens (human)					
SOURCE Homo sapiens					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE					
1 Liu, N. and Mueller, R.					
TITLE Purified transposon factor cdf-1 and its use					
JOURNAL Patent: WO 9927092-A 1 03-JUN-1999;					
Liu NINGSHU (DE); MOELLER ROUF (DE)					
FEATURES					
source Location/Qualifiers					
1..15					
/organism="Homo sapiens"					
/mol_type="genomic DNA"					
/db_xref="taxon:9606"					
BASE COUNT 4 a 1 c 7 g 3 t					
Query Match 0.8%; Score 12.4; DB 1; Length 15;					
Best Local Similarity 92.9%; Pred.No. 6.5e+02;					
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY 327 CGGAGCGTATGAA 340					
Db 2 CGGAAGCTTTGAA 15					
RESULT 634					
AX028356/c 15 bp DNA linear PAT 16-SEP-2000					
LOCUS					
DEFINITION Sequence 175 from Patent WO0036143.					
ACCESSION AX028356					
VERSION AX028356.1 GI:10189569					
KEYWORDS Sus scrofa (pig)					
SOURCE Sus scrofa					
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.					
REFERENCE					
1 Georges, M., Spincemalle, G. and Andersson, L.					
TITLE Selecting animals for parentally imprinted traits					
JOURNAL Patent: WO 0036143-A 175 22-JUN-2000;					
SECHERGENTECC N V (BE) ; GEORGES MICHEL (BE) ; UNIV LIEGE (BE) ; SPINCEMALLE GERST (BE) ; MELICA HB (SE) ; ANDERSSON LEIF (SE)					
FEATURES					
source Location/Qualifiers					
1..15					
/organism="Sus scrofa"					
/mol_type="genomic DNA"					
/db_xref="taxon:9823"					
/note="Polymorphism in coding region"					
BASE COUNT 0 a 11 c 4 g 0 t					
Query Match 0.8%; Score 12.4; DB 1; Length 15;					
Best Local Similarity 92.9%; Pred.No. 6.5e+02;					
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY 1551 CCGGGGAGGGCGC 1564					
Db 14 CCGGGGAGGGCGC 1					
RESULT 635					
AX328726 15 bp DNA linear PAT 08-JAN-2000					
LOCUS					
DEFINITION Sequence 223 from Patent EP1164203.					
ACCESSION AX328726					
VERSION AX328726.1 GI:18101925					
KEYWORDS					

```

SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE 1
AUTHORS     Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
            Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
TITLE       Dna diagnostics based on mass spectrometry
JOURNAL     Patent: EP 1164203-A 223 19-DEC-2001;
            SEQUENOM, INC. (US)
FEATURES    Location/Qualifiers
            1..15
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
BASE COUNT  2 a 5 c 3 g 4 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 GCACCTGGCTCTCTG 1492
Db 2 GCACCTGACTCTG 15

RESULT 636
AX535794
LOCUS      AX535794 15 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 33 from Patent WO02068684.
ACCESSION  AX535794
VERSION     AX535794.1 GI:25262262
KEYWORDS    synthetic construct
SOURCE      synthetic construct
            artificial sequences.
REFERENCE 1
AUTHORS     Lundeberg,J., Ahmadian,A. and Nyren,P.
TITLE       Allele-specific primer extension assay
JOURNAL     Patent: WO 02068684-A 33 06-SEP-2002;
            Pyrosequencing AB (SE) ; DZIEGLEWSKA, Hanna Eva (GB)
FEATURES    Location/Qualifiers
            1..15
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Extension Probe"
BASE COUNT  2 a 6 c 5 g 2 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 738 GAGCGTCTCCCG 751
Db 2 GAGCGTCTCCCG 15

RESULT 637
AX636188/c
LOCUS      AX636188 15 bp mRNA linear PAT 21-FEB-2003
DEFINITION Sequence 3327 from Patent EP1260586.
ACCESSION  AX636188
VERSION     AX636188.1 GI:28471802
KEYWORDS    .
SOURCE      unidentified
            unclassified.
REFERENCE 1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
genes
JOURNAL     Patent: EP 1260586-A 3327 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            1..15
            /organism="unidentified"
            /mol_type="mRNA"
            /db_xref="taxon:32644"
BASE COUNT  3 a 7 c 1 g 4 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 GGGGTTTCGGGAAGA 248
Db 15 GGGGTTTCGAGAAGA 2

RESULT 639
BD065499
LOCUS      BD065499 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065499
VERSION     BD065499.1 GI:22611102
KEYWORDS    JP 2001511000-A/134.
SOURCE      unidentified
            unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 134 07-AUG-2001;
            BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
            OS Unknown
            PN JP 2001511000-A/134

```

```

TITLE       Method and reagent for inhibiting the expression of disease related
genes
JOURNAL     Patent: EP 1260586-A 3327 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            1..15
            /organism="unidentified"
            /mol_type="mRNA"
            /db_xref="taxon:32644"
BASE COUNT  1 a 5 c 3 g 2 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 644 GCGGTGGAGCGCG 657
Db 14 GAGGTGGAGCGCG 1

RESULT 638
AX636693/c
LOCUS      AX636693 15 bp mRNA linear PAT 24-FEB-2003
DEFINITION Sequence 3832 from Patent EP1260586.
ACCESSION  AX636693
VERSION     AX636693.1 GI:28472307
KEYWORDS    .
SOURCE      unidentified
            unclassified.
REFERENCE 1
AUTHORS     Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
TITLE       Method and reagent for inhibiting the expression of disease related
genes
JOURNAL     Patent: EP 1260586-A 3832 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
            1..15
            /organism="unidentified"
            /mol_type="mRNA"
            /db_xref="taxon:32644"
BASE COUNT  3 a 7 c 1 g 4 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 GGGGTTTCGGGAAGA 248
Db 15 GGGGTTTCGAGAAGA 2

RESULT 639
BD065499
LOCUS      BD065499 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065499
VERSION     BD065499.1 GI:22611102
KEYWORDS    JP 2001511000-A/134.
SOURCE      unidentified
            unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 134 07-AUG-2001;
            BIOLOGISTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
            OS Unknown
            PN JP 2001511000-A/134

```

LOCUS	I12919	15 bp	DNA	linear	PAT 26-JUL-1999
DEFINITION	Sequence 4 from patent US 5429948.				
ACCESSION	I12919				
VERSION	I12919.1	GI:910896			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 15)				
TITLE	Crespi, C.L., Penman, B.W. and Davies, R.L. Human cell line stably expressing 5cDNAs encoding procarcinogen-activating enzymes and related mutagenicity assays				
JOURNAL	Patent: US 5429948-A 4 04-JUL-1995;				
FEATURES	Location/Qualifiers 1..15 /organism="unknown"				
BASE COUNT	2 a 4 c 5 g 4 t				
Query Match	0.8%; Score 12.4; DB 1; Length 15;				
Best Local Similarity	92.9%; Pred. No. 6.5e+02;				
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	165 CGAGATCTCTGCTG 178				
Db	2 CGAGATCTCTGCCG 15				
RESULT 642					
I51784/c					
LOCUS	I51784	15 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 52 from patent US 5645986.				
ACCESSION	I51784				
VERSION	I51784.1	GI:2472985			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 15)				
TITLE	West, M.D., Harley, C.B., Strahl, C.M., McEachern, M.J., Shay, J., Wright, W.E., Blackburn, E.H. and Vaziri, H. Therapy and diagnosis of conditions related to telomere length and/or telomerase activity				
JOURNAL	Patent: US 5645986-A 52 08-JUL-1997;				
FEATURES	Location/Qualifiers 1..15 /organism="unknown"				
BASE COUNT	0 a 0 c 8 g 7 t				
Query Match	0.8%; Score 12.4; DB 1; Length 15;				
Best Local Similarity	92.9%; Pred. No. 6.5e+02;				
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	72 CACACGCACACACC 85				
Db	15 CACACACACACACC 2				
RESULT 643					
I61712/c					
LOCUS	I61712	15 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 266 from patent US 5658780.				
ACCESSION	I61712				
VERSION	I61712.1	GI:2479660			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 15)				
TITLE	Stinchcomb, D.T., Draper, K.G. and McSwiggen, J. Rel a targeted ribozymes				
JOURNAL	Patent: US 5658780-A 266 19-AUG-1997;				
FEATURES	Location/Qualifiers 1..15 /organism="unknown"				

```

BASE COUNT      1 a      9 c      3 g      2 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      644 GCGGTGGAGCCGG 657
Db      14 GAGGTGGAGCCGG 1

RESULT 644
LOCUS      I84393              15 bp      DNA      linear      PAT 04-APR-1998
DEFINITION Sequence 51 from patent US 5695932.
ACCESSION  I84393
VERSION     I84393.1 GI:3021913
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS    West,M.D., Shay,J., Wright,W., Blackburn,E.H. and McEachern,M.J.
TITLE      Telomerase activity assays for diagnosing pathogenic infections
JOURNAL    Patent: US 5695932-A 51 09-DEC-1997;
FEATURES   Location/Qualifiers
            source
            1..15
            /organism="unknown"
BASE COUNT      0 a      0 c      8 g      7 t
Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      72 CACACGACACACC 85
Db      15 CACACACACACC 2

RESULT 645
LOCUS      AR050052              16 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5824857.
ACCESSION  AR050052
VERSION     AR050052.1 GI:5972044
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Beachy,R.N. and Bhattacharyya,M.
TITLE      Plant promoter
JOURNAL    Patent: US 5824857-A 1 20-OCT-1998;
FEATURES   Location/Qualifiers
            source
            1..16
            /organism="unknown"
BASE COUNT      7 a      3 c      2 g      4 t
Query Match      0.8%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      897 AGAAGTCTTCTAC 910
Db      1 AGAAGATCTTCTAC 14

RESULT 646
LOCUS      AX007859              16 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 401 from Patent WO9967428.
ACCESSION  AX007859

```

```

VERSION      AX007859.1 GI:9995556
KEYWORDS     Aids-associated retrovirus
SOURCE       Aids-associated retrovirus
ORGANISM     Viruses; Retrovirdae.
REFERENCE    1
AUTHORS      Stuyver,L.
TITLE        Method for detection of drug-selected mutations in the hiv protease
JOURNAL      gene
JOURNAL      Patent: WO 9967428-A 401 29-DEC-1999;
JOURNAL      INNOGENETICS NV (BE); STUYVER LIEVEN (BE)
FEATURES     Location/Qualifiers
            1..16
            /organism="Aids-associated retrovirus"
            /mol_type="genomic DNA"
            /db_xref="taxon:11966"
BASE COUNT   4 a      3 c      4 g      5 t
Query Match   0.8%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      440 CTGATGACTCAGAG 453
Db      3 CTGTTGACTCAGAG 16

RESULT 647
LOCUS      AX042425              16 bp      DNA      linear      PAT 23-NOV-2000
DEFINITION Sequence 5 from Patent WO0065038.
ACCESSION  AX042425
VERSION     AX042425.1 GI:11341033
KEYWORDS
SOURCE      unidentified
ORGANISM     unclassified.
REFERENCE    1
AUTHORS      Lockert,D.H. and Lynch,C.M.
TITLE        Methods, compositions, and cells for encapsidating recombinant vec
            tors in aav particles
JOURNAL      Patent: WO 0065038-A 5 02-NOV-2000;
JOURNAL      TARGETED GENETICS CORPORATION (US)
FEATURES     Location/Qualifiers
            source
            1..16
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
            /note="Rep68/Rep78 binding site sequence"
BASE COUNT   0 a      7 c      4 g      3 t      2 others
Query Match   0.8%; Score 12.4; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      20 AGAGCGGAGCGGGC 34
Db      15 AGCGAGCGGCGGNC 1

RESULT 648
LOCUS      AX317220              16 bp      DNA      linear      PAT 14-DEC-2001
DEFINITION Sequence 223 from Patent WO0190337.
ACCESSION  AX317220
VERSION     AX317220.1 GI:17900208
KEYWORDS
SOURCE      synthetic construct
ORGANISM     synthetic construct
REFERENCE    1
AUTHORS      Allawi,H., Bartholomay,C.T., Chehak,L., Curtis,M.L., Eis,P.S.,
            Hall,J.G., Ip,H.S., Kaiser,M., Kwiatkowski,R.W., Lukowiak,A.A.,

```


Lyamichev,V., Ma,W., Olson-Munoz,M.C., Olson,S.M., Schaefer,J.J., Skrzypczynski,Z., Takova,T.Y., Vedvik,K.L. and Lyamichev,N.E.
 TITLE
 JOURNAL
 Patent: WO 0150337-A 223 29-NOV-2001;
 THIRD WAVE TECHNOLOGIES, INC. (US)
 FEATURES
 source
 1..16
 Location/Qualifiers
 misc_feature
 1 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 misc_feature
 6 /note="TH 5' end has a fluorescein label."
 /note="The residue at th position is a cy3 abasic linker group."
 BASE COUNT 0 a 7 c 3 g 4 t 2 others
 Query Match 0.8%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 13 GCGAGGGAGAGAGCG 27
 Db 16 GCGAGCGAGAGAGCG 2
 RESULT 649
 AX328727
 LOCUS
 DEFINITION
 Sequence 224 from Patent EP1164203.
 ACCESSION
 AX328727
 VERSION
 AX328727.1 GI:18101926
 KEYWORDS
 unidentified
 SOURCE
 unidentified
 ORGANISM
 unclassified.
 REFERENCE
 1
 AUTHORS
 Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D., Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
 TITLE
 JOURNAL
 Patent: EP 1164203-A 224 19-DEC-2001;
 SEQUENOW, INC. (US)
 FEATURES
 source
 1..16
 Location/Qualifiers
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"
 BASE COUNT 2 a 6 c 3 g 5 t
 Query Match 0.8%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1479 GCACCTGGCTCCTG 1492
 Db 2 GCACCTGACTCCTG 15
 RESULT 650
 AX716641/c
 LOCUS
 DEFINITION
 Sequence 3325 from Patent EP1293569.
 ACCESSION
 AX716641
 VERSION
 AX716641.1 GI:29889956
 KEYWORDS
 synthetic construct
 SOURCE
 synthetic construct
 ORGANISM
 artificial sequences.
 REFERENCE
 1
 AUTHORS
 Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.

Full-length cDNAs
 Patent: EP 1293569-A 3325 19-MAR-2003;
 Helix Research Institute (JP) ; Research Association for Biotechnology (JP)
 TITLE
 JOURNAL
 Patent: WO 03027328-A 17 03-APR-2003;
 Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
 FEATURES
 source
 1..16
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="an artificially synthesized primer sequence"
 BASE COUNT 2 a 5 c 4 g 5 t
 Query Match 0.8%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 712 AGAGAACTCGGTGG 725
 Db 14 ACAGAACTCGGTGG 1
 RESULT 651
 AX741031
 LOCUS
 DEFINITION
 Sequence 5 from Patent WO03027328.
 ACCESSION
 AX741031
 VERSION
 AX741031.1 GI:30523892
 KEYWORDS
 synthetic construct
 SOURCE
 synthetic construct
 ORGANISM
 artificial sequences.
 REFERENCE
 1
 AUTHORS
 Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
 TITLE
 JOURNAL
 Patent: WO 03027328-A 5 03-APR-2003;
 Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
 FEATURES
 source
 1..16
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Description of Combined Probe Sequence"
 /note="Oligomer Sequence-Synthetic Probe Sequence"
 BASE COUNT 2 a 3 c 11 g 0 t
 Query Match 0.8%; Score 12.4; DB 1; Length 16;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 999 GGGAGCCGAGGCG 1012
 Db 1 GGGAGCCGAGGCG 14
 RESULT 652
 AX741043/c
 LOCUS
 DEFINITION
 Sequence 17 from Patent WO03027328.
 ACCESSION
 AX741043
 VERSION
 AX741043.1 GI:30523904
 KEYWORDS
 synthetic construct
 SOURCE
 synthetic construct
 ORGANISM
 artificial sequences.
 REFERENCE
 1
 AUTHORS
 Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
 TITLE
 JOURNAL
 Patent: WO 03027328-A 17 03-APR-2003;
 Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)

```

FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
      /notes="Description of Combined DNA/RNA Molecule:Synthetic
      Oligomer Sequence-Synthetic Probe Sequence"
BASE COUNT      0 a 11 c 3 g
      Query Match      0.8%; Score 12.4; DB 1; Length 16;
      Best Local Similarity 92.9%; Pred. No. 6.6e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 999 GGGAGCCGAGGCG 1012
      |||||
Db 16 GGGAGCCGAGGCG 3

RESULT 653
LOCUS      BD132292      16 bp      DNA      linear      PAT 18-SEP-2002
DEFINITION DNA diagnosis method based on mass spectrometry.
ACCESSION  BD132292
VERSION     BD132292.1 GI:23227237
KEYWORDS   JP 2002507883-A/224.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
          Boom,D.V.D., Jurinke,C. and Rupert A.
TITLE     DNA diagnosis method based on mass spectrometry
JOURNAL   Patent: JP 2002507883-A 224 12-MAR-2002;
          SEQUENOM INC
COMMENT   PN JP 2002507883-A/224
          PD 12-MAR-2002
          PF 06-NOV-1997 JP 1998521832
          PR 06-NOV-1996 US 08/744481,06-NOV-1996 US 08/746036 PR
          23-JAN-1997 US 08/746055,06-NOV-1996 US 08/744590 PR
          06-NOV-1996 US 08/786988,23-JAN-1997 US 08/787639 PR
          19-SEP-1997 US 08/933792,08-OCT-1997 US 08/947801 PI
          KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI
          XIANG,
          PI DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
          C12Q1/68,C07H21/00,C07F9/24
          CC Strandedness: Single;
          CC Topology: Unknown;
          FH Key Location/Qualifiers.
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
BASE COUNT      2 a 6 c 3 g 5 t
      Query Match      0.8%; Score 12.4; DB 1; Length 16;
      Best Local Similarity 92.9%; Pred. No. 6.6e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 GCACCTGGCTCTTG 1492
      |||||
Db 2 GCACCTGACTCTTG 15

RESULT 654
LOCUS      I28863      16 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 8 from patent US 5574142.
ACCESSION  I28863
VERSION     I28863.1 GI:1819650
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unknown.

```

```

Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Meyer,R.B. Jr., Gall,A.A. and Reed,M.W.
TITLE     Peptide linkers for improved oligonucleotide delivery
JOURNAL   Patent: US 5574142-A 8 12-NOV-1996;
          Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
BASE COUNT      3 a 7 c 1 g 5 t
      Query Match      0.8%; Score 12.4; DB 1; Length 16;
      Best Local Similarity 92.9%; Pred. No. 6.6e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 533 TGGGACGAAGATGG 546
      |||||
Db 16 TGTGACGAAGATGG 3

RESULT 655
LOCUS      I35381      16 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 349 from patent US 5599706.
ACCESSION  I35381
VERSION     I35381.1 GI:2088349
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 16)
AUTHORS   Stinchcomb,D.T., McSwiggen,J., Newton,R.S. and Ramharack,R.
TITLE     Ribozymes targeted to apo(a) mRNA
JOURNAL   Patent: US 5599706-A 349 04-FEB-1997;
          Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..16
      /organism="unknown"
BASE COUNT      2 a 6 c 7 g 1 t
      Query Match      0.8%; Score 12.4; DB 1; Length 16;
      Best Local Similarity 92.9%; Pred. No. 6.6e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1485 GGCTCTCGACAGC 1498
      |||||
Db 16 GGCTCTGGGCAGC 3

RESULT 656
LOCUS      A25087      17 bp      DNA      linear      PAT 27-FEB-1995
DEFINITION Synthetic Streptomyces nodosus sequencing primer P321.
ACCESSION  A25087
VERSION     A25087.1 GI:833539
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS   SECONDARY-METABOLITE BIOSYNTHESIS GENES FROM ACTINOMYCETES, METHOD
          OF ISOLATING THEM, AND THEIR USE
TITLE     Patent: WO 9306219-A 8 01-APR-1993;
          Location/Qualifiers
FEATURES
  source
    Location/Qualifiers
      1..17
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"
BASE COUNT      6 a 4 c 7 g 0 t
      Query Match      0.8%; Score 12.4; DB 1; Length 17;
      Best Local Similarity 92.9%; Pred. No. 6.6e+02;
      Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1277 GCCTTCGGCGCCTT 1290
Db 17 GCCTTCGGCGCCTT 4

RESULT 657
LOCUS A25088 17 bp DNA linear PAT 27-FEB-1995
DEFINITION Synthetic Streptomyces nodosus sequencing primer Prev337.
ACCESSION A25088
VERSION A25088.1 GI:8333540
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Hampel, A.E., Tritz, R.H. and Hicks, M.F.
TITLE HIV targeted hairpin ribozymes
JOURNAL Patent: US 5869339-A 27 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 1 a 9 c 5 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1277 GCCTTCGGCGCCTT 1290
Db 1 GCCTTCGGCGCCTT 14

RESULT 658
LOCUS A76795 17 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 11 from Patent WO9315208.
ACCESSION A76795
VERSION A76795.1 GI:6088649
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Wilks, H.M. and Holbrook, J.J.
TITLE CHIRAL SYNTHESIS WITH MODIFIED ENZYMES
JOURNAL Patent: WO 9315208-A 11 05-AUG-1993;
FEATURES Location/Qualifiers
source 1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 0 a 7 c 4 g 6 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1277 GCCTTCGGCGCCTT 1290
Db 1 GCCTTCGGCGCCTT 14

RESULT 659
LOCUS A76795 17 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 11 from Patent WO9315208.
ACCESSION A76795
VERSION A76795.1 GI:6088649
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Wilks, H.M. and Holbrook, J.J.
TITLE CHIRAL SYNTHESIS WITH MODIFIED ENZYMES
JOURNAL Patent: WO 9315208-A 11 05-AUG-1993;
FEATURES Location/Qualifiers
source 1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
BASE COUNT 3 a 7 c 5 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1173 CCGCGGGCGCCTAC 1186
Db 3 CCGCGGGCGCCTAC 16

RESULT 659
LOCUS AR027367/c 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 27 from patent US 5856188.
ACCESSION AR027367
VERSION AR027367.1 GI:5938187

```

```

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hampel, A.E., Tritz, R.H. and Hicks, M.F.
TITLE HIV targeted hairpin ribozymes
JOURNAL Patent: US 5856188-A 27 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 1 a 9 c 5 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 CGGGGACAGCGGCG 1358
Db 15 CGGGGACAGCGGCG 2

RESULT 660
LOCUS AR028821/c 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 27 from patent US 5858785.
ACCESSION AR028821
VERSION AR028821.1 GI:5940794
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hampel, A.E. and Tritz, R.H.
TITLE HIV targeted ribozymes
JOURNAL Patent: US 5858785-A 27 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 1 a 9 c 5 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 CGGGGACAGCGGCG 1358
Db 15 CGGGGACAGCGGCG 2

RESULT 661
LOCUS AR034358/c 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 27 from patent US 5869339.
ACCESSION AR034358
VERSION AR034358.1 GI:5949963
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Hampel, A.E., Tritz, R.H. and Hicks, M.F.
TITLE HIV targeted hairpin ribozymes
JOURNAL Patent: US 5869339-A 27 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 1 a 9 c 5 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. NO. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1345 CGGGACAGCGCG 1358
Db 15 CGGGACAGCGCG 2

RESULT 662
LOCUS AR074719 17 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 16 from patent US 5955276.
ACCESSION AR074719
VERSION AR074719.1 GI:10001472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic
polymorphisms
JOURNAL Patent: US 5955276-A 16 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 7 a 8 c 2 g 0 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 71 GCACAGCACACAC 84
Db 3 GCACACACACAC 16

RESULT 663
LOCUS AR091418 17 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 8 from patent US 5994109.
ACCESSION AR091418
VERSION AR091418.1 GI:10018173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
TITLE Nucleic acid transporter system and methods of use
JOURNAL Patent: US 5994109-A 8 30-NOV-1999;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 8 c 0 g 9 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 AGGGAGAGAGAG 29
Db 17 AGGGAGAGAGAG 4

RESULT 664
LOCUS AR125623 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 8 from patent US 6177554.
ACCESSION AR125623
VERSION AR125623.1 GI:1411695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)

AUTHORS Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S. and Sparrow,J.
TITLE Nucleic acid transporter systems
JOURNAL Patent: US 6177554-A 8 23-JAN-2001;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 8 c 0 g 9 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 AGGGAGAGAGAG 29
Db 17 AGGGAGAGAGAG 4

RESULT 665
LOCUS ARI89922 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5410 from patent US 6346398.
ACCESSION ARI89922
VERSION ARI89922.1 GI:20235887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwigen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 5410 12-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 6 a 4 c 4 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 483 TCTCGGTGATGAAC 496
Db 16 TCTCGGTGATGTAC 3

RESULT 666
LOCUS AR286227 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 599 from patent US 6528640.
ACCESSION AR286227
VERSION AR286227.1 GI:29723823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpelsky,A.,
Matulic-Adamic,J., Sneedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 599 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 3 a 6 c 6 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGAGGACCCAGC 14
Db 4 GCGAGGACCCAGC 17

```

RESULT 667
 AR286325/c
 LOCUS 17 bp RNA linear PAT 10-APR-2003
 DEFINITION Sequence 697 from patent US 6528640.
 ACCESSION AR286325
 VERSION AR286325.1 GI:29723921
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
 TITLE Synthetic ribonucleic acids with RNase activity
 JOURNAL Patent: US 6528640-A 697 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..17
 BASE COUNT 3 a 3 c 9 g 2 t
 Query Match 0.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1301 CACGCGCTCTGGC 1314
 Db 15 CACGCACTCTGGC 2
 RESULT 668
 AR286386
 LOCUS 17 bp RNA linear PAT 10-APR-2003
 DEFINITION Sequence 758 from patent US 6528640.
 ACCESSION AR286386
 VERSION AR286386.1 GI:29723982
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
 TITLE Synthetic ribonucleic acids with RNase activity
 JOURNAL Patent: US 6528640-A 758 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..17
 BASE COUNT 3 a 6 c 5 g 3 t
 Query Match 0.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 759 CCACGGTGACCTG 772
 Db 4 CCACGGTGACGCTG 17
 RESULT 669
 AR286446
 LOCUS 17 bp RNA linear PAT 10-APR-2003
 DEFINITION Sequence 818 from patent US 6528640.
 ACCESSION AR286446
 VERSION AR286446.1 GI:29724042
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A., Matulic-Adamic,J., Sweedler,D. and Zinnen,S.

TITLE Synthetic ribonucleic acids with RNase activity
 JOURNAL Patent: US 6528640-A 818 04-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..17
 BASE COUNT 5 a 5 c 7 g 0 t
 Query Match 0.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 245 AAGAGGAGGACCC 258
 Db 1 AAGAGGAGGACCC 14
 RESULT 670
 AX139192/c
 LOCUS 17 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 40 from Patent EP1076099.
 ACCESSION AX139192
 VERSION AX139192.1 GI:14274865
 KEYWORDS
 SOURCE Mycobacterium tuberculosis
 ORGANISM Mycobacterium tuberculosis
 Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 REFERENCE 1
 AUTHORS Suzuki,Y., Nishida,M. and Takenishi,S.
 TITLE Kit for diagnosis of tubercle bacilli
 JOURNAL Patent: EP 1076099-A 40 14-FEB-2001;
 NISSHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
 (JP)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Mycobacterium tuberculosis"
 /mol_type="genomic DNA"
 /db_xref="taxon:1773"
 /note="capture"
 BASE COUNT 4 a 2 c 8 g 3 t
 Query Match 0.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 6.6e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 394 CCCGACATCATAT 407
 Db 17 CCCGACATCCTAT 4
 RESULT 671
 AX139212/c
 LOCUS 17 bp DNA linear PAT 30-MAY-2001
 DEFINITION Sequence 60 from Patent EP1076099.
 ACCESSION AX139212
 VERSION AX139212.1 GI:14274885
 KEYWORDS
 SOURCE Mycobacterium tuberculosis
 ORGANISM Mycobacterium tuberculosis
 Bacteria; Actinobacteri; Actinobacteridae; Actinomycetales;
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
 tuberculosis complex.
 REFERENCE 1
 AUTHORS Suzuki,Y., Nishida,M. and Takenishi,S.
 TITLE Kit for diagnosis of tubercle bacilli
 JOURNAL Patent: EP 1076099-A 60 14-FEB-2001;
 NISSHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
 (JP)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Mycobacterium tuberculosis"
 /mol_type="genomic DNA"

Query	Subject	Score	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	
-------	---------	-------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--

```

Db      16  AACTGGTGAAGGA 3
RESULT 676
LOCUS   AX216348
DEFINITION
Sequence 1790 from Patent WO0159103.
ACCESSION
AX216348
VERSION
AX216348.1 GI:15526409
KEYWORDS
SYNTHETIC CONSTRUCT
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 1790 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1..17
source
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT      2 a      6 c      8 g      1 t
Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1373  GCGCGGGGCGGCAG 1386
|||||
Db      2  GCGCGGGGCGGCAG 15

RESULT 677
LOCUS   AX216954
DEFINITION
Sequence 2396 from Patent WO0159103.
ACCESSION
AX216954
VERSION
AX216954.1 GI:15527015
KEYWORDS
SYNTHETIC CONSTRUCT
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2396 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1..17
source
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT      1 a      9 c      6 g      1 t
Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      807  GCCCGGGGACCCG 820
|||||
Db      2  GCCCGGGGACCCG 15

RESULT 678
LOCUS   AX216955
DEFINITION
Sequence 2397 from Patent WO0159103.
ACCESSION
AX216955
VERSION
AX216955.1 GI:15527016
KEYWORDS
SYNTHETIC CONSTRUCT
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE
Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2397 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
Location/Qualifiers
1..17
source
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT      1 a      9 c      6 g      1 t
Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      807  GCCCGGGGACCCG 820
|||||
Db      1  GCCCGGGGACCCG 14

RESULT 679
LOCUS   AX227482
DEFINITION
Sequence 854 from Patent WO0157206.
ACCESSION
AX227482
VERSION
AX227482.1 GI:15556623
KEYWORDS
SYNTHETIC CONSTRUCT
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
Fattaey, A.R., Jarvis, T., McSwiggen, J., Bocher, R.N. and Holman, P.S.
TITLE
Method and reagent for the inhibition of checkpoint kinase-1 (chk
1) enzyme
JOURNAL
Patent: WO 0157206-A 854 09-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)
FEATURES
Location/Qualifiers
1..17
source
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
BASE COUNT      3 a      5 c      4 g      5 t
Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      261  AAAAGCTGACCCCT 274
|||||
Db      14  AAAAGCTGACCCCT 1

RESULT 680
LOCUS   AX227592
DEFINITION
Sequence 964 from Patent WO0157206.
ACCESSION
AX227592
VERSION
AX227592.1 GI:15556733
KEYWORDS
SYNTHETIC CONSTRUCT
SOURCE
ORGANISM
synthetic construct
artificial sequences.

```

artificial sequences.

REFERENCE 1
 AUTHORS Fattaey,A.R., Jarvis,T., Mcswiggen,J., Bocher,R.N. and Holman,P.S.
 TITLE Method and reagent for the inhibition of checkpoint kinase-1 (CHK)

JOURNAL 1) enzyme
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)

FEATURES Location/Qualifiers
 1..17

source
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630" 5 t

BASE COUNT 5 a 3 c 4 g 5 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 262 AAAGCTGACCCCTT 275

Db 17 AAAGCTGATCCCTT 4

RESULT 681

AX328728

LOCUS AX328728 17 bp DNA linear PAT 08-JAN-2002

DEFINITION Sequence 225 from Patent EP1164203.

ACCESSION AX328728

VERSION AX328728.1 GI:18101927

KEYWORDS unidentifed

SOURCE unidentifed

ORGANISM unclassified.

REFERENCE 1

AUTHORS Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,

Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,P.

Dna diagnostics based on mass spectrometry

Patient: EP 1164203-A 225 19-DEC-2001;

SEQUENOM, INC. (US)

FEATURES Location/Qualifiers

1..17

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644" 5 t

BASE COUNT 2 a 6 c 4 g 5 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 GCACCTGCTCTG 1492

Db 2 GCACCTGACTCTG 15

RESULT 682

AX498854

LOCUS AX498854 17 bp DNA linear PAT 27-SEP-2002

DEFINITION Sequence 161 from Patent EP1229046.

ACCESSION AX498854

VERSION AX498854.1 GI:23381147

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Zhan,J.

Human testis expressed patched like protein

Patient: EP 1229046-A 161 07-AUG-2002;

Aeomica, Inc. (US)

FEATURES Location/Qualifiers

1..17

/organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606" 2 t

BASE COUNT 2 a 8 c 5 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 986 GACTCGGCCACCGG 999

Db 4 GACTCTGCCACCGG 17

RESULT 683

AX498858

LOCUS AX498858 17 bp DNA linear PAT 27-SEP-2002

DEFINITION Sequence 165 from Patent EP1229046.

ACCESSION AX498858

VERSION AX498858.1 GI:23381151

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Zhan,J.

Human testis expressed patched like protein

Patient: EP 1229046-A 165 07-AUG-2002;

Aeomica, Inc. (US)

FEATURES Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606" 2 t

BASE COUNT 2 a 8 c 5 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 987 ACTCGGCCACCGGG 1000

Db 1 ACTCTGCCACCGGG 14

RESULT 684

AX532312/c

LOCUS AX532312 17 bp DNA linear PAT 22-NOV-2002

DEFINITION Sequence 1821 from Patent EP1239051.

ACCESSION AX532312

VERSION AX532312.1 GI:25256407

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Shaanon,M.

Human posh-like protein 1

Patient: EP 1239051-A 1821 11-SEP-2002;

Aeomica, Inc. (US)

FEATURES Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606" 2 t

BASE COUNT 3 a 9 c 3 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	557 GAGGAGTCTCTGCA 570
Db	17 GAGGGGTCTCTGCA 4
RESULT 685	
AX532313/c	
LOCUS	AX532313 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 1822 from Patent EP1239051.
ACCESSION	AX532313
VERSION	AX532313.1 GI:25256409
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Shannon,M. Homo posh-like protein 1
AUTHORS	TITLE
JOURNAL	Patient: EP 1239051-A 1822 11-SEP-2002;
FEATURES	Location/Qualifiers
source	1..17
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
BASE COUNT	3 a 9 c 3 g 2 t
Query Match	0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity	92.9%; Pred. No. 6.6e+02;
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	557 GAGGAGTCTCTGCA 570
Db	16 GAGGGTCTCTGCA 3
RESULT 686	
AX532314/c	
LOCUS	AX532314 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 1823 from Patent EP1239051.
ACCESSION	AX532314
VERSION	AX532314.1 GI:25256411
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Shannon,M. Homo posh-like protein 1
AUTHORS	TITLE
JOURNAL	Patient: EP 1239051-A 1823 11-SEP-2002;
FEATURES	Location/Qualifiers
source	1..17
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
BASE COUNT	4 a 8 c 3 g 2 t
Query Match	0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity	92.9%; Pred. No. 6.6e+02;
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	557 GAGGAGTCTCTGCA 570
Db	15 GAGGGGTCTCTGCA 2
RESULT 687	
AX532315/c	
LOCUS	AX532315 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 1824 from Patent EP1239051.
ACCESSION	AX532315
VERSION	AX532315.1 GI:25256413
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Shannon,M. Homo posh-like protein 1
AUTHORS	TITLE
JOURNAL	Patient: EP 1239051-A 1824 11-SEP-2002;
FEATURES	Location/Qualifiers
source	1..17
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
BASE COUNT	4 a 7 c 4 g 2 t
Query Match	0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity	92.9%; Pred. No. 6.6e+02;
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	557 GAGGAGTCTCTGCA 570
Db	14 GAGGGGTCTCTGCA 1
RESULT 688	
AX532475	
LOCUS	AX532475 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 1984 from Patent EP1239051.
ACCESSION	AX532475
VERSION	AX532475.1 GI:25256722
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Shannon,M. Human posh-like protein 1
AUTHORS	TITLE
JOURNAL	Patient: EP 1239051-A 1984 11-SEP-2002;
FEATURES	Location/Qualifiers
source	1..17
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
BASE COUNT	2 a 7 c 7 g 1 t
Query Match	0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity	92.9%; Pred. No. 6.6e+02;
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	994 CACCGGGGAGCCGC 1007
Db	4 CACGGGGGAGCCGC 17
RESULT 689	
AX532476	
LOCUS	AX532476 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 1985 from Patent EP1239051.
ACCESSION	AX532476
VERSION	AX532476.1 GI:25256724
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Shannon,M. Human posh-like protein 1
AUTHORS	TITLE
JOURNAL	Patient: EP 1239051-A 1985 11-SEP-2002;
FEATURES	Location/Qualifiers
source	1..17
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
BASE COUNT	2 a 7 c 7 g 1 t
Query Match	0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity	92.9%; Pred. No. 6.6e+02;
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	994 CACCGGGGAGCCGC 1007
Db	4 CACGGGGGAGCCGC 17
RESULT 690	
AX532476	
LOCUS	AX532476 17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 1985 from Patent EP1239051.
ACCESSION	AX532476
VERSION	AX532476.1 GI:25256724
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Shannon,M. Human posh-like protein 1
AUTHORS	TITLE
JOURNAL	Patient: EP 1239051-A 1985 11-SEP-2002;
FEATURES	Location/Qualifiers
source	1..17
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
BASE COUNT	2 a 7 c 7 g 1 t
Query Match	0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity	92.9%; Pred. No. 6.6e+02;
Matches	13

```

TITLE      Human posh-like protein 1
JOURNAL    Patent: EP 1239051-A 1985 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"
BASE COUNT      2 a      7 c      1 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      994 CACCGGGAGCCCG 1007
Db      3 CACGGGGAGCCCG 16

RESULT 690
LOCUS      AX532477      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1986 from Patent EP1239051.
ACCESSION  AX532477
VERSION     AX532477.1 GI:25256726
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1985 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES    source
           1..17
           /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"
BASE COUNT      2 a      7 c      1 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      994 CACCGGGAGCCCG 1007
Db      2 CACGGGGAGCCCG 15

RESULT 691
LOCUS      AX532478      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1987 from Patent EP1239051.
ACCESSION  AX532478
VERSION     AX532478.1 GI:25256728
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M.
TITLE       Human posh-like protein 1
JOURNAL     Patent: EP 1239051-A 1987 11-SEP-2002;
           Aeomica, Inc. (US)
FEATURES    source
           1..17
           /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"
BASE COUNT      2 a      8 c      7 g      0 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      994 CACCGGGAGCCCG 1007
Db      2 CACGGGGAGCCCG 15

RESULT 692
LOCUS      AX673727      17 bp      DNA      linear      PAT 27-MAR-2003
DEFINITION Sequence 2172 from Patent WO03004526.
ACCESSION  AX673727
VERSION     AX673727.1 GI:29332075
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijinder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and their use as
            medicines
JOURNAL     Patent: WO 03004526-A 2172 16-JAN-2003;
           Molecular Engines Laboratories (FR)
FEATURES    source
           1..17
           /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"
BASE COUNT      5 a      4 c      5 g      3 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      869 ACTTTCCTGGACCG 882
Db      17 ACTTTCGTGGACCG 4

RESULT 693
LOCUS      AX687671      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 403 from Patent EP1281758.
ACCESSION  AX687671
VERSION     AX687671.1 GI:29410367
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL     Patent: EP 1281758-A 403 05-FEB-2003;
           Aeomica, Inc. (US)
FEATURES    source
           1..17
           /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="taxon:9606"
BASE COUNT      2 a      9 c      1 g      5 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      864 TCCTCATTCTCTCG 877

```

```

Db      1 TCTCACTATCCTG 14
|||||
RESULT 694
AX687746
LOCUS      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 478 from Patent EP1281758.
ACCESSION AX687746
VERSION    AX687746.1 GI:29410442
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    Patent: EP 1281758-A 478 05-FEB-2003;
FEATURES   Acomica, Inc. (US)
source     1. .17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 3 a 4 c 7 g 3 t
            1 a 6 c 7 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 792 TCGTGAAGGACCTG 805
|||||
Db 4 TCGTGAAGGACCTG 17
|||||

RESULT 695
AX687750
LOCUS      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 482 from Patent EP1281758.
ACCESSION AX687750
VERSION    AX687750.1 GI:29410446
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    Patent: EP 1281758-A 482 05-FEB-2003;
FEATURES   Acomica, Inc. (US)
source     1. .17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 4 a 3 c 8 g 2 t
            0 a 7 c 7 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 793 GGTGAAGGACTGA 806
|||||
Db 1 GGTGAAGGACTGA 14
|||||

RESULT 696
AX688007
LOCUS      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 739 from Patent EP1281758.
ACCESSION AX688007
VERSION    AX688007.1 GI:29410705
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    Patent: EP 1281758-A 739 05-FEB-2003;
FEATURES   Acomica, Inc. (US)
source     1. .17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 1 a 6 c 7 g 3 t
            1 a 6 c 7 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1223 CGGTGCTGGCCTC 1236
|||||
Db 4 CGGTGCTGGCCTC 17
|||||

RESULT 697
AX688008
LOCUS      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 740 from Patent EP1281758.
ACCESSION AX688008
VERSION    AX688008.1 GI:29410706
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    Patent: EP 1281758-A 740 05-FEB-2003;
FEATURES   Acomica, Inc. (US)
source     1. .17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 0 a 7 c 7 g 3 t
            0 a 7 c 7 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1223 CGGTGCTGGCCTC 1236
|||||
Db 3 CGGTGCTGGCCTC 16
|||||

RESULT 698
AX688009
LOCUS      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 741 from Patent EP1281758.
ACCESSION AX688009
VERSION    AX688009.1 GI:29410707
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL    Patent: EP 1281758-A 741 05-FEB-2003;
FEATURES   Acomica, Inc. (US)
source     1. .17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 0 a 7 c 7 g 3 t
            0 a 7 c 7 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1223 CGGTGCTGGCCTC 1236
|||||
Db 3 CGGTGCTGGCCTC 16
|||||

```

```

REFERENCE
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
              mdz12
JOURNAL      Patent: EP 1281758-A 741 05-FEB-2003;
              Aeomica, Inc. (US)
FEATURES
source       Location/Qualifiers
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   0 a      8 c      6 g      3 t
              Query Match      0.8%; Score 12.4; DB 1; Length 17;
              Best Local Similarity 92.9%; Pred. No. 6.6e+02;
              Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1223 CGGGTCTGGCCTC 1236
Db      ||||| ||||| |||||
        2 CGGGTCTGGCCTC 15

RESULT 699
AX688010 AX688010 17 bp DNA linear PAT 31-MAR-2003
LOCUS     Sequence 742 from Patent EP1281758.
DEFINITION
ACCESSION AX688010
VERSION    AX688010.1 GI:29410708
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 742 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source     Location/Qualifiers
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   0 a      9 c      5 g      3 t
              Query Match      0.8%; Score 12.4; DB 1; Length 17;
              Best Local Similarity 92.9%; Pred. No. 6.6e-02;
              Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1223 CGGGTCTGGCCTC 1236
Db      ||||| ||||| |||||
        1 CGGGTCTGGCCTC 14

RESULT 700
AX688727/c AX688727/c 17 bp DNA linear PAT 31-MAR-2003
LOCUS       Sequence 1459 from Patent EP1281758.
DEFINITION
ACCESSION  AX688727
VERSION     AX688727.1 GI:29411431
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 1459 05-FEB-2003;
            Aeomica, Inc. (US)

```

```

FEATURES
source       Location/Qualifiers
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   4 a      6 c      6 g      1 t
              Query Match      0.8%; Score 12.4; DB 1; Length 17;
              Best Local Similarity 92.9%; Pred. No. 6.6e+02;
              Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1401 CTCAGGTGCTGCC 1414
Db      ||||| ||||| |||||
        17 CTCAGGTGCTGCC 4

RESULT 701
AX688728/c AX688728 17 bp DNA linear PAT 31-MAR-2003
LOCUS       Sequence 1460 from Patent EP1281758.
DEFINITION
ACCESSION  AX688728
VERSION     AX688728.1 GI:29411432
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 1460 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source     Location/Qualifiers
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   4 a      6 c      6 g      1 t
              Query Match      0.8%; Score 12.4; DB 1; Length 17;
              Best Local Similarity 92.9%; Pred. No. 6.6e+02;
              Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1401 CTCAGGTGCTGCC 1414
Db      ||||| ||||| |||||
        16 CTCAGGTGCTGCC 3

RESULT 702
AX688729/c AX688729 17 bp DNA linear PAT 31-MAR-2003
LOCUS       Sequence 1461 from Patent EP1281758.
DEFINITION
ACCESSION  AX688729
VERSION     AX688729.1 GI:29411433
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE      Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL    Patent: EP 1281758-A 1461 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source     Location/Qualifiers
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   4 a      5 c      6 g      2 t

```

```

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1401 CTCACGGTCTGCC 1414
Db 15 CTCACGGTCTGCC 2

RESULT 703
AX688730/c
LOCUS AX688730 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1462 from Patent EP1281758.
ACCESSION AX688730
VERSION AX688730.1 GI:29411434
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 5 c 7 g 2 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1401 CTCACGGTCTGCC 1414
Db 14 CTCACGGTCTGCC 1

RESULT 704
AX688735/c
LOCUS AX688735 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1467 from Patent EP1281758.
ACCESSION AX688735
VERSION AX688735.1 GI:29411439
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 7 c 5 g 2 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAG 775
Db 17 CGGTGCACCTGGAG 4

RESULT 707
AX688738/c
LOCUS AX688738 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1470 from Patent EP1281758.
ACCESSION AX688738

```

```

RESULT 705
AX688736/c
LOCUS AX688736 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1468 from Patent EP1281758.
ACCESSION AX688736
VERSION AX688736.1 GI:29411440
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 6 c 6 g 2 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAG 775
Db 16 CGGTGCACCTGGAG 3

RESULT 706
AX688737/c
LOCUS AX688737 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1469 from Patent EP1281758.
ACCESSION AX688737
VERSION AX688737.1 GI:29411441
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 6 c 6 g 2 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAG 775
Db 15 CGGTGCACCTGGAG 2

RESULT 707
AX688738/c
LOCUS AX688738 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1470 from Patent EP1281758.
ACCESSION AX688738

```

```

VERSION      AX698738.1  GI:29411442
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL      mdz12
JOURNAL      Patent: EP 1281758-A 1470 05-FEB-2003;
FEATURES     Aeomica, Inc. (US)
SOURCE       1. .17
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"

BASE COUNT   3 a 5 c 7 g 2 t

Query Match   0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 762 CGGTGCACCTGGAG 775
Db 14 CGGTGCACCTGCAG 1

RESULT 708
AX690457
LOCUS        AX690457 17 bp DNA linear PAT 31-MAR-2003
DEFINITION   Sequence 3189 from Patent EP1281758.
ACCESSION    AX690457
VERSION      AX690457.1 GI:29413338
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL      mdz12
JOURNAL      Patent: EP 1281758-A 3189 05-FEB-2003;
FEATURES     Aeomica, Inc. (US)
SOURCE       1. .17
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"

BASE COUNT   7 a 1 c 9 g 0 t

Query Match   0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 243 GGAAGAGGAGGCAC 256
Db 4 GGAAGAGGAGGAAC 17

RESULT 709
AX690458
LOCUS        AX690458 17 bp DNA linear PAT 31-MAR-2003
DEFINITION   Sequence 3190 from Patent EP1281758.
ACCESSION    AX690458
VERSION      AX690458.1 GI:29413339
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

```

```

AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL      mdz12
JOURNAL      Patent: EP 1281758-A 3190 05-FEB-2003;
FEATURES     Aeomica, Inc. (US)
SOURCE       1. .17
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"

BASE COUNT   8 a 1 c 8 g 0 t

Query Match   0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 243 GGAAGAGGAGGCAC 256
Db 3 GGAAGAGGAGGAAC 16

RESULT 710
AX690459
LOCUS        AX690459 17 bp DNA linear PAT 31-MAR-2003
DEFINITION   Sequence 3191 from Patent EP1281758.
ACCESSION    AX690459
VERSION      AX690459.1 GI:29413340
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL      mdz12
JOURNAL      Patent: EP 1281758-A 3191 05-FEB-2003;
FEATURES     Aeomica, Inc. (US)
SOURCE       1. .17
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"

BASE COUNT   8 a 1 c 7 g 1 t

Query Match   0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 243 GGAAGAGGAGGCAC 256
Db 2 GGAAGAGGAGGAAC 15

RESULT 711
AX690460
LOCUS        AX690460 17 bp DNA linear PAT 31-MAR-2003
DEFINITION   Sequence 3192 from Patent EP1281758.
ACCESSION    AX690460
VERSION      AX690460.1 GI:29413341
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS      Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE        Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL      mdz12
JOURNAL      Patent: EP 1281758-A 3192 05-FEB-2003;
FEATURES     Aeomica, Inc. (US)
SOURCE       1. .17

```

```

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

BASE COUNT      7 a      1 c      7 g      2 t

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

QY 243 GGAAGAGGAGGCAC 256
|||||
Db 1 GGAAGAGGAGGCAC 14

RESULT 712
LOCUS      AX696158      17 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 57 from Patent WO03008640.
ACCESSION  AX696158
VERSION     AX696158.1 GI:29419318
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE    1
AUTHORS     Whittaker P.A., Meyers, D.A., Postma, D.S. and Bleecker, E.R.
TITLE       Asthma-associated gene
JOURNAL     Patent: WO 03008640-A 57 30-JAN-2003;
            Novartis AG (CH); Novartis Pharma GmbH (AT); Wake Forest
            University Health Sciences (US); Rijksuniversiteit te Groningen
            (NL)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

BASE COUNT      2 a      6 c      5 g      4 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 971 GTGGGCGCCGACAA 984
|||||
Db 1 GTGGGCGCCGCTCAA 14

RESULT 713
AX722711/c
LOCUS      AX722711      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 398 from Patent WO03025176.
ACCESSION  AX722711
VERSION     AX722711.1 GI:30423212
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    1
AUTHORS     Telerman, A., Anson, R. and Tuijthof, M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 398 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"

BASE COUNT      3 a      3 c      6 g      5 t

```

```

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 681 CCAAGGCACATATC 694
|||||
Db 14 CCAAGGCACATATC 1

RESULT 714
AX724356
LOCUS      AX724356      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2043 from Patent WO03025176.
ACCESSION  AX724356
VERSION     AX724356.1 GI:30503699
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    1
AUTHORS     Telerman, A., Anson, R. and Tuijthof, M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 2043 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"

BASE COUNT      4 a      5 c      3 g      5 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 293 ATCCCAATGTGGC 306
|||||
Db 2 ATCCCAATGTGGC 15

RESULT 715
AX724898
LOCUS      AX724898      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2585 from Patent WO03025176.
ACCESSION  AX724898
VERSION     AX724898.1 GI:30504241
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    1
AUTHORS     Telerman, A., Anson, R. and Tuijthof, M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL     Patent: WO 03025176-A 2585 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    Location/Qualifiers
            source
            1..17
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"

BASE COUNT      3 a      8 c      4 g      2 t

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 873 TCCTGGACCGGAC 886

```

```

Db      3 TCTTGGACCGCCAC 16
|||||
RESULT 716
AX726731
LOCUS      AX726731
DEFINITION Sequence 4418 from Patent WO03025176.
ACCESSION AX726731
VERSION    AX726731.1 GI:30506074
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 4418 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
            1..17
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
BASE COUNT 6 a 5 c 3 g 3 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      346 GATCTCCAGAAACT 359
|||||
Db      1 GATCCCCAGAAACT 14

RESULT 717
AX727805
LOCUS      AX727805
DEFINITION Sequence 5492 from Patent WO03025176.
ACCESSION AX727805
VERSION    AX727805.1 GI:30507148
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 5492 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
            1..17
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
BASE COUNT 7 a 5 c 3 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      548 CACCACTCAGAGGA 561
|||||
Db      4 CACCACTCAGAGAA 17

RESULT 718
AX728285
LOCUS      AX728285
DEFINITION Sequence 5972 from Patent WO03025176.
ACCESSION AX728285
VERSION    AX728285.1 GI:30507628
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025176-A 5972 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
            1..17
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
BASE COUNT 2 a 11 c 2 g 2 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1549 GCGCGGGGAGGGG 1562
|||||
Db      17 GCGTGGGGGAGGGG 4

RESULT 719
AX729359
LOCUS      AX729359
DEFINITION Sequence 993 from Patent WO03025175.
ACCESSION AX729359
VERSION    AX729359.1 GI:30508702
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS    Telerman,A., Amson,R. and Tuijinder,M.
TITLE      Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
JOURNAL    Patent: WO 03025175-A 993 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES   source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT 2 a 3 g 4 t
Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      944 CTGCTCACCAGCGGC 957
|||||
Db      4 CTCTCACCAGCGGC 17

RESULT 720
AX729407/c
LOCUS      AX729407
DEFINITION Sequence 1041 from Patent WO03025175.
ACCESSION AX729407
VERSION    AX729407.1 GI:30508750

```



```

KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 4836 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     Location/Qualifiers
              source
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   4 a 8 c 3 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1513 GCTGGGCGATGGCG 1526
Db 17 GCTGGGCGATGGTG 4

RESULT 721
LOCUS      AX732545 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4179 from Patent WO03025175.
ACCESSION  AX732545
VERSION     AX732545.1 GI:30511888
KEYWORDS    Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 4179 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     Location/Qualifiers
              source
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   3 a 6 c 6 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1192 GTCACGGCCGCG 1205
Db 1 GATCACGGCCGCG 14

RESULT 722
LOCUS      AX733202/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 4836 from Patent WO03025175.
ACCESSION  AX733202
VERSION     AX733202.1 GI:30512545
KEYWORDS    Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 4836 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     Location/Qualifiers
              source
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   5 a 4 c 5 g 3 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 869 ACTTCTCGGACCG 882
Db 17 ACTTCTCGGACCG 4

RESULT 723
LOCUS      AX735559/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1149 from Patent WO03025177.
ACCESSION  AX735559
VERSION     AX735559.1 GI:30514836
KEYWORDS    Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments
JOURNAL      Patent: WO 03025177-A 1149 27-MAR-2003;
              Molecular Engines Laboratories (FR)
FEATURES     Location/Qualifiers
              source
              1..17
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   9 a 1 c 5 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 903 TCTTCTACGTGATC 916
Db 14 TCTTCTACTTGATC 1

RESULT 724
LOCUS      AX737927 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3517 from Patent WO03025177.
ACCESSION  AX737927
VERSION     AX737927.1 GI:30517215
KEYWORDS    Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or resistance to viruses and the use
              thereof as medicaments

```

JOURNAL Patent: WO 03025177-A 3517 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 7 a 5 c 2 g 3 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 254 CACCCCAAAAAGCT 267

|||||

4 CACCTCAAAAAGCT 17

RESULT 725

AX738886

LOCUS AX738886 17 bp DNA linear PAT 08-MAY-2003

DEFINITION Sequence 4476 from Patent WO03025177.

ACCESSION AX738886

VERSION AX738886.1 GI:30518176

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Telerman, A., Amson, R. and Tuijinder, M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments

JOURNAL Patent: WO 03025177-A 4476 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)

source Location/Qualifiers

1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 5 a 4 c 4 g 4 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1525 GGTCAAGTCCAGCT 1538

|||||

1 GATCAAGTCCAGCT 14

RESULT 726

ED013476/c

LOCUS ED013476 17 bp DNA linear PAT 27-AUG-2002

DEFINITION Diagnosis kit of tubercle bacillus.

ACCESSION ED013476

VERSION ED013476.1 GI:22553790

KEYWORDS JP 2001103981-A/40.

SOURCE Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 17)

Suzuki, S., Nishida, M. and Takenishi, S.

TITLE Diagnosis kit of tubercle bacillus

JOURNAL Patent: JP 2001103981-A 40 17-APR-2001;

COMMENT NISSHINO IND INC, SYSTEM RESEARCH CO LTD

OS Mycobacterium tuberculosis

PN JP 2001103981-A/40

PD 17-APR-2001

PF 26-JUL-2000 JP 2000225985

PI SADAHIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, C12Q1/68, C12R1/32, PC
(C12Q1/68, C12R1/32), (C12Q1/68, C12R1/33), C12N15/00, C12N15/00 CC

capture

FT Key Location/Qualifiers

FT source 1. .17

FT /organism="Mycobacterium tuberculosis".

FEATURES Location/Qualifiers

source 1. .17

/organism="Mycobacterium tuberculosis"

/mol_type="genomic DNA"

/db_xref="taxon:1773"

BASE COUNT 4 a 2 c 8 g 3 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 394 CCCGACATCATAT 407

|||||

17 CCCGACATCTTAT 4

RESULT 727

BD013496/c

LOCUS BD013496

DEFINITION Diagnosis kit of tubercle bacillus.

ACCESSION BD013496

VERSION BD013496.1 GI:22553810

KEYWORDS JP 2001103981-A/60.

SOURCE Mycobacterium tuberculosis

ORGANISM Mycobacterium tuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 17)

Suzuki, S., Nishida, M. and Takenishi, S.

TITLE Diagnosis kit of tubercle bacillus

JOURNAL Patent: JP 2001103981-A 60 17-APR-2001;

COMMENT NISSHINO IND INC, SYSTEM RESEARCH CO LTD

OS Mycobacterium tuberculosis

PN JP 2001103981-A/60

PD 17-APR-2001

PF 26-JUL-2000 JP 2000225985

PI SADAHIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/09, C12M1/00, C12Q1/68, C12Q1/68, C12R1/32, PC
(C12Q1/68, C12R1/32), (C12Q1/68, C12R1/33), C12N15/00, C12N15/00 CC

capture

FT Key Location/Qualifiers

FT source 1. .17

FT /organism="Mycobacterium tuberculosis".

FEATURES Location/Qualifiers

source 1. .17

/organism="Mycobacterium tuberculosis"

/mol_type="genomic DNA"

/db_xref="taxon:1773"

BASE COUNT 5 a 4 c 5 g 3 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 6.6e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 125 TCGGAGTCATCATG 138

|||||

16 TCGGAGTCATCTG 3

RESULT 728

BD067380/c

LOCUS BD067380

DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.

ACCESSION BD067380

17 bp RNA linear PAT 27-AUG-2002
Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.

```

VERSION BD067380.1 GI:22612983
KEYWORDS JP 2001511003-A/220.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
        to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 220 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
PN JP 2001511003-A/220
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Unidentified'.

FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644' 4 t

BASE COUNT 5 a 0 c 8 g 4 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 348 TCTCCAGAAACTCC 361
Db 17 TCTCCAGAAACTCC 4

RESULT 729
LOCUS BD067381/c 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067381
VERSION BD067381.1 GI:22612984
KEYWORDS JP 2001511003-A/221.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 221 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
PN JP 2001511003-A/221
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..17

```

```

FEATURES
source
Location/Qualifiers
1..17
/organism='Unidentified'.

BASE COUNT 5 a 0 c 8 g 4 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 348 TCTCCAGAAACTCC 361
Db 16 TCTCCAGAAACTCC 3

RESULT 730
LOCUS BD104453 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104453
VERSION BD104453.1 GI:22650027
KEYWORDS WO 0192572-A/557.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and
        Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 557 06-DEC-2001;
        NISSHINBO INDUSTRIES INC.SYSTEM RESEARCH INC.HIDETOSHI INOKO, TAEKO
        KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
        NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/557
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
        MATSUMURA,
        SHOGO MORIYA, MICHIO NISHIDA
        PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
        CC Description of Artificial Sequence:capture
        FH Key Location/Qualifiers
        FT source 1..17
        FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630' 2 t

BASE COUNT 0 a 7 c 8 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1024 GGGGCCGCGCTTCCG 1037
Db 4 GGGGCCGCGCTGCG 17

RESULT 731
LOCUS BD104759/c 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104759
VERSION BD104759.1 GI:22650333
KEYWORDS WO 0192572-A/863.
SOURCE synthetic construct
ORGANISM synthetic construct

```

```

T. . I. /
/organism="synthetic construct"
/mol_type="genomic DNA"
/db xref="taxon:32630"

```

RESULT 735
I38726
I38726
LOCUS
I38726 17 bp DNA linear PAT 13-MAY-1997

BASE COUNT	0 a	7 c	4 g	6 t	
Query Match	0.8%;	Score 12.4;	DB 1;	Length 17;	
Best Local Similarity	92.9%;	Pred. No. 6.6e+02;			
Matches 13;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
QY	1277	GCCTTCGGCCCTT 1290			
Db	1	GCCTTCGGGCTT 14			
RESULT 738					
LOCUS	184401		30 bp	DNA	linear
DEFINITION	Sequence 2 from patent US 5695933.				
ACCESSION	184401				
VERSION	184401.1	GI:3021921			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 30)				
AUTHORS	Schalling, M., Hudson, T.J. and Housman, D.E.				
TITLE	Direct detection of expanded nucleotide repeats in the human genome				
JOURNAL	Patent: US 5695933-A 2 09-DEC-1997;				
FEATURES	Location/Qualifiers				
source	1..30				
BASE COUNT	0 a	20 c	10 g	0 t	
Query Match	0.8%;	Score 12.4;	DB 1;	Length 30;	
Best Local Similarity	63.3%;	Pred. No. 6.6e+02;			
Matches 19;	Conservative 0;	Mismatches 11;	Indels 0;	Gaps 0;	
QY	1410	CTGCGGACGCTCGGGTGCGGGGCCACCG 1439			
Db	1	CCGCGCGCGCGCGCGCGCGCGCGCG 30			
RESULT 739					
LOCUS	AX216373		17 bp	mRNA	linear
DEFINITION	Sequence 1815 from Patent WO0159103.				
ACCESSION	AX216373				
VERSION	AX216373.1	GI:15526434			
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1				
AUTHORS	Blatt, L., McSwiggen, J. and Chowrira, B.M.				
TITLE	Method and reagent for the modulation and diagnosis of cd20 and				
JOURNAL	nogo gene expression				
Patent:	WO 0159103-A 1815 16-AUG-2001;				
RIBOZYME PHARMACEUTICALS, INC. (US) ;	Blatt, Lawrence (US) ;				
McSwiggen, James (US) ;	Chowrira, Bharat M. (US)				
Location/Qualifiers					
source	1..17				
BASE COUNT	0 a	9 c	7 g	1 t	
Query Match	0.8%;	Score 12.2;	DB 1;	Length 17;	
Best Local Similarity	82.4%;	Pred. No. 7.1e+02;			
Matches 14;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;	
QY	1408	TGCTGCCGACGCTCGG 1424			
Db	1	TGCCGCGCGCGCCCGG 17			

```

RESULT 740
AX216946
LOCUS AX216946 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2388 from Patent WO0159103.
ACCESSION AX216946
VERSION AX216946.1 GI:15527007
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 10 c 6 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1319 CTGCGCCGCGCGCCAC 1335
Db 1 CTGCGCCGCGCGCCCGCC 17

RESULT 741
AX216951
LOCUS AX216951 17 bp mRNA linear PAT 07-SEP-2001
DEFINITION Sequence 2393 from Patent WO0159103.
ACCESSION AX216951
VERSION AX216951.1 GI:15527012
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
BASE COUNT 0 a 9 c 7 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1407 GTGCTGCCGACGCTCCG 1423
Db 1 GTGCGCCGCGCGCCCGCC 17

RESULT 742
AX499046/c
LOCUS AX499046 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 353 from Patent EP1229046.

```

```

ACCESSION AX499046
VERSION AX499046.1 GI:23381339
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 353 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 9 c 5 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1532 TCCAGCTGAAGCGGG 1548
Db 17 TCCAGCGCGAGCGGG 1

RESULT 743
A27313
LOCUS A27313 17 bp DNA linear PAT 26-SEP-1995
DEFINITION Synthetic betaGlc linker 1.
ACCESSION A27313
VERSION A27313.1 GI:1248429
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sedlacek, H.H.
TITLE Fusion proteins with monoclonal antibody, linker and beta
JOURNAL Glucuronidase for prodrug activation; Preparation and use thereof
Patent: EP 0501215-A 5 02-SEP-1992;
BEHRINGERWERKE Aktiengesellschaft
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 1 a 5 c 10 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1374 GCGCGCGCGCGAGTA 1390
Db 1 GCGCGCGCGCGGTGCA 17

RESULT 744
A87923/c
LOCUS A87923 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 71 from Patent WO9833904.
ACCESSION A87923
VERSION A87923.1 GI:6736493
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Brysch, W. and Schlingensiepen, K.

```

TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 71 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)

FEATURES

source
1..17
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 6 a 3 c 5 g 3 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GCTCTACAGCGACTTCC 866
Db 17 GCTGTACATTGACTTCC 1

RESULT 745

LOCUS A89890 17 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 71 from Patent EP0856579.
ACCESSION A89890
VERSION A89890.1 GI:6738404

KEYWORDS unidentified

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Brysch,W.D. and Schlingensiepen,K.D.

TITLE An antisense oligonucleotide preparation method

JOURNAL Patent: EP 0856579-A 71 05-AUG-1998;
BIOGOSTIK GES (DE)

FEATURES

source 1..17
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

BASE COUNT 6 a 3 c 5 g 3 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GCTCTACAGCGACTTCC 866
Db 17 GCTGTACATTGACTTCC 1

RESULT 746

LOCUS AR024080 17 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 30 from patent US 5795778.
ACCESSION AR024080
VERSION AR024080.1 GI:3977374

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Draper,K.G.

TITLE Method and reagent for inhibiting herpes simplex virus replication

JOURNAL Patent: US 5795778-A 30 18-AUG-1998;
BIOGOSTIK GES (DE)

FEATURES

source 1..17
Location/Qualifiers
/organism="unknown"

BASE COUNT 0 a 13 c 3 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GCTCTACAGCGACTTCC 866
Db 17 GCTGTACATTGACTTCC 1

RESULT 747

LOCUS AR039607 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 455 from patent US 5807743.
ACCESSION AR039607
VERSION AR039607.1 GI:5958970

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.

TITLE Interleukin-2 receptor gamma-chain ribozymes

JOURNAL Patent: US 5807743-A 11 15-SEP-1998;
BIOGOSTIK GES (DE)

FEATURES

source 1..17
Location/Qualifiers
/organism="unknown"

BASE COUNT 6 a 5 c 2 g 4 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 128 GAAGTCATCATTCAT 144
Db 1 GAAGCCATCATTCAT 17

QY 1549 GGCGCGGGAGGGGCGC 1565
Db 17 GGCGCGGGAGGGGCGC 1

RESULT 747

LOCUS AR029907 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 96 from patent US 5861244.
ACCESSION AR029907
VERSION AR029907.1 GI:5943121

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Wang,C.-G. and Heburn,A.G.

TITLE Genetic sequence assay using DNA triple strand formation

JOURNAL Patent: US 5861244-A 96 19-JAN-1999;
BIOGOSTIK GES (DE)

FEATURES

source 1..17
Location/Qualifiers
/organism="unknown"

BASE COUNT 0 a 14 c 1 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1558 AGGGCGCGGGAGGGG 1574
Db 17 AGGGCGCGGGAGGGG 1

RESULT 748

LOCUS AR039163 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5807743.
ACCESSION AR039163
VERSION AR039163.1 GI:5958526

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.

TITLE Interleukin-2 receptor gamma-chain ribozymes

JOURNAL Patent: US 5807743-A 11 15-SEP-1998;
BIOGOSTIK GES (DE)

FEATURES

source 1..17
Location/Qualifiers
/organism="unknown"

BASE COUNT 6 a 5 c 2 g 4 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 128 GAAGTCATCATTCAT 144
Db 1 GAAGCCATCATTCAT 17

RESULT 749

LOCUS AR039607 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 455 from patent US 5807743.
ACCESSION AR039607
VERSION AR039607.1 GI:5958970

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.

TITLE Interleukin-2 receptor gamma-chain ribozymes

JOURNAL Patent: US 5807743-A 11 15-SEP-1998;
BIOGOSTIK GES (DE)

FEATURES

source 1..17
Location/Qualifiers
/organism="unknown"

BASE COUNT 6 a 5 c 2 g 4 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 128 GAAGTCATCATTCAT 144
Db 1 GAAGCCATCATTCAT 17

```

TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 455 15-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1. .17
BASE COUNT 0 a 11 c 0 g 6 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 15 GAGGAGGAGCGAGCG 31
Db 17 GAGGAGGAGGAGGAGG 1

RESULT 750
AR039609/c
LOCUS AR039609
DEFINITION Sequence 457 from patent US 5807743.
ACCESSION AR039609
VERSION AR039609.1 GI:5958972
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 457 15-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1. .17
BASE COUNT 0 a 11 c 0 g 6 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 GCGAGGAGAGCGAGCG 29
Db 17 GCGAGGAGGAGGAGGAGG 1

RESULT 751
AR039611/c
LOCUS AR039611
DEFINITION Sequence 459 from patent US 5807743.
ACCESSION AR039611
VERSION AR039611.1 GI:5958974
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 459 15-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1. .17
BASE COUNT 0 a 10 c 0 g 7 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 AGCGAGGAGAGAGCGA 28
Db 17 AGCGAGGAGGAGGAGG 1

RESULT 752
AR039615/c
LOCUS AR039615
DEFINITION Sequence 463 from patent US 5807743.
ACCESSION AR039615
VERSION AR039615.1 GI:5958978
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 463 15-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1. .17
BASE COUNT 0 a 10 c 0 g 7 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 41 GAGCGAGGAGGAGGAG 57
Db 17 GAGGAGGAGGAGGAGG 1

RESULT 753
AR039963/c
LOCUS AR039963
DEFINITION Sequence 811 from patent US 5807743.
ACCESSION AR039963
VERSION AR039963.1 GI:5959326
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 811 15-SEP-1998;
FEATURES Location/Qualifiers
SOURCE 1. .17
BASE COUNT 2 a 6 c 6 g 3 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 426 CCGGAGGCGACAGGCTG 442
Db 17 CCGGAGGCGACAGGCTG 1

RESULT 754
AR046684
LOCUS AR046684
DEFINITION Sequence 1477 from patent US 5817796.
ACCESSION AR046684
VERSION AR046684.1 GI:5968149
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myc ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 1477 06-OCT-1998;
FEATURES Location/Qualifiers
SOURCE 1. .17
BASE COUNT 5 a 5 c 4 g 3 t

```



```

Query Match          0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1205 GGCACCATTCATCAAA 1221
|||||
Db 1 GGCACCATTCGACAA 17

RESULT 755
AR074706          17 bp      DNA      linear      PAT 28-AUG-2000
LOCUS
DEFINITION      Sequence 3 from patent US 5955276.
ACCESSION      AR074706
VERSION      AR074706.1 GI:10001459
KEYWORDS      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Morgante,M. and Vogel,J.Marie.
TITLE      Compound microsatellite primers for the detection of genetic
POLYMERPHISMS
JOURNAL      Patent: US 5955276-A 3 21-SEP-1999;
FEATURES      Location/Qualifiers
source      1. .17
/organism="unknown"
BASE COUNT      9 a      0 c      8 g      0 t

Query Match          0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 AGCGAGGAGAGAGCGCA 28
|||||
Db 1 AGAGAGAGAGAGAGAGA 17

RESULT 756
AR074707          17 bp      DNA      linear      PAT 28-AUG-2000
LOCUS
DEFINITION      Sequence 4 from patent US 5955276.
ACCESSION      AR074707
VERSION      AR074707.1 GI:10001460
KEYWORDS      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Morgante,M. and Vogel,J.Marie.
TITLE      Compound microsatellite primers for the detection of genetic
POLYMERPHISMS
JOURNAL      Patent: US 5955276-A 4 21-SEP-1999;
FEATURES      Location/Qualifiers
source      1. .17
/organism="unknown"
BASE COUNT      8 a      0 c      9 g      0 t

Query Match          0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 GCGAGGAGAGAGCGCAG 29
|||||
Db 1 GAGAGAGAGAGAGAGAG 17

RESULT 757
AR074708          17 bp      DNA      linear      PAT 28-AUG-2000
LOCUS
DEFINITION      Sequence 5 from patent US 5955276.
ACCESSION      AR074708

```

```

VERSION      AR074708.1 GI:10001461
KEYWORDS      Unknown.
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Morgante,M. and Vogel,J.Marie.
TITLE      Compound microsatellite primers for the detection of genetic
POLYMERPHISMS
JOURNAL      Patent: US 5955276-A 5 21-SEP-1999;
FEATURES      Location/Qualifiers
source      1. .17
/organism="unknown"
BASE COUNT      0 a      8 c      0 g      9 t

Query Match          0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 AGCGAGGAGAGAGCGCA 28
|||||
Db 17 AGAGAGAGAGAGAGAGA 1

RESULT 758
AR074709/c
LOCUS
DEFINITION      Sequence 6 from patent US 5955276.
ACCESSION      AR074709
VERSION      AR074709.1 GI:10001462
KEYWORDS      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Morgante,M. and Vogel,J.Marie.
TITLE      Compound microsatellite primers for the detection of genetic
POLYMERPHISMS
JOURNAL      Patent: US 5955276-A 6 21-SEP-1999;
FEATURES      Location/Qualifiers
source      1. .17
/organism="unknown"
BASE COUNT      0 a      9 c      0 g      8 t

Query Match          0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 GCGAGGAGAGAGCGCAG 29
|||||
Db 17 GAGAGAGAGAGAGAGAG 1

RESULT 759
AR107651
LOCUS
DEFINITION      Sequence 4 from patent US 6110665.
ACCESSION      AR107651
VERSION      AR107651.1 GI:12823138
KEYWORDS      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Fenger,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
TITLE      Sarcocystis neuronadagnostic primer and its use in methods of
equine protozoal myeloencephalitis diagnosis
JOURNAL      Patent: US 6110665-A 4 29-AUG-2000;
FEATURES      Location/Qualifiers
source      1. .17
/organism="unknown"
BASE COUNT      2 a      5 c      8 g      2 t

```



```
QY 734 TCGGAGGCTGCTTCCC 750
Db 1 TCGGGTGTCTGCTTCTC 17

RESULT 770
LOCUS AR195605 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 70 from patent US 6350934.
ACCESSION AR195605
VERSION AR195605.1 GI:20245042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 70 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 1 a 5 c 10 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1364 GACCGCGGGCGCGCG 1380
Db 1 GACGGCGTCGGCGCGG 17

RESULT 771
LOCUS AR195753 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 218 from patent US 6350934.
ACCESSION AR195753
VERSION AR195753.1 GI:20245190
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 218 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 1 a 7 c 6 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 CTCGGGCTCGGGCGCG 1031
Db 1 CTCAGCCTCGGGGTGCG 17

RESULT 772
LOCUS AR195755 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 220 from patent US 6350934.
ACCESSION AR195755
VERSION AR195755.1 GI:20245192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 220 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 6 c 9 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1367 CGCGGGCGCGCGCGG 1383
Db 1 CTCGGGGTCGGCGCGG 17

RESULT 773
LOCUS AR195755/c 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 220 from patent US 6350934.
ACCESSION AR195755
VERSION AR195755.1 GI:20245192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 220 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 6 c 9 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 993 CCACCGGGGAGCCCGAG 1009
Db 17 CCGCGGGGACCCCGAG 1

RESULT 774
LOCUS AR196227 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 692 from patent US 6350934.
ACCESSION AR196227
VERSION AR196227.1 GI:20245664
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 692 26-FEB-2002;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 0 a 11 c 3 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 941 CTGCTGCTCAGCGCGC 957
```

```

||||| |||| |||| |||| ||||
1 CTGCGCTCTCCGCGCGC 17

RESULT 775
AR200322/c
LOCUS AR200322 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 79 from patent US 6355785.
ACCESSION AR200322
VERSION AR200322.1 GI:20250396
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Fennewald,S., Zendegeui,J.G., Ojwang,J.O., Hogan,M.E.,
Pommier,Y. and Mazumder,A.
TITLE Guanosine-rich oligonucleotide integrase inhibitors
JOURNAL Patent: US 6355785-A 79 12-MAR-2002;
FEATURES
source Location/Qualifiers
BASE COUNT 0 a 1 c 12 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 75 ACCGACACACCGCGCGC 91
Db 17 ACCGACCGCGCGCGC 1

RESULT 776
AR224299/c
LOCUS AR224299 17 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 30 from patent US 6440719.
ACCESSION AR224299
VERSION AR224299.1 GI:23333076
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting herpes simplex virus replication
JOURNAL Patent: US 6440719-A 30 27-AUG-2002;
FEATURES
source Location/Qualifiers
BASE COUNT 0 a 13 c 3 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1549 GCGCGCGGGAGGGCGCGC 1565
Db 17 GCGCGCGGGAGGGCGGC 1

RESULT 777
AR242713
LOCUS AR242713 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6475486.
ACCESSION AR242713
VERSION AR242713.1 GI:27289217
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kolar,C., Czech,J., Bosslet,K., Seemann,G., Sedlacek,H.-H. and

Hoffman,D.
Glycosyl-etosopside prodrugs, a process for preparation thereof and
the use thereof in combination with functionalized tumor-specific
enzyme conjugates
Patent: US 6475486-A 1 05-NOV-2002;
FEATURES
source Location/Qualifiers
BASE COUNT 1 a 5 c 10 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1374 GCGCGCGCGCGAGGTA 1390
Db 1 GCGCGCGCGCGCGTGCA 17

RESULT 778
AR243452/c
LOCUS AR243452 17 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 245 from patent US 6475789.
ACCESSION AR243452
VERSION AR243452.1 GI:27290663
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Czech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit: diagnostic and therapeutic
methods
JOURNAL Patent: US 6475789-A 245 05-NOV-2002;
FEATURES
source Location/Qualifiers
BASE COUNT 2 a 10 c 4 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1362 GGGACCGCGCGCGCGC 1378
Db 17 GGCATCGCGCGCGGTGGC 1

RESULT 779
AR262453/c
LOCUS AR262453 17 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 79 from patent US 6323185.
ACCESSION AR262453
VERSION AR262453.1 GI:28073884
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Rando,R.F., Fennewald,S., Zendegeui,J.G., Ojwang,J.O. and Hogan,M.E.
TITLE Anti-viral guanosine-rich oligonucleotides and method of treating
HIV
JOURNAL Patent: US 6323185-A 79 27-NOV-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 0 a 1 c 12 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 75 ACCGACACCCCGCGC 91
Db 17 ACCGACACCCCGCGC 1

RESULT 780
AR285947/c
LOCUS AR285947 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 319 from patent US 6528640.
ACCESSION AR285947
VERSION AR285947.1 GI:29723543
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpaisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 319 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 0 a 11 c 6 g 0 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1548 GGGCCGGGGGAGGGCG 1564
Db 17 GGGCCGGGGGAGGGCG 1

RESULT 781
AR286005
LOCUS AR286005 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 377 from patent US 6528640.
ACCESSION AR286005
VERSION AR286005.1 GI:29723601
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpaisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 377 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 0 a 10 c 3 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 184 CCTCGTCTCTCCGCTGC 200
Db 1 CCTCGTCTCTCCGCTGC 17

RESULT 782
AR286300
LOCUS AR286300 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 672 from patent US 6528640.
ACCESSION AR286300
VERSION AR286300.1 GI:29723896
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

```

```

REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpaisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 672 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 3 a 4 c 7 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1505 CTGCACCGCTGGGCAT 1521
Db 1 CTGCACCGCTGGGCAT 17

RESULT 783
AR286317/c
LOCUS AR286317 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 689 from patent US 6528640.
ACCESSION AR286317
VERSION AR286317.1 GI:29723913
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpaisky,A.,
Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 689 04-MAR-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 2 a 7 c 5 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1256 GAGCACAGCTGGGGCA 1272
Db 17 GAGCACAGCTGGGGCA 1

RESULT 784
AX060340/c
LOCUS AX060340 17 bp DNA linear PAT 22-JAN-2001
DEFINITION Sequence 48 from Patent WO0078802.
ACCESSION AX060340
VERSION AX060340.1 GI:12405829
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Shinkets,R.A., Fernandes,E., Vernet,C., Yang,M., Boldog,F.L. and
Herrmann,J.L.
TITLE Secreted polypeptides and corresponding polynucleotides
JOURNAL Patent: WO 0078802-A 48 28-DEC-2000;
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="chemically synthesized"
BASE COUNT 3 a 10 c 2 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;

```

```

Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1113 GTGACGGGACCGCGG 1129
DB 17 GTGATGGGAGCGCTGG 1

RESULT 785
AX074458/c
LOCUS AX074458 17 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 18 from Patent WO0104319.
ACCESSION AX074458
VERSION AX074458.1 GI:12710586
KEYWORDS Infectious bursal disease virus (Gumboro virus)
SOURCE Viruses; deRNA viruses; Birnaviridae; Avibirnavirus.
ORGANISM
REFERENCE 1
AUTHORS Boot,H.J., ter Huurne,A.A. and Peeters,B.P.
TITLE Mosaic infectious bursal disease virus vaccines
JOURNAL Patent: WO 0104319-A 18 JAN-2001;
Stichting Dienst Landbouwkundig Onderzoek (NL)
FEATURES
source
1..17
/organism="infectious bursal disease virus"
/mol_type="genomic DNA"
/db_xref="taxon:10995"
BASE COUNT 3 a 4 c 7 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 977 CGCACACGACTCGGC 993
DB 17 CTGCACCGACTTGGC 1

RESULT 786
AX074465/c
LOCUS AX074465 17 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 25 from Patent WO0104319.
ACCESSION AX074465
VERSION AX074465.1 GI:12710593
KEYWORDS Infectious bursal disease virus (Gumboro virus)
SOURCE Viruses; deRNA viruses; Birnaviridae; Avibirnavirus.
REFERENCE 1
AUTHORS Boot,H.J., ter Huurne,A.A. and Peeters,B.P.
TITLE Mosaic infectious bursal disease virus vaccines
JOURNAL Patent: WO 0104319-A 25 JAN-2001;
Stichting Dienst Landbouwkundig Onderzoek (NL)
FEATURES
source
1..17
/organism="infectious bursal disease virus"
/mol_type="genomic DNA"
/db_xref="taxon:10995"
BASE COUNT 1 a 7 c 5 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1485 GGCTCTGTGACAGCGAG 1501
DB 17 GGCTCCAGGACAGCGAG 1

RESULT 787
AX133871/c
LOCUS AX133871 17 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 25 from Patent WO0104319.
ACCESSION AX133871
VERSION AX133871.1 GI:14547018
KEYWORDS Infectious bursal disease virus (Gumboro virus)
SOURCE Viruses; deRNA viruses; Birnaviridae; Avibirnavirus.
REFERENCE 1
AUTHORS Shimkets,R.A., Fernandes,E., Herrmann,J.L., Liu,X., Yang,M. and
Boldog,F.L.
TITLE Secreted human proteins, polynucleotides encoding them and methods
of using the same
JOURNAL Patent: WO 0119856-A 57 22-MAR-2001;
Curagen Corporation (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Agi74 reverse primer"
BASE COUNT 3 a 10 c 2 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1113 GTGACGGGACCGCGG 1129
DB 17 GTGATGGGAGCGCTGG 1

RESULT 788
AX139210
LOCUS AX139210 17 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 58 from Patent EP1076099.
ACCESSION AX139210
VERSION AX139210.1 GI:14274883
KEYWORDS Mycobacterium tuberculosis
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
REFERENCE 1
AUTHORS Suzuki,Y., Nishida,M. and Takenishi,S.
TITLE Kit for diagnosis of tubercle bacilli
JOURNAL Patent: EP 1076099-A 58 14-FEB-2001;
NISHINBO INDUSTRIES, INC. (JP) ; System Research Incorporation
(JP)
FEATURES
source
1..17
/organism="Mycobacterium tuberculosis"
/mol_type="genomic DNA"
/db_xref="taxon:1773"
/note="capture"
BASE COUNT 3 a 6 c 7 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1365 ACCCGGGGGCGCGGC 1381
DB 1 ACCGCATGAGCGCGGC 17

RESULT 789
AX166743
LOCUS AX166743 17 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 234 from Patent WO0138503.
ACCESSION AX166743
VERSION AX166743.1 GI:14547018
KEYWORDS
```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
TITLE       Novel human protein kinases and protein kinase-like enzymes
JOURNAL     Patent: WO 0138503-A 234 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES    source
            1..17
            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  5 a 8 c 2 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1203 AGGCACCAATTCATC 1219
|||||
Db 1 AGGCACCACTCATC 17

RESULT 790
LOCUS      AX173375/c
DEFINITION Sequence 29 from Patent WO0142445.
ACCESSION AX173375
VERSION    AX173375.1 GI:14598150
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Murphy,B.R., Collins,P.L., Schmidt,A.C., Durbin,A.P.,
            Skiadopoulos M.H. and Tao,T.
TITLE      Use of recombinant parainfluenza viruses (pivs) as vectors to
            protect against infection and disease caused by piv and other human
            pathogens
JOURNAL    Patent: WO 0142445-A 29 14-JUN-2001;
            The Secretary of the Department of Health and Human Services (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            /note="Oligomer insert for rule-of-six conformity"
BASE COUNT  1 a 8 c 7 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1008 AGGCCTCTCGGCTCG 1024
|||||
Db 17 AGGCCTCGCGGCGCG 1

RESULT 791
LOCUS      AX214609
DEFINITION Sequence 51 from Patent WO0159103.
ACCESSION AX214609
VERSION    AX214609.1 GI:15524652
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
JOURNAL    Patent: WO 0159103-A 51 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
            McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"
BASE COUNT  1 a 6 c 7 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1009 GCGCTCTCGGCTCGG 1025
|||||
Db 1 GCGCTCTCGGCTCG 17

RESULT 792
LOCUS      AX215322
DEFINITION Sequence 764 from Patent WO0159103.
ACCESSION AX215322
VERSION    AX215322.1 GI:15525365
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
JOURNAL    Patent: WO 0159103-A 764 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
            McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="synthetic construct"
            /mol_type="mRNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"
BASE COUNT  0 a 8 c 9 g 0 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1367 CGCGGGCGCGCGCGG 1383
|||||
Db 1 CGCGGGCGCGCGCGG 17

RESULT 793
LOCUS      AX215328/c
DEFINITION Sequence 770 from Patent WO0159103.
ACCESSION AX215328
VERSION    AX215328.1 GI:15525371
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
JOURNAL    Patent: WO 0159103-A 770 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
            McSwiggen, James (US); Chowrira, Bharat M. (US)

```


[illegible]

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1163 AGCGAGGAGCGCGGG 1179
 Db 17 AGCGGGATGCGCGGG 1

RESULT 798
 AX215459/c
 LOCUS AX215459 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 901 from Patent WO0159103.
 ACCESSION AX215459
 VERSION AX215459.1 GI:15525502
 KEYWORDS synthetic construct
 ORGANISM synthetic construct
 SOURCE artificial sequences.

REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 Patent: WO 0159103-A 901 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
 source
 1..17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

BASE COUNT 0 a 13 c 2 g 2 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1550 GCCGGGGAGGCGG 1566
 Db 17 GCCGGGGAGGCGG 1

RESULT 799
 AX216129/c
 LOCUS AX216129 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 1571 from Patent WO0159103.
 ACCESSION AX216129
 VERSION AX216129.1 GI:15526172
 KEYWORDS synthetic construct
 ORGANISM synthetic construct
 SOURCE artificial sequences.

REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 Patent: WO 0159103-A 1571 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
 source
 1..17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

BASE COUNT 0 a 9 c 8 g 0 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1367 CGCGGGGCGCGCGG 1383
 Db 17 CGCGGGGCGCGCGG 1

RESULT 800
 AX216149/c

LOCUS AX216149 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 1591 from Patent WO0159103.
 ACCESSION AX216149
 VERSION AX216149.1 GI:15526192
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 Patent: WO 0159103-A 1591 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
 source
 1..17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

BASE COUNT 0 a 13 c 3 g 1 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1370 GCGGGCGCGCGG 1386
 Db 17 GCGGGCGCGCGG 1

RESULT 801
 AX216199/c
 LOCUS AX216199 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 1641 from Patent WO0159103.
 ACCESSION AX216199
 VERSION AX216199.1 GI:15526242
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and
 JOURNAL nogo gene expression
 Patent: WO 0159103-A 1641 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
 source
 1..17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

BASE COUNT 5 a 2 c 7 g 3 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 860 GACTTCTCACTTCT 876
 Db 17 GACTTCTCACTTCT 1

RESULT 802
 AX216349/c
 LOCUS AX216349 17 bp mRNA linear PAT 07-SEP-2001

DEFINITION Sequence 1791 from Patent WO0159103.
 ACCESSION AX216349
 VERSION AX216349.1 GI:15526410
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
 FEATURES
 source
 1. .17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 3 a 6 c 7 g 1 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1402 TCCAGTGTCTGCGGCG 1418
 Db 17 TGCAGTGTCTGCGGCG 1
 RESULT 803
 AX216893
 LOCUS AX216893 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2335 from Patent WO0159103.
 ACCESSION AX216893
 VERSION AX216893.1 GI:15526954
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
 FEATURES
 source
 1. .17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 0 a 8 c 9 g 0 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1368 GCGGCGGCGGCGGCGG 1384
 Db 1 GCGGCGGCGGCGGCGG 17
 RESULT 804
 AX216928
 LOCUS AX216928 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2370 from Patent WO0159103.
 ACCESSION AX216928
 VERSION AX216928.1 GI:15526989
 KEYWORDS
 SOURCE synthetic construct

ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
 FEATURES
 source
 1. .17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 7 a 2 c 8 g 0 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 527 GAGGCTGGGACGAGA 543
 Db 1 GAGGACGAGGACGAGA 17
 RESULT 805
 AX218199
 LOCUS AX218199 17 bp mRNA linear PAT 07-SEP-2001
 DEFINITION Sequence 3641 from Patent WO0159103.
 ACCESSION AX218199
 VERSION AX218199.1 GI:15528260
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)
 FEATURES
 source
 1. .17
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"
 BASE COUNT 11 a 0 c 3 g 3 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 409 TAAGGATGAGAGAAACA 425
 Db 1 TAAGGATGATATAAAA 17
 RESULT 806
 AX262672/c
 LOCUS AX262672 17 bp DNA linear PAT 26-OCT-2001
 DEFINITION Sequence 63 from Patent WO0173002.
 ACCESSION AX262672
 VERSION AX262672.1 GI:16511471
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Kmiec, E.B., Camper, H.B. and Rice, M.C.

TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
PATENT: WO 0173002-A 63 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 4 c 8 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 589 GGACATCACCACTGCTG 605
Db 17 GCCACCACTGCTG 1
RESULT 807
AX262673
LOCUS AX262673 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 64 from Patent WO0173002.
ACCESSION AX262673
VERSION AX262673.1 GI:16511472
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL Patent: WO 0173002-A 64 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 8 c 4 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 589 GGACATCACCACTGCTG 605
Db 1 GCCACCACTGCTG 17
RESULT 808
AX262856/c
LOCUS AX262856/c 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 247 from Patent WO0173002.
ACCESSION AX262856
VERSION AX262856.1 GI:16511655
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL Patent: WO 0173002-A 247 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"

/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 11 c 5 g 0 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 921 CGCGGGAGCGCGCGAG 937
Db 17 CGCGGGTCCGGCGGG 1
RESULT 809
AX262857
LOCUS AX262857 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 248 from Patent WO0173002.
ACCESSION AX262857
VERSION AX262857.1 GI:16511656
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL Patent: WO 0173002-A 248 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 0 a 5 c 11 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 921 CGCGGGAGCGCGCGAG 937
Db 1 CGCGGGTCCGGCGGG 17
RESULT 810
AX263984
LOCUS AX263984 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 1375 from Patent WO0173002.
ACCESSION AX263984
VERSION AX263984.1 GI:16512783
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Kmiec,E.B., Gamper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL Patent: WO 0173002-A 1375 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 5 c 8 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kniec,E.B., Ganper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
Patent: WO 0173002-A 3695 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 4 c 9 g 0 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 574 CGAGGCGCGCGCAGTGG 590
Db 1 CGAAGCGCGAGCAGGGG 17
RESULT 816
AX266571
LOCUS AX266571 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3962 from Patent WO0173002.
ACCESSION AX266571
VERSION AX266571.1 GI:16515370
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kniec,E.B., Ganper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
JOURNAL stranded oligonucleotides
Patent: WO 0173002-A 3962 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 0 a 6 c 5 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 838 CGAGGCGCGCGTGTCT 854
Db 1 CCTGGCGCTGCTGTGT 17
RESULT 817
AX266572/c
LOCUS AX266572 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3963 from Patent WO0173002.
ACCESSION AX266572
VERSION AX266572.1 GI:16515371
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kniec,E.B., Ganper,H.B. and Rice,M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides

```

```

JOURNAL Patent: WO 0173002-A 3963 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 6 c 6 g 0 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 838 CGAGGCGCGCGTGTCT 854
Db 17 CCTGGCGCTGCTGTGT 1
RESULT 818
AX272790/c
LOCUS AX272790 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 359 from Patent WO0162911.
ACCESSION AX272790
VERSION AX272790.1 GI:16545527
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 359 30-AUG-2001;
RIBOZYNE PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 9 c 3 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 151 GATGCTGCTGTGCGGA 167
Db 17 GGTGCTGCTGCAGGGA 1
RESULT 819
AX273293
LOCUS AX273293 17 bp mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 862 from Patent WO0162911.
ACCESSION AX273293
VERSION AX273293.1 GI:16546030
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 862 30-AUG-2001;
RIBOZYNE PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

```

```

BASE COUNT      0 a      5 c      9 g      3 t
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1048 GGGGCTCGGGCGCTGT 1064
Db 1 GTGGCCCGGGCGCTGT 17

RESULT 820
AX273310
LOCUS AX273310 mRNA linear PAT 29-OCT-2001
DEFINITION Sequence 879 from Patent WO0162911.
ACCESSION AX273310
VERSION AX273310.1 GI:16546047
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., Hamblin, P.A. and Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 879 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT      2 a      2 c      9 g      4 t
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 789 AGCTGTTGAGGACCTG 805
Db 1 AGGTGTTGAGGCTCTG 17

RESULT 821
AX284039/c
LOCUS AX284039 DNA linear PAT 20-NOV-2001
DEFINITION Sequence 4 from Patent WO0179487.
ACCESSION AX284039
VERSION AX284039.1 GI:17044749
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Degitz, K.K. and Besch, R.
TITLE Polydesoxyribonucleotides for inhibiting the expression of the icam-1-gene
JOURNAL Patent: WO 0179487-A 4 25-OCT-2001;
Degitz, Klaus Karl (DE); Besch, Robert (DE)
FEATURES
source
1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/noE="Beschreibung der kuenstlichen Sequenz: Polydesoxyribonukleotid"
BASE COUNT      0 a      13 c      0 g      4 t
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1553 GGGGAGGGCGCGCGGA 1569
Db 17 GAGGGAGGGCGAGGGGA 1

RESULT 822
AX325917/c
LOCUS AX325917 DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2055 from Patent WO0192512.
ACCESSION AX325917
VERSION AX325917.1 GI:18096677
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 2055 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
BASE COUNT      1 a      5 c      10 g      1 t
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1069 CAGCCGCGTGC GCCCG 1085
Db 17 CCGCCGCGCTACGCCCG 1

RESULT 823
AX325918
LOCUS AX325918 DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2056 from Patent WO0192512.
ACCESSION AX325918
VERSION AX325918.1 GI:18096678
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.
TITLE Targeted chromosomal genomic alterations in plants using modified single stranded oligonucleotides
JOURNAL Patent: WO 0192512-A 2056 06-DEC-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1..17
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
BASE COUNT      1 a      10 c      5 g      1 t
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1069 CAGCCGCGTGC GCCCG 1085
Db 1 CCGCCGCGCTACGCCCG 17

```

```

RESULT 824
AX326181/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 825
AX326182
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
Query Match
Best Local Similarity
Matches
QY
Db
RESULT 826
AX406535
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
Query Match
Best Local Similarity
Matches
QY
Db

```

Sequence 12 from Patent WO0222686.

AX406535

AX406535.1 GI:21439550

synthetic construct

synthetic construct

artificial sequences.

REFERENCE

1 Kwak,L.W. and Biragyn,A.

Defensin-antigen fusion proteins

PATENT: WO 022686-A 12 21-MAR-2002;

The Secretary, Dept. of Health and Human services, NIH (US)

Location/Qualifiers

1..17

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Description of Artificial Sequence; Note = Synthetic Construct"

0 a 0 c 13 g 0 t 4 others

BASE COUNT

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 827

AX421748

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1

AX421748

Sequence 84 from Patent WO0188124.

AX421748

AX421748.1 GI:21525130

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.

Method and reagent for the inhibition of erg

PATENT: WO 0188124-A 84 22-NOV-2001;

RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

Location/Qualifiers

1..17

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

4 a 9 c 3 g 1 t

BASE COUNT

Query Match

Best Local Similarity

Matches

QY

Db

RESULT 828

AX422335

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1

AX422335

Sequence 671 from Patent WO0188124.

AX422335

AX422335.1 GI:21525717

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 671 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
2 t
BASE COUNT 4 a 10 c 2 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 381 CCCCCAATTACACCC 397
Db 1 CCCCCAGTACACGCC 17
RESULT 829
AX422336 17 bp mRNA linear PAT 18-JUN-2002
LOCUS Sequence 672 from Patent WO0188124.
DEFINITION AX422336
ACCESSION AX422336
VERSION AX422336.1 GI:21525718
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 672 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
3 g 1 t
BASE COUNT 5 a 8 c 3 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 384 CCAATTACACCCCGAC 400
Db 1 CCGCTACACCCCGAC 17
RESULT 830
AX422818/c 17 bp mRNA linear PAT 18-JUN-2002
LOCUS Sequence 1154 from Patent WO0188124.
DEFINITION AX422818
ACCESSION AX422818
VERSION AX422818.1 GI:21526200
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1154 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)

FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
2 t
BASE COUNT 0 a 8 c 7 g 9
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1174 CCGGGGGCTAGCGC 1190
Db 17 CCGGGGGCGGACACGC 1
RESULT 831
AX423030/c 17 bp mRNA linear PAT 18-JUN-2002
LOCUS Sequence 1366 from Patent WO0188124.
DEFINITION AX423030
ACCESSION AX423030
VERSION AX423030.1 GI:21526412
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1366 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
3 t
BASE COUNT 0 a 8 c 6 g 9
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1189 GCGGCTCAGCGCCAGG 1205
Db 17 GCGGCGCAGCGCCAGG 1
RESULT 832
AX423222 17 bp mRNA linear PAT 18-JUN-2002
LOCUS Sequence 1558 from Patent WO0188124.
DEFINITION AX423222
ACCESSION AX423222
VERSION AX423222.1 GI:21526604
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1558 22-NOV-2001; GLAXO GROUP LIMITED (GB)
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
9 g 0 t
BASE COUNT 1 a 7 c 9 g 0 t

```

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1342 CGCGGGGACAGCGGCG 1358
Db 1 CGCGGGGACAGCGGCG 17

RESULT 833
AX423276
LOCUS AX423276 17 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 1612 from Patent WO0188124.
ACCESSION AX423276
VERSION AX423276.1 GI:21526658
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1612 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 6 a 7 c 3 g 1 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 385 CAATTACACCCCGACA 401
Db 1 CAGCTACACCCCGACA 17

RESULT 834
AX423546/c
LOCUS AX423546 17 bp mRNA linear PAT 18-JUN-2002
DEFINITION Sequence 1882 from Patent WO0188124.
ACCESSION AX423546
VERSION AX423546.1 GI:21526928
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1882 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 7 c 6 g 2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1391 GCCCTAACCGGTCACAGG 1407
Db 17 GCCGTGACCGGTCACAGG 1

```

```

RESULT 835
AX474905
LOCUS AX474905 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 126 from Patent WO0224750.
ACCESSION AX474905
VERSION AX474905.1 GI:22214190
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 126 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 5 a 5 c 5 g 2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 543 ATGGCCACCTCAGAG 559
Db 1 ATGACGACCGCTCAGAG 17

RESULT 836
AX474906
LOCUS AX474906 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 127 from Patent WO0224750.
ACCESSION AX474906
VERSION AX474906.1 GI:22214191
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 127 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
Location/Qualifiers
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 5 c 6 g 2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 544 TGGCCACCTCAGAG 560
Db 1 TGACGACCGCTCAGAG 17

RESULT 837
AX498859
LOCUS AX498859 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 166 from Patent BP1229046.
ACCESSION AX498859
VERSION AX498859.1 GI:23381152
KEYWORDS

```

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 166 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  1 a 9 c 5 g 2 t
            Query Match      0.8%; Score 12.2; DB 1; Length 17;
            Best Local Similarity 82.4%; Pred. No. 7.1e+02;
            Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 988 CTCGCCACCGGGAGC 1004
Db 1 CTCGCCACCGGGCGC 17

RESULT 838
AX498979
LOCUS       AX498979                17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 286 from Patent EP1229046.
ACCESSION  AX498979
VERSION    AX498979.1 GI:23381272
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 286 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a 6 c 6 g 1 t
            Query Match      0.8%; Score 12.2; DB 1; Length 17;
            Best Local Similarity 82.4%; Pred. No. 7.1e+02;
            Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 243 GGAGGAGGAGGACCC 259
Db 1 GGAGGAGGAGGACCC 17

RESULT 839
AX499230
LOCUS       AX499230                17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 537 from Patent EP1229046.
ACCESSION  AX499230
VERSION    AX499230.1 GI:23381523
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 537 07-AUG-2002;
            Aeomica, Inc. (US)

```

```

FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  3 a 5 c 6 g 3 t
            Query Match      0.8%; Score 12.2; DB 1; Length 17;
            Best Local Similarity 82.4%; Pred. No. 7.1e+02;
            Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 942 TGCTGCTCACCAGCGCG 958
Db 1 TGATGCTGACAGCGCG 17

RESULT 840
AX499231
LOCUS       AX499231                17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 538 from Patent EP1229046.
ACCESSION  AX499231
VERSION    AX499231.1 GI:23381524
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 538 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  3 a 6 c 6 g 2 t
            Query Match      0.8%; Score 12.2; DB 1; Length 17;
            Best Local Similarity 82.4%; Pred. No. 7.1e+02;
            Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 943 GCTGCTCACCAGCGCG 959
Db 1 GATGCTGACAGCGCG 17

RESULT 841
AX499490/c
LOCUS       AX499490                17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 797 from Patent EP1229046.
ACCESSION  AX499490
VERSION    AX499490.1 GI:23381783
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 797 07-AUG-2002;
            Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  3 a 4 c 9 g 1 t
            Query Match      0.8%; Score 12.2; DB 1; Length 17;
            Best Local Similarity 82.4%; Pred. No. 7.1e+02;

```

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 873 TCCTGGACCGGACGAC 889
 Db 17 TCCTGGACCGGCGGTC 1

RESULT 842
 AX499660
 LOCUS AX499660 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 967 from Patent EP1229046.
 ACCESSION AX499660
 VERSION AX499660.1 GI:23381953
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Zhan,J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 967 07-AUG-2002;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 3 a 9 c 4 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1434 CCACCGCGGCATCCAC 1450
 Db 1 CCACCGCAGGCATCCCC 17

RESULT 843
 AX499661
 LOCUS AX499661 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 968 from Patent EP1229046.
 ACCESSION AX499661
 VERSION AX499661.1 GI:23381954
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Zhan,J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 968 07-AUG-2002;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 3 a 8 c 4 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1435 CACCGCGGCATCCACT 1451
 Db 1 CACGCGCAGGCATCCCT 17

RESULT 844
 AX527194

LOCUS AX527194 17 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 224 from Patent WO0226818.
 ACCESSION AX527194
 VERSION AX527194.1 GI:25171809
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Gu,Y. and Corrigan,A.
 TITLE Human nedg-1
 JOURNAL Patent: WO 0226818-A 224 04-APR-2002;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 8 a 0 c 3 g 6 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 406 ATTTAAGGATGAAGAA 422
 Db 1 ATTTAAGGATGTTGAA 17

RESULT 845
 AX531219
 LOCUS AX531219 17 bp DNA linear PAT 22-NOV-2002
 DEFINITION Sequence 728 from Patent EP1239051.
 ACCESSION AX531219
 VERSION AX531219.1 GI:25254229
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shannon,M.
 TITLE Human posh-like protein 1
 JOURNAL Patent: EP 1239051-A 728 11-SEP-2002;
 Aeomica, Inc. (US)
 FEATURES Location/Qualifiers
 source
 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 5 a 2 c 5 g 5 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1209 CCATTCTCATCAACCGG 1225
 Db 17 CAATTCTCATCAAGCTG 1

RESULT 846
 AX531299
 LOCUS AX531299 17 bp DNA linear PAT 22-NOV-2002
 DEFINITION Sequence 808 from Patent EP1239051.
 ACCESSION AX531299
 VERSION AX531299.1 GI:25254384
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 808 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT   2 a 9 c 5 g 1 t
              0.8%; Score 12.2; DB 1; Length 17;
Query Match  Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1341 GCGCGGGGACAGCGGC 1357
      |||||
Db 17 GCGGTGGGGACGCTGC 1

RESULT 847
AX532022/c
LOCUS        AX532022 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 1531 from Patent EP1239051.
ACCESSION   AX532022
VERSION     AX532022.1 GI:25255809
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 1531 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT   3 a 6 c 7 g 1 t
              0.8%; Score 12.2; DB 1; Length 17;
Query Match  Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1411 TGCCGACTCGCCGGTG 1427
      |||||
Db 17 TGCCGACTCGCCGGTG 1

RESULT 848
AX532235
LOCUS        AX532235 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 1744 from Patent EP1239051.
ACCESSION   AX532235
VERSION     AX532235.1 GI:25256257
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 1744 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT   2 a 9 c 5 g 1 t
              0.8%; Score 12.2; DB 1; Length 17;
Query Match  Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1253 GAGGAGCACAGCTGGGC 1269
      |||||
Db 1 GAGAAGCACAGCGCGC 17

RESULT 849
AX532237/c
LOCUS        AX532237 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 1746 from Patent EP1239051.
ACCESSION   AX532237
VERSION     AX532237.1 GI:25256261
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 1746 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT   4 a 7 c 5 g 1 t
              0.8%; Score 12.2; DB 1; Length 17;
Query Match  Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 840 AGGCGCGCTGCTCTAC 856
      |||||
Db 17 AGGCGCGCTGCTCTTC 1

RESULT 850
AX532413
LOCUS        AX532413 17 bp DNA linear PAT 22-NOV-2002
DEFINITION  Sequence 1922 from Patent EP1239051.
ACCESSION   AX532413
VERSION     AX532413.1 GI:25256601
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Shannon,M.
TITLE        Human posh-like protein 1
JOURNAL      Patent: EP 1239051-A 1922 11-SEP-2002;
              Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT   4 a 7 c 5 g 1 t
              0.8%; Score 12.2; DB 1; Length 17;
Query Match  Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 990 CGGCCACGGGAGCCC 1006
      |||||

```

```

Db      1  CAGCCACAGGGGATCCC 17

RESULT 851
AX544648/c
LOCUS      17 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 161 from Patent EP1243660.
ACCESSION  AX544648
VERSION     AX544648.1  GI:25809859
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS     Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE       Human udp-galnac:polypeptide n-acetylglalatosaminyltransferase 10
JOURNAL     Patent: EP 1243660-A 161 25-SEP-2002;
            Aecomica, Inc. (US)

FEATURES
source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  2 a      5 c      9 g      1 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1138  CGCGCTGTGCACAGCG 1154
Db      17  CTCGCTGCGCACCGCG 1

RESULT 852
AX545028
LOCUS      17 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 541 from Patent EP1243660.
ACCESSION  AX545028
VERSION     AX545028.1  GI:25810239
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS     Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE       Human udp-galnac:polypeptide n-acetylglalatosaminyltransferase 10
JOURNAL     Patent: EP 1243660-A 541 25-SEP-2002;
            Aecomica, Inc. (US)

FEATURES
source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      4 c      4 g      5 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      903  TCCTTCTAGTGTGATCGAG 919
Db      1  TCATCTTCTGTGACGAG 17

RESULT 853
AX545089
LOCUS      17 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 602 from Patent EP1243660.
ACCESSION  AX545089
VERSION     AX545089.1  GI:25810300
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS     Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE       Human udp-galnac:polypeptide n-acetylglalatosaminyltransferase 10
JOURNAL     Patent: EP 1243660-A 701 25-SEP-2002;
            Aecomica, Inc. (US)

FEATURES
source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      5 c      6 g      2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1118  GGGGACCGCGGCTCCT 1134
Db      17  GGGGACCTTCAGCTCCT 1

RESULT 855
AX545188
LOCUS      17 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 701 from Patent EP1243660.
ACCESSION  AX545188
VERSION     AX545188.1  GI:25810399
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS     Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE       Human udp-galnac:polypeptide n-acetylglalatosaminyltransferase 10
JOURNAL     Patent: EP 1243660-A 701 25-SEP-2002;
            Aecomica, Inc. (US)

FEATURES
source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      5 c      6 g      2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1118  GGGGACCGCGGCTCCT 1134
Db      17  GGGGACCTTCAGCTCCT 1

RESULT 855
AX545188
LOCUS      17 bp      DNA      linear      PAT 26-NOV-2002
DEFINITION Sequence 701 from Patent EP1243660.
ACCESSION  AX545188
VERSION     AX545188.1  GI:25810399
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS     Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE       Human udp-galnac:polypeptide n-acetylglalatosaminyltransferase 10
JOURNAL     Patent: EP 1243660-A 701 25-SEP-2002;
            Aecomica, Inc. (US)

FEATURES
source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
BASE COUNT  4 a      5 c      6 g      2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1118  GGGGACCGCGGCTCCT 1134
Db      17  GGGGACCTTCAGCTCCT 1

```

```

FEATURES
  source
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
  1..17
  2 a 5 c 8 g 2 t
  BASE COUNT      2 a 5 c 8 g 2 t
    Query Match      0.8%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 7.1e+02;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 784 CACCAAGCTGTGAAGG 800
Db 1 CCCCAGGCTGTGAAGG 17

RESULT 856
AX578339
LOCUS      AX578339      17 bp mRNA linear PAT 10-JAN-2003
DEFINITION Sequence 177 from Patent WO0211674.
ACCESSION AX578339
VERSION    AX578339.1 GI:27647541
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 Thompson,J., McSwiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
    and Grupe,A.
    Method and reagent for the inhibition of calcium activated chloride
    channel-1 (clca-1)
  JOURNAL
    Patent: WO 0211674-A 177 14-FEB-2002;
    RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
    Thompson, James (US)
  FEATURES
    source
      Location/Qualifiers
        1..17
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        6 a 5 c 3 g 3 t
  BASE COUNT      6 a 5 c 3 g 3 t
    Query Match      0.8%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 7.1e+02;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1459 GCAGCTGCTCTACCAA 1475
Db 1 GCAGCTGTTACACCAA 17

RESULT 857
AX578995
LOCUS      AX578995      17 bp mRNA linear PAT 10-JAN-2003
DEFINITION Sequence 833 from Patent WO0211674.
ACCESSION AX578995
VERSION    AX578995.1 GI:27648197
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 Thompson,J., McSwiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
    and Grupe,A.
    Method and reagent for the inhibition of calcium activated chloride
    channel-1 (clca-1)
  JOURNAL
    Patent: WO 0211674-A 833 14-FEB-2002;
    RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
    Thompson, James (US)
  FEATURES
    source
      Location/Qualifiers
        1..17
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        5 a 7 c 4 g 1 t
  BASE COUNT      5 a 7 c 4 g 1 t
    Query Match      0.8%; Score 12.2; DB 1; Length 17;
    Best Local Similarity 82.4%; Pred. No. 7.1e+02;
    Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 731 AAATCGGAGGCTGCTT 747
Db 17 AATTGGGAGGCTCCTT 1

RESULT 859
AX579334
LOCUS      AX579334      17 bp mRNA linear PAT 10-JAN-2003
DEFINITION Sequence 1172 from Patent WO0211674.
ACCESSION AX579334
VERSION    AX579334.1 GI:27648536
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 Thompson,J., McSwiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E.
    and Grupe,A.
    Method and reagent for the inhibition of calcium activated chloride
    channel-1 (clca-1)
  JOURNAL
    Patent: WO 0211674-A 1172 14-FEB-2002;
    RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
    Thompson, James (US)
  FEATURES
    source
      Location/Qualifiers
        1..17
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"

```

```

BASE COUNT      1 a      7 c      3 g      6 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 169 ATGCTGCTGCTAGTCC 185
Db 1 ACGTCTGCTTGTCC 17

RESULT 860
AX615281
LOCUS AX615281 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 88 from Patent EP1262488.
ACCESSION AX615281
VERSION AX615281.1 GI:28446180
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y. and Nguyen, C.T.
TITLE Human local-domain containing protein
JOURNAL Patent: EP 1262488-A 88 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      2 a      4 c      1 g      10 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 409 TAAGGATGAGAGAAACA 425
Db 1 TAAGGATGAGCAAAA 1

RESULT 863
AX649376
LOCUS AX649376 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1216 from Patent EP1273660
ACCESSION AX649376
VERSION AX649376.1 GI:29152194
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen-exchanger like protein 1
JOURNAL Patent: EP 1273660-A 1216 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT      2 a      4 c      4 g      7 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 132 TCATCAGTTCATGGGC 148
Db 1 TCTTCTGTTACATGGGC 17

RESULT 864
AX649524
LOCUS AX649524 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 1364 from Patent EP1273660.
ACCESSION AX649524
VERSION AX649524.1 GI:29152342
KEYWORDS

```


SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Gu.Y.
 TITLE Human sodium-hydrogen exchanger like protein 1
 JOURNAL Patent: EP 1273660-A 1364 08-JAN-2003;
 Aemica, Inc. (US)

FEATURES
 source 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 5 a 5 c 4 g 3 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 343 GAAGATCTCCAGAACT 359
 |||||
 1 GAAGATCCCTGGAAT 17

DB AX671955 17 bp DNA linear PAT 27-MAR-2003
 AX671955/c
 LOCUS Sequence 400 from Patent WO03004526.
 DEFINITION AX671955
 ACCESSION AX671955
 VERSION AX671955.1 GI:29330303
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or resistance to viruses and their use as
 medicines
 JOURNAL Patent: WO 03004526-A 400 16-JAN-2003;
 Molecular Engines Laboratories (FR)

FEATURES
 source 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 3 c 5 g 5 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 120 ACAGCTCGGAAGTCATC 136
 |||||
 17 ACATCTCGCAAGTGATC 1

DB AX672132 17 bp DNA linear PAT 27-MAR-2003
 AX672132/c
 LOCUS Sequence 577 from Patent WO03004526.
 DEFINITION AX672132
 ACCESSION AX672132
 VERSION AX672132.1 GI:29330480
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour

reversion, apoptosis and/or resistance to viruses and their use as
 medicines
 JOURNAL Patent: WO 03004526-A 577 16-JAN-2003;
 Molecular Engines Laboratories (FR)

FEATURES
 source 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 6 a 4 c 5 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 773 GAGCAGGGGGCACCMA 789
 |||||
 1 GATCAGGGCAGCACTMA 17

DB AX672333 17 bp DNA linear PAT 27-MAR-2003
 AX672333/c
 LOCUS Sequence 778 from Patent WO03004526.
 DEFINITION AX672333
 ACCESSION AX672333
 VERSION AX672333.1 GI:29330681
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or resistance to viruses and their use as
 medicines
 JOURNAL Patent: WO 03004526-A 778 16-JAN-2003;
 Molecular Engines Laboratories (FR)

FEATURES
 source 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 2 a 5 c 6 g 4 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1200 CCCAGGGCACCATTCTC 1216
 |||||
 17 CCCAGGGCAGCATGATC 1

DB AX673341 17 bp DNA linear PAT 27-MAR-2003
 AX673341/c
 LOCUS Sequence 1786 from Patent WO03004526.
 DEFINITION AX673341
 ACCESSION AX673341
 VERSION AX673341.1 GI:29331689
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or resistance to viruses and their use as
 medicines
 JOURNAL Patent: WO 03004526-A 1786 16-JAN-2003;
 Molecular Engines Laboratories (FR)

FEATURES
 source 1..17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match	Score	DB 1	Length	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379
-------------	-------	------	--------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

RESULT 873
AX687673
LOCUS AX687673 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 405 from Patent EP1281758.
ACCESSION AX687673
KEYWORDS AX687673.1 GI:29410369
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 405 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 2 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 866 CTCACCTTCCTGGACCG 882
Db 1 CTCACATCTCTGCCCG 17
RESULT 874
AX687674
LOCUS AX687674 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 406 from Patent EP1281758.
ACCESSION AX687674
VERSION AX687674.1 GI:29410370
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 406 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 2 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 867 TCACCTTCCTGGACCG 883
Db 1 TCACATCTCTGCCCG 17
RESULT 875
AX687675
LOCUS AX687675 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 407 from Patent EP1281758.
ACCESSION AX687675

VERSION AX687675.1 GI:29410371
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 407 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 2 a 3 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 868 CACTTTCCTGGACCG 884
Db 1 CACTATCTCTGCCCG 17
RESULT 876
AX687676
LOCUS AX687676 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 408 from Patent EP1281758.
ACCESSION AX687676
VERSION AX687676.1 GI:29410372
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 408 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 8 c 3 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 869 ACTTTCCTGGACCG 885
Db 1 ACTATCTCTGCCCG 17
RESULT 877
AX688006
LOCUS AX688006 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 738 from Patent EP1281758.
ACCESSION AX688006
VERSION AX688006.1 GI:29410704
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 738 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 1 a 6 c 7 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1219 CAGCGGGTCTGGCT 1235
Db 1 CAGCGGGTCTGGCT 17
RESULT 878
AX688332/c
LOCUS AX688332 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1064 from Patent EPI281758.
ACCESSION AX688332
VERSION AX688332.1 GI:29411032
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1064 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 3 c 8 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1480 CAGCTGCTCTGGACA 1496
Db 17 CAGCAGGCTCTGCTCA 1
RESULT 879
AX688570
LOCUS AX688570 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1302 from Patent EPI281758.
ACCESSION AX688570
VERSION AX688570.1 GI:29411272
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1302 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 6 a 4 c 5 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 791 CTGGTGAAGGACCTGAG 807
Db 1 CTGGTGAAGCACCAG 17
RESULT 880
AX688660/c
LOCUS AX688660 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1392 from Patent EPI281758.
ACCESSION AX688660
VERSION AX688660.1 GI:29411362
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1392 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 7 c 5 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1311 TGGCTGCACTGGCGCCC 1327
Db 17 TGGCTGCGCTGGTGAC 1
RESULT 881
AX688669/c
LOCUS AX688669 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1401 from Patent EPI281758.
ACCESSION AX688669
VERSION AX688669.1 GI:29411371
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1401 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1. .17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 6 c 6 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 294 TCCCAATGTCGCCGAG 310
 17 TCCCAATGTCGCCG 1

Db

RESULT 882
 AX688671/c
 LOCUS 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1403 from Patent EP1281758.
 ACCESSION AX688671
 VERSION AX688671.1 GI:29411373
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 1403 05-FEB-2003;
 FEATURES
 source
 1. .17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 5 a 5 c 6 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 292 TATCCCAATGTCGCCG 308
 17 TCTCCCAATGTCGCTG 1

Db

RESULT 883
 AX688674/c
 LOCUS 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1406 from Patent EP1281758.
 ACCESSION AX688674
 VERSION AX688674.1 GI:29411376
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 1406 05-FEB-2003;
 FEATURES
 source
 1. .17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 5 a 5 c 6 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 289 GTTATCCCAATGTCG 305
 17 GCTTCCCAATGTCG 1

Db

RESULT 886
 AX690675
 LOCUS 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 3407 from Patent EP1281758.
 ACCESSION AX690675
 VERSION AX690675.1 GI:29413556
 KEYWORDS

RESULT 884
 AX688726/c
 LOCUS 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 1458 from Patent EP1281758.
 ACCESSION AX688726
 VERSION AX688726.1 GI:29411430
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 1458 05-FEB-2003;
 FEATURES
 source
 1. .17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 7 c 5 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1402 TCCAGTGTCTGCCGACG 1418
 17 TGCAGTGTCTGCCGCG 1

Db

RESULT 885
 AX690657
 LOCUS 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 3389 from Patent EP1281758.
 ACCESSION AX690657
 VERSION AX690657.1 GI:29413538
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
 TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
 JOURNAL Patent: EP 1281758-A 3389 05-FEB-2003;
 FEATURES
 source
 1. .17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 2 a 3 c 8 g 4 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 150 AGATGCTGCTGCTGCG 166
 1 AGCTGCTGCTGCTGAG 17

Db

RESULT 886
 AX690675
 LOCUS 17 bp DNA linear PAT 31-MAR-2003
 DEFINITION Sequence 3407 from Patent EP1281758.
 ACCESSION AX690675
 VERSION AX690675.1 GI:29413556
 KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 3407 05-FEB-2003;
Aemica, Inc. (US)
FEATURES source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 3 a 5 c 3 g 6 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 861 ACTTCCTCAGCTTCCTG 877 17 bp DNA linear PAT 31-MAR-2003
Db 1 AGTTCCTGACTATCCTG 17
RESULT 887
LOCUS AX693203 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5935 from Patent EP1281758.
ACCESSION AX693203
VERSION AX693203.1 GI:29416167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5935 05-FEB-2003;
Aemica, Inc. (US)
FEATURES source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
BASE COUNT 4 a 3 c 9 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 27 GAGCGCGGAGCCGAG 43
Db 1 GAGAGCGCCAGCTGGAG 17
RESULT 888
LOCUS AX711072/c 17 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 372 from Patent EP1288296.
ACCESSION AX711072
VERSION AX711072.1 GI:29787453
KEYWORDS
SOURCE Herpes simplex virus unknown type
ORGANISM Herpes simplex virus unknown type
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphan herpesvirinae; Simplexvirus.
REFERENCE 1
AUTHORS Draper, K.G., Mcswiggen, J.A., Holecsek, J.J., Dudycz, L.W., Macejak, D.G. and Mamone, J.A.

TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 372 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES source
Location/Qualifiers
1..17
/organism="Herpes simplex virus unknown type"
/mol_type="genomic RNA"
/db_xref="taxon:126283"
BASE COUNT 0 a 13 c 3 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1549 GGCGCGGGGAGGGGCGC 1565
Db 17 GGCGCGGGGAGGGGCGC 1
RESULT 889
LOCUS AX721791 17 bp DNA linear PAT 07-MAY-2003
DEFINITION Sequence 12 from Patent WO03025002.
ACCESSION AX721791
VERSION AX721791.1 GI:30422379
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Biragyn, A. and Kwak, L.W.
TITLE Method and compositions of defensin-antigen fusion proteins and chemokine-antigen fusion proteins as vaccines for tumors and viral infection
JOURNAL Patent: WO 03025002-A 12 27-MAR-2003;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 0 a 13 g 0 t 4 others
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 7.1e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1547 GGCGCGGGGAGGGGCGC 1563
Db 1 GCGGCGGGGAGGGGCGS 17
RESULT 890
LOCUS AX723336/c 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1023 from Patent WO03025176.
ACCESSION AX723336
VERSION AX723336.1 GI:30423837
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 1023 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES source
Location/Qualifiers
1..17
/organism="Mus musculus"

```

BASE COUNT      4 a      5 c      3 t
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 740 GGCTGCTTCCCGGCTC 756
Db 17 GGATGCTTCCCGAGATC 1

RESULT 891
AX723519/c
LOCUS      AX723519      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1206 from Patent WO03025176.
ACCESSION  AX723519
VERSION     AX723519.1 GI:30424020
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT      4 a      1 c      6 g      6 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 378 TCACCCCAATTACAC 394
Db 17 TCACCCCAATTAGATC 1

RESULT 892
AX724912
LOCUS      AX724912      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2599 from Patent WO03025176.
ACCESSION  AX724912
VERSION     AX724912.1 GI:30504255
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT      4 a      4 c      7 g      2 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;

```

```

Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 913 GATCGAGCGCGGAGC 929
Db 1 GATCGAGCTCGGAAGC 17

RESULT 893
AX725292
LOCUS      AX725292      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2979 from Patent WO03025176.
ACCESSION  AX725292
VERSION     AX725292.1 GI:30504635
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT      5 a      5 c      6 g      1 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1486 GCTCCTGGACGCGAGG 1502
Db 1 GATCCAGGACAGCCAGG 17

RESULT 894
AX725622/c
LOCUS      AX725622      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3309 from Patent WO03025176.
ACCESSION  AX725622
VERSION     AX725622.1 GI:30504965
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT      2 a      5 c      4 g      6 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 342 GGAAGATCTCCAGAAC 358
Db 1 GGAAGATCTCCAGAAC 358

```

```

Db      17  GGAGAGACTCCAGATC 1
LOCUS
DEFINITION Sequence 3345 from Patent WO03025176.
ACCESSION AX725658
VERSION AX725658.1 GI:30505001
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3345 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 3 a 5 c 3 g 6 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 469 GAACGCTTGGCCATCT 485
Db 1 GATCTCATGGCCATCT 17
LOCUS
DEFINITION Sequence 3685 from Patent WO03025176.
ACCESSION AX725998
VERSION AX725998.1 GI:30505341
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3685 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 7 a 4 c 5 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1246 GGTCTATCGAGGAGCACA 1262
Db 1 GATCAGCAGGAGGAGCACA 17
LOCUS
DEFINITION Sequence 3345 from Patent WO03025176.
ACCESSION AX726458
VERSION AX726458.1 GI:30505801
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4145 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 4 a 6 c 3 g 4 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 510 TGAACCTGCGGGTGACC 526
Db 17 TGCAACTGAGGGTGATC 1
LOCUS
DEFINITION Sequence 4267 from Patent WO03025176.
ACCESSION AX726580
VERSION AX726580.1 GI:30505923
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4267 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
BASE COUNT 6 a 4 c 5 g 2 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1246 GGTCTATCGAGGAGCACA 1262
Db 1 GATCAGCAGGAGGAGCACA 17
LOCUS
DEFINITION Sequence 5178 from Patent WO03025176.
ACCESSION AX727491
VERSION AX727491.1 GI:30505834
KEYWORDS

```


SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025176-A 5178 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 FEATURES source
 1..17
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090" 6 t
 BASE COUNT 1 a 2 g 6 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 333 GGTATGGAAGGGAAGATC 349
 Db 17 GGAGCGAAGGGAAGATC 1
 RESULT 900
 AX728148/c
 LOCUS AX728148 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 5835 from Patent WO03025176.
 ACCESSION AX728148
 VERSION AX728148.1 GI:30507491
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025176-A 5835 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 FEATURES source
 1..17
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090" 5 t
 BASE COUNT 4 a 4 g 5 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 361 CGAGCGATTAGGAAC 377
 Db 17 CGAGCGATTAGGATC 1
 RESULT 901
 AX728634
 LOCUS AX728634 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 268 from Patent WO03025175.
 ACCESSION AX728634
 VERSION AX728634.1 GI:30507977
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1

AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025175-A 268 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 FEATURES source
 1..17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606" 4 t
 BASE COUNT 2 a 6 c 5 g 4 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 346 GATCTCCAGAACTCCG 362
 Db 1 GAICTCTGGGACTCCG 17
 RESULT 902
 AX728654/c
 LOCUS AX728654 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 288 from Patent WO03025175.
 ACCESSION AX728654
 VERSION AX728654.1 GI:30507997
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025175-A 288 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 FEATURES source
 1..17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606" 5 t
 BASE COUNT 3 a 1 c 8 g 5 t
 Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 592 CATCACCCGCTGACC 608
 Db 17 CAACACCCCTCTGATC 1
 RESULT 903
 AX729739/c
 LOCUS AX729739 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 1373 from Patent WO03025175.
 ACCESSION AX729739
 VERSION AX729739.1 GI:30509082
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 JOURNAL Patent: WO 03025175-A 1373 27-MAR-2003;

FEATURES	source	Location/Qualifiers	Score	DB	Length	Indels	Gaps
BASE COUNT	6 a	2 c	5 g	4 t			
Query Match		0.8%;	Score 12.2;	DB 1;	Length 17;		
Best Local Similarity		82.4%;	Pred. No. 7.1e+02;				
Matches	14;	Conservative	0;	Mismatches	3;	Indels	0;
QY	279	CCTACAGGAGTTATC	295				
Db	17	CCTACATTGATGATC	1				
RESULT 904							
LOCUS	AX731101/c						
DEFINITION	Sequence 2735 from Patent WO03025175.						
ACCESSION	AX731101						
VERSION	AX731101.1	GI:30510444					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
BASE COUNT	3 a	6 c	1 g	7 t			
Query Match		0.8%;	Score 12.2;	DB 1;	Length 17;		
Best Local Similarity		82.4%;	Pred. No. 7.1e+02;				
Matches	14;	Conservative	0;	Mismatches	3;	Indels	0;
QY	333	GGTATGAGGAGATC	349				
Db	17	GGTATATAGAGGATC	1				
RESULT 905							
LOCUS	AX731108/c						
DEFINITION	Sequence 2742 from Patent WO03025175.						
ACCESSION	AX731108						
VERSION	AX731108.1	GI:30510451					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
BASE COUNT	3 a	6 c	1 g	7 t			
Query Match		0.8%;	Score 12.2;	DB 1;	Length 17;		
Best Local Similarity		82.4%;	Pred. No. 7.1e+02;				
Matches	14;	Conservative	0;	Mismatches	3;	Indels	0;
QY	333	GGTATGAGGAGATC	349				
Db	17	GGTATATAGAGGATC	1				
RESULT 905							
LOCUS	AX731108/c						
DEFINITION	Sequence 2742 from Patent WO03025175.						
ACCESSION	AX731108						
VERSION	AX731108.1	GI:30510451					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
BASE COUNT	3 a	6 c	1 g	7 t			
Query Match		0.8%;	Score 12.2;	DB 1;	Length 17;		
Best Local Similarity		82.4%;	Pred. No. 7.1e+02;				
Matches	14;	Conservative	0;	Mismatches	3;	Indels	0;
QY	333	GGTATGAGGAGATC	349				
Db	17	GGTATATAGAGGATC	1				
RESULT 905							
LOCUS	AX731108/c						
DEFINITION	Sequence 2742 from Patent WO03025175.						
ACCESSION	AX731108						
VERSION	AX731108.1	GI:30510451					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
FEATURES							
source							
BASE COUNT	3 a	6 c	1 g	7 t			
Query Match		0.8%;	Score 12.				

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1467 TCTACCAATAGGCACC 1483
 |||||
 Db 17 TCTACCAAGTAGGCATC 1

RESULT 908

AX735717
 LOCUS AX735717 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 1307 from Patent WO03025177.
 ACCESSION AX735717
 VERSION AX735717.1 GI:30514994
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 1307 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 2 a 6 c 5 g 4 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 346 GATCTCCAGAACTCCG 362
 |||||
 Db 1 GATCTCCGGACTCCG 17

AX737405
 LOCUS AX737405 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 2995 from Patent WO03025177.
 ACCESSION AX737405
 VERSION AX737405.1 GI:30516693
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 2995 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 4 c 4 g 5 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1467 TCTACCAATAGGCACC 1483
 |||||
 Db 17 TCTACCAAGTAGGCATC 1

AX737846
 LOCUS AX737846 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 3436 from Patent WO03025177.
 ACCESSION AX737846
 VERSION AX737846.1 GI:30517134
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 3436 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 4 c 4 g 5 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1142 GCTCTGCACACGCGAC 1158
 |||||
 Db 1 GATCTGCACACGCGAC 17

AX738466
 LOCUS AX738466 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 3938 from Patent WO03025177.
 ACCESSION AX738466
 VERSION AX738466.1 GI:30517636
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 3938 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 5 c 6 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 910

AX737846
 LOCUS AX737846 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 3436 from Patent WO03025177.
 ACCESSION AX737846
 VERSION AX737846.1 GI:30517134
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 3436 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 6 a 4 c 6 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 913 GATCGAGACGCGGACG 929
 |||||
 Db 1 GATCGAGAGCGGACG 17

AX738348
 LOCUS AX738348 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 3938 from Patent WO03025177.
 ACCESSION AX738348
 VERSION AX738348.1 GI:30517636
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 3938 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 5 c 6 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1142 GCTCTGCACACGCGAC 1158
 |||||
 Db 1 GATCTGCACACGCGAC 17

AX738466
 LOCUS AX738466 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 3938 from Patent WO03025177.
 ACCESSION AX738466
 VERSION AX738466.1 GI:30517636
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 3938 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 5 c 6 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1142 GCTCTGCACACGCGAC 1158
 |||||
 Db 1 GATCTGCACACGCGAC 17

AX738466
 LOCUS AX738466 17 bp DNA linear PAT 08-MAY-2003
 DEFINITION Sequence 3938 from Patent WO03025177.
 ACCESSION AX738466
 VERSION AX738466.1 GI:30517636
 KEYWORDS Homo sapiens (human)
 SOURCE ORGANISM

REFERENCE 1
 AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
 JOURNAL Patent: WO 03025177-A 3938 27-MAR-2003;
 FEATURES Molecular Engines Laboratories (FR)
 source Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

BASE COUNT 4 a 5 c 6 g 2 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

DEFINITION      Sequence 4056 from Patent WO03025177.
ACCESSION       AX738466
VERSION         AX738466.1  GI:30517754
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Telerman,A., Anson,R. and Tuijnder,M.
TITLE           Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL         Patent: WO 03025177-A 4056 27-MAR-2003;
                Molecular Engines Laboratories (FR)
FEATURES        Location/Qualifiers
                source
                1..17
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT      3 a 5 c 3 g 6 t
                Query Match      0.8%; Score 12.2; DB 1; Length 17;
                Best Local Similarity 82.4%; Pred. No. 7.1e+02;
                Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 456 GTAAGGACAAAGTTGAAC 472
Db 17 GTAAGGACAAAGTTGATC 1

RESULT 913
LOCUS           AX738561/c
DEFINITION      Sequence 4151 from Patent WO03025177.
ACCESSION       AX738561
VERSION         AX738561.1  GI:30517849
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Telerman,A., Anson,R. and Tuijnder,M.
TITLE           Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL         Patent: WO 03025177-A 4151 27-MAR-2003;
                Molecular Engines Laboratories (FR)
FEATURES        Location/Qualifiers
                source
                1..17
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT      3 a 5 g 3 t
                Query Match      0.8%; Score 12.2; DB 1; Length 17;
                Best Local Similarity 82.4%; Pred. No. 7.1e+02;
                Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1442 GGCATCCACTGGTACTC 1458
Db 17 GGCATCCACTGGGGATC 1

RESULT 914
LOCUS           AX739235/c
DEFINITION      Sequence 4825 from Patent WO03025177.
ACCESSION       AX739235
VERSION         AX739235.1  GI:30518532
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Telerman,A., Anson,R. and Tuijnder,M.
TITLE           Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL         Patent: WO 03025177-A 4825 27-MAR-2003;
                Molecular Engines Laboratories (FR)
FEATURES        Location/Qualifiers
                source
                1..17
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT      3 a 5 g 3 t
                Query Match      0.8%; Score 12.2; DB 1; Length 17;
                Best Local Similarity 82.4%; Pred. No. 7.1e+02;
                Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1486 GCTCTGGACAGCGAGG 1502
Db 1 GATCTGGACAGCGTGG 17

RESULT 916
LOCUS           AX741041
DEFINITION      Sequence 15 from Patent WO03027328.
ACCESSION       AX741041
VERSION         AX741041.1  GI:30523902
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
REFERENCE       1
AUTHORS         Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE           Methods, kits and compositions pertaining to the suppression of

```

```

ORGANISM        Homo sapiens
REFERENCE       1
AUTHORS         Telerman,A., Anson,R. and Tuijnder,M.
TITLE           Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL         Patent: WO 03025177-A 4825 27-MAR-2003;
                Molecular Engines Laboratories (FR)
FEATURES        Location/Qualifiers
                source
                1..17
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT      2 a 4 c 5 t
                Query Match      0.8%; Score 12.2; DB 1; Length 17;
                Best Local Similarity 82.4%; Pred. No. 7.1e+02;
                Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 255 ACCCCAAAAGCTGACC 271
Db 17 ACCCCAGGAGCTGATC 1

RESULT 915
LOCUS           AX739841
DEFINITION      Sequence 5431 from Patent WO03025177.
ACCESSION       AX739841
VERSION         AX739841.1  GI:30519138
KEYWORDS        Homo sapiens (human)
SOURCE          Homo sapiens
ORGANISM        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
AUTHORS         Telerman,A., Anson,R. and Tuijnder,M.
TITLE           Sequences involved in phenomena of tumour suppression, tumour
                reversion, apoptosis and/or resistance to viruses and the use
                thereof as medicaments
JOURNAL         Patent: WO 03025177-A 5431 27-MAR-2003;
                Molecular Engines Laboratories (FR)
FEATURES        Location/Qualifiers
                source
                1..17
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT      3 a 7 g 4 t
                Query Match      0.8%; Score 12.2; DB 1; Length 17;
                Best Local Similarity 82.4%; Pred. No. 7.1e+02;
                Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1486 GCTCTGGACAGCGAGG 1502
Db 1 GATCTGGACAGCGTGG 17

RESULT 916
LOCUS           AX741041
DEFINITION      Sequence 15 from Patent WO03027328.
ACCESSION       AX741041
VERSION         AX741041.1  GI:30523902
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
REFERENCE       1
AUTHORS         Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE           Methods, kits and compositions pertaining to the suppression of

```

detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
Patent: WO 03027328-A 15 03-APR-2003;
Boston Probes, Inc. (US); DakoCytomation Denmark A/S (DK)

FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

BASE COUNT 2 a 10 c 5 g 0 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1185 ACGCGCGCTCACGGCC 1201
D5 1 ACGCACCGCGCGGCC 17

RESULT 917
AX744246
LOCUS AX744246 17 bp DNA linear PAT 14-MAY-2003
DEFINITION Sequence 211 from Patent WO03031621.
ACCESSION AX744246

VERSION AX744246.1 GI:30722913
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Zhang, J.
TITLE A human G protein coupled receptor
JOURNAL Patent: WO 03031621-A 211 17-APR-2003;
Amersham Biosciences (SV) Corp. (US)

FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 4 a 3 c 7 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 788 AAGCTGGTGAAGGACCT 804
D5 1 AAGCTGGTGAAGGACCT 17

RESULT 918
BD001184/c
LOCUS BD001184 17 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.

ACCESSION BD001184
VERSION BD001184.1 GI:18625743
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
AUTHORS Draper, K.G., Dadykzt, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J., and Mamone, A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 344 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC

COMMENT
OS Artificial Sequence
PN JP 2000342285-A/344
PD 12-DEC-2000

PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKZT, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00,C12N9/22//(C12N5/10,C12R1:91), PC
C12N15/00,
PC C12N5/00,(C12N5/00,C12R1:91)
CC
FT Key Location/Qualifiers
1..17
/organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

BASE COUNT 0 a 13 c 3 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1549 GGCGGGGGGAGGGGCGC 1565
D5 17 GGCGGGGGGAGGGGCGC 1

RESULT 919
BD001613/c
LOCUS BD001613 17 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.

ACCESSION BD001613
VERSION BD001613.1 GI:18626172
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
AUTHORS Draper, K.G., Dadykzt, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J., and Mamone, A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342286-A 344 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC

COMMENT
OS Artificial Sequence
PN JP 2000342286-A/344
PD 12-DEC-2000

PF 01-MAY-2000 JP 2000132651
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889,14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR

15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
 07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
 KENNETH G DRAPER, LEC W DADYITZ, JAMES A MACSWIGEN, PI DENNIS G
 MAYSEJAK,
 PI JAMES J HOLESEK, ANTHONY J MAMONE
 PC C12N15/09, C12N5/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
 A61K39/135,
 PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
 PC A61P1/16,
 PC A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/68, PC
 (C12N15/09, C12R1:93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
 C12R1:93)
 CC

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 BASE COUNT 0 a _ 13 c 3 g 1 t

FEATURES

source 1. .17
 Location/Qualifiers
 /organism="Artificial Sequence".

1. .17
 /organism="synthetic construct"
 /mol_type="genomic RNA"
 /db_xref="taxon:32630"

BASE COUNT 0 a _ 13 c 3 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 BASE COUNT 0 a _ 13 c 3 g 1 t

Qy 1549 GCGCGGGGAGGGCGC 1565
 Db 17 GCGCGGGGAGGGGGC 1

RESULT 920

BD011182/c
 LOCUS Human telomerase catalytic subunit. 17 bp DNA linear PAT 31-JAN-2002

DEFINITION Human telomerase catalytic subunit.
 ACCESSION BD011182
 VERSION BD011182.1 GI:18639555

KEYWORDS JP 2001081042-A/139.
 SOURCE unclassified

ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,
 Harley, C.B. and Andrews, W.H.

TITLE Human telomerase catalytic subunit
 JOURNAL Patent: JP 2001081042-A 139 27-MAR-2001;
 GERON CORP, UNIVERSITY TECHNOLOGY CORP

COMMENT OS Unidentified
 PN JP 2001081042-A/139
 PD 27-MAR-2001

PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR
 25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR
 09-MAY-1997 US 08/854050, 14-AUG-1997 US 08/911312 PR

14-AUG-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI THOMAS
 R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
 MORIN,

PI CALVIN B HARLEY, WILLIAM H ANDREWS
 PC A61K38/00, A61K31/7088, A61K39/00, A61K48/00, A61P35/00, A61P43/00,
 PC C07K5/10,
 PC C07K5/107, C07K5/117, C07K7/06, C07K7/08, C07K16/40, C12N9/12, PC

C12N15/09,
 PC C12Q1/02, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
 G01N33/53,
 PC G01N33/566, G01N33/573//C12P21/08, A61K37/02, C12N15/00 CC

Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers

FT /organism="Unidentified".
 Location/Qualifiers
 1. .17

FEATURES source

/organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644" 1 t
 BASE COUNT 2 a _ 10 c 4 g

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1362 GGGACCGGGGGGGCGC 1378
 Db 17 GGCATCGGGGGGTGC 1

RESULT 921

BD012716
 LOCUS Novel DNA fragment increasing gene expression dose. 17 bp DNA linear PAT 02-AUG-2002

DEFINITION Novel DNA fragment increasing gene expression dose.
 ACCESSION BD012716
 VERSION BD012716.1 GI:22092905

KEYWORDS WO 0114543-A/25.
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Takakura, Y. and Ueki, J.
 JOURNAL Patent: WO 0114543-A 25 01-MAR-2001;
 JAPAN TOBACCO INC, YOSHIMITSU TAKAKURA, JUN UEKI

COMMENT OS Artificial Sequence
 PN WO 0114543-A/25
 PD 01-MAR-2001

PF 18-AUG-2000 WO 2000JP005539
 PR 19-AUG-1999 JP 99P 232815
 PI YOSHIMITSU TAKAKURA, JUN UEKI

PC C12N15/11, C12P21/02
 CC

FH Key Location/Qualifiers
 source 1. .17
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

BASE COUNT 3 a _ 10 c 3 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1137 CCGCGCTGTGCACAGC 1153
 Db 1 CCGCGCAGTCACACC 17

RESULT 922

BD012716/c
 LOCUS Novel DNA fragment increasing gene expression dose. 17 bp DNA linear PAT 02-AUG-2002

DEFINITION Novel DNA fragment increasing gene expression dose.
 ACCESSION BD012716
 VERSION BD012716.1 GI:22092905

KEYWORDS WO 0114543-A/25.
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Takakura, Y. and Ueki, J.
 JOURNAL Patent: WO 0114543-A 25 01-MAR-2001;
 JAPAN TOBACCO INC, YOSHIMITSU TAKAKURA, JUN UEKI

COMMENT OS Artificial Sequence
 PN WO 0114543-A/25
 PD 01-MAR-2001

PF 18-AUG-2000 WO 2000JP005539

FEATURES source

```

PR 19-AUG-1999 JP 99P 232815
PI YOSHIMITSU TAKAKURA, JUN UEKI
PC C12N15/11, C12P21/02
CC
FH Key Location/Qualifiers.
FEATURES
  source
    Location/Qualifiers
    1..17
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
BASE COUNT 3 a 10 c 3 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1343 GCGCGGACAGCGGCGG 1359
    |||||
Db 17 GGTGTGACTGCGGCGG 1

RESULT 923
BD065436/c
LOCUS
DEFINITION Diagnosis kit of tubercle bacillus.
ACCESSION BD013494
VERSION BD013494.1 GI:22553808
KEYWORDS JP 2001103981-A/58.
SOURCE Mycobacterium tuberculosis
ORGANISM Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
1 (bases 1 to 17)
Suzuki, S., Nishida, M. and Takenishi, S.
Diagnosis kit of tubercle bacillus
Patent: JP 200103981-A 58 17-APR-2001;
NISHINBO IND INC, SYSTEM RESEARCH CO LTD
OS Mycobacterium tuberculosis
PN JP 2001103981-A/58
PD 17-APR-2001
PF 26-JUL-2000 JP 200225985
PI SADAIKO SUZUKI, MICHIO NISHIDA, SOICHIRO TAKENISHI PC
C12N15/09, C12N15/00, C12Q1/68, C12Q1/32, PC
C12Q1/68, C12R1/325, C12Q1/68, C12R1/33, C12N15/00, C12N15/00 CC
capture
FH Key Location/Qualifiers
FT source 1..17
/organism="Mycobacterium tuberculosis".
FEATURES
  source
    Location/Qualifiers
    1..17
    /organism="Mycobacterium tuberculosis"
    /mol_type="genomic DNA"
    /db_xref="taxon:1773"
BASE COUNT 3 a 6 c 7 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1365 ACCGCGGGGCGGCGG 1381
    |||||
Db 1 ACCGATGAGCGGCGG 17

RESULT 924
BD065436/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065436
VERSION BD065436.1 GI:22611039
KEYWORDS JP 2001511000-A/71.
SOURCE unidentified
  
```

```

ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Schlingensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 71 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/71
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN, WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A51K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..17
/organism="Unknown".
FEATURES
  source
    Location/Qualifiers
    1..17
    /organism="unidentified"
    /mol_type="genomic DNA"
    /db_xref="taxon:32644"
BASE COUNT 6 a 3 c 5 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 850 GCTCTACGCGACTTCC 866
    |||||
Db 17 GCTGTACATTGACTTCC 1

RESULT 925
BD067713/c
LOCUS
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067713
VERSION BD067713.1 GI:22613316
KEYWORDS JP 2001511003-A/553.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Akhtar, S., Fell, P. and McSwiggen, J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 553 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
OS Unidentified
PN JP 2001511003-A/553
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476, 04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
C12N3/00, C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..17
/organism="unidentified".
FEATURES
  source
    Location/Qualifiers
    1..17
    /organism="unidentified"
    /mol_type="genomic RNA"
    /db_xref="taxon:32844"
BASE COUNT 3 a 6 c 5 g 3 t
  
```

```

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 891 GGCCCAAGAGGCTTC 907
DB 17 GGCCCATGAAGGCTTC 1

RESULT 926
BD067714/c
LOCUS BD067714 17 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION BD067714.1 GI:226213317
VERSION JP 2001511003-A/554.
KEYWORDS unidentifed
SOURCE unidentifed
ORGANISM unclassified.
1 (bases 1 to 17)
REFERENCE Akhtar, S., Fell, P. and McSwiggen, J.A.
AUTHORS Enzymatic nucleic acid treatment of diseases or conditions related
TITLE to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A/554 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC, ASTON UNIV
OS Unidentifed
PN JP 2001511003-A/554
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476, 04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC
C12N9/00, C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1.17 /organism='Unidentifed'.
1.17 Location/Qualifiers
/organism='unidentifed'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
BASE COUNT 3 a 7 c 4 g 3 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 890 GGCCCAAGAGGCTTC 906
DB 17 GGCCCATGAAGGCTTC 1

RESULT 927
BD104504/c
LOCUS BD104504 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104504
VERSION BD104504.1 GI:22650078
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 17)
REFERENCE Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and
AUTHORS Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 608 06-DEC-2001;
NISSHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TAEKO
INOKO, H., KAGIYA, T., ICHIHARA, T., MATSUMURA, Y., MORIYA, S. and
NISHIDA, M.
OS Artificial Sequence
PN WO 0192572-A/608
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
MATSUMURA,
SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1.17 /organism='Artificial Sequence'.
1.17 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 4 a 3 c 9 g 1 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
NISHIDA
OS Artificial Sequence
PN WO 0192572-A/608
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
MATSUMURA,
SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1.17 /organism='Artificial Sequence'.
1.17 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 1 a 4 c 8 g 4 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1498 CGAGCCCTGCACCCGC 1514
DB 17 CCAGGAAGTGCACCCGC 1

RESULT 928
BD104826
LOCUS BD104826 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104826
VERSION BD104826.1 GI:22650400
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
1 (bases 1 to 17)
REFERENCE Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and
AUTHORS Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 930 06-DEC-2001;
NISSHINBO INDUSTRIES INC, SYSTEM RESEARCH INC, HIDETOSHI INOKO, TAEKO
KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO
NISHIDA
OS Artificial Sequence
PN WO 0192572-A/930
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI PI
MATSUMURA,
SHOGO MORIYA, MICHIO NISHIDA
PC C12Q1/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence:capture
FH Key Location/Qualifiers
FT source 1.17 /organism='Artificial Sequence'.
1.17 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 4 a 3 c 9 g 1 t

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```



```

QY 33 CGGAGCCGGACGAGGA 49
Db 1 CGGAGCCGGAGGATGGA 17

RESULT 929
LOCUS BD105168 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Kit and method for determining HLA type.
ACCESSION BD105168
VERSION BD105168.1 GI:22650742
KEYWORDS WO 0192572-A/1272.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1272 06-DEC-2001; NISHINOBO INDUSTRIES INC,SYSTEM RESEARCH INC,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1272
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDETOSHI INOKO,TAEKO KAGIYA,TATSUO ICHIHARA,YOSHIYUKI MATSUMURA,SHOGO MORIYA,MICHIO NISHIDA
PI SHOGO MORIYA,MICHIO NISHIDA
PC C12Q1/68,C12M1/00,C12N15/09,G01N33/53
CC Description of Artificial Sequence:capture
FH Key
FT source 1..17
/organism='Artificial Sequence'
/Location/Qualifiers
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
3 a 7 c 6 g 1 t

FEATURES
source
BASE COUNT 3 a 7 c 6 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 804 TGAGCCCGGACCGC 820
Db 17 TGAGCCCGGTGTCGC 1

RESULT 930
LOCUS BD182250 17 bp DNA linear PAT 15-MAY-2003
DEFINITION Polynucleotide probe and primer for detecting beer-clouding lactic acid bacterium and method of detecting beer-clouding lactic acid bacterium.
ACCESSION BD182250
VERSION BD182250.1 GI:30793168
KEYWORDS WO 02095028-A/53.
SOURCE Lactobacillus brevis
ORGANISM Lactobacillus brevis
REFERENCE 1 (bases 1 to 17)
AUTHORS Fujii,T.
TITLE Polynucleotide probe and primer for detecting beer-clouding lactic acid bacterium and method of detecting beer-clouding lactic acid bacterium.
JOURNAL Patent: WO 02095028-A 63 28-NOV-2002; KIRIN BREWERY CO LTD,TOSHIO FUJII
COMMENT OS Lactobacillus brevis
PN WO 02095028-A/63

```

```

PD 28-NOV-2002
PF 23-MAY-2002 WO 2002JP005022
PR 23-MAY-2001 JP 01P 154085
PI TOSHIO FUJII
PC C12N15/11,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C07K14/335, PC C07K16/12
PC C12P21/02,C12Q1/04,C12Q1/68
CC Polynucleotide probe and primer for detecting beer-clouding lactic acid bacterium and method of detecting beer-clouding lactic acid bacterium
CC Key
FH Key
FT source 1..17
/organism='Lactobacillus brevis'
/Location/Qualifiers
1..17
/organism='Lactobacillus brevis'
/Location/Qualifiers
1..17
/organism='genomic DNA'
/db_xref='taxon:1580'
5 a 4 c 5 g 3 t

BASE COUNT 5 a 4 c 5 g 3 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 725 GCGGCCCAATCGGAGG 741
Db 1 GCGGCCCAATCGTGATG 17

RESULT 931
LOCUS E12897/c 17 bp RNA linear PAT 27-APR-1998
DEFINITION Modified antisense oligonucleotide.
ACCESSION E12897
VERSION E12897.1 GI:5708629
KEYWORDS JP 1997095495-A/1.
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsuda,A. and Ono,A.
TITLE ANTISENSE OLIGONUCLEOTIDE, NUCLEOSIDE AND INTERMEDIATE FOR PRODUCING THE SAME, ITS SYNTHESIS, OLIGONUCLEOTIDE SYNTHESIZING UNIT AND ITS
JOURNAL Patent: JP 1997095495-A 1 08-APR-1997; KANSAI SHIN GIUTSU KENKYUSHO:KK, MATSUDA AKIRA
COMMENT OS None
OC Artificial sequences.
PN JP 1997095495-A/1
PD 08-APR-1997
PF 29-SEP-1995 JP 1995277168
PI MATSUDA AKIRA, ONO AKIRA
PC C07H21/04//A61K31/70,A61K31/70,C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key
FT source 1..17
/organism='Artificial sequences'
FT misc_feature 1
FT misc_feature 2
/Note='5-(N,N-dimethylaminoethyl) carbamoyl-2'-deoxyuridine' FT
FT misc_feature 4
/Note='5-methyl-2'-deoxycytidine' FT
FT misc_feature 6
/Note='5-methyl-2'-deoxycytidine' FT
FT misc_feature 7
/Note='5-methyl-2'-deoxycytidine' FT
FT

```

```

/note='5-(N,N-dimethylaminohexyl)carbamoyl-2'-deoxyuridine' FT
misc_feature 8 /note='5-methyl-2'-deoxycytidine' FT
FT
misc_feature 10 /note='5-methyl-2'-deoxycytidine' FT
FT
misc_feature 11 /note='5-methyl-2'-deoxycytidine' FT
FT
FT
/note='5-(N,N-dimethylaminohexyl)carbamoyl-2'-deoxyuridine' FT
misc_feature 12 /note='5-methyl-2'-deoxycytidine' FT
FT
misc_feature 14 /note='5-methyl-2'-deoxycytidine' FT
FT
misc_feature 16 /note='5-methyl-2'-deoxycytidine' FT
FT
misc_feature 17 /note='5-methyl-2'-deoxycytidine' FT
FT
FT
/note='5-aminohexylcarbamoyl-2'-deoxyuridine'
Location/Qualifiers
1. .17
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
BASE COUNT 0 a 8 c 0 g 9 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 ACGAGGGAGAGAGCA 28
||| ||| ||| ||| ||| ||| |||
DB 17 AGAGAGAGAGAGAGA 1

RESULT 932
E36931/C
LOCUS Human telomerase catalytic subunit promoter. 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36931
VERSION E36931.1 GI:13022894
KEYWORDS JP 1999253177-A/139.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 139 21-SEP-1999;
JERON CORP. UNIVERSITY TECHNOLOGY CORP
COMMENT OS Unidentified
PN JP 1999253177-A/139
PD 21-SEP-1999
PF 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HAREI,WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
PC C12Q1/02
PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
C07K16/40,
PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
C12R1:84),
PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .17
/organism='Unidentified'.

```

```

FEATURES
source
Location/Qualifiers
1. .17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
BASE COUNT 2 a 10 c 4 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1362 GGGACCGGGGGGGCGGC 1378
||| ||| ||| ||| ||| ||| |||
DB 17 GGCATCGGGGGGGTGGC 1

RESULT 933
E42982
LOCUS Novel DNA fragment enlarging gene expression dose. 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel DNA fragment enlarging gene expression dose.
ACCESSION E42982
VERSION E42982.1 GI:18633441
KEYWORDS JP 2001057886-A/25.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Takakura,Y. and Ueki,J.
TITLE Novel DNA fragment enlarging gene expression dose
JOURNAL Patent: JP 2001057886-A 25 06-MAR-2001;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2001057886-A/25
PD 06-MAR-2001
PF 19-AUG-1999 JP 1999232815
PR YOSHIMITSU TAKAKURA,JUN UEKI
PC C12N15/09//C12Q1/68,C12N15/00
CC Key Location/Qualifiers
FT source 1. .17
/organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1. .17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
BASE COUNT 3 a 10 c 3 g 1 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1137 CCGCGCGGTGCGACAGC 1153
||| ||| ||| ||| ||| ||| |||
DB 1 CCGCGCGGTGCGACAGC 17

RESULT 934
E42982/C
LOCUS Novel DNA fragment enlarging gene expression dose. 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel DNA fragment enlarging gene expression dose.
ACCESSION E42982
VERSION E42982.1 GI:18633441
KEYWORDS JP 2001057886-A/25.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Takakura,Y. and Ueki,J.
TITLE Novel DNA fragment enlarging gene expression dose
JOURNAL Patent: JP 2001057886-A 25 06-MAR-2001;
JAPAN TOBACCO INC

```

BASE COUNT	1 a	7 c	3 g	6 t
Query Match	0.8%;	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	82.4%;	Pred. NO. 7.1e+02;		
Matches	14;	Conservative	0; Mismatches	3; Indels
0;	Gaps	0;		
QY	44	CGAGGAAGGAAAGCG	60	
DB	17	CGAGGAAGGGAATC	1	
RESULT 937				
LOCUS	I46955			
DEFINITION	Sequence 48 from patent US 5639655.			linear
ACCESSION	I46955			
VERSION	I46955.1	GI:2470920		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Thompson, J.D. and Draper, K.G.			
TITLE	PML-RARA targeted ribozymes			
JOURNAL	Patent: US 5639655-A 48 17-JUN-1997;			
FEATURES	Location/Qualifiers			
source	1. .17			
BASE COUNT	1 a	2 c	13 g	1 t
Query Match	0.8%;	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	82.4%;	Pred. NO. 7.1e+02;		
Matches	14;	Conservative	0; Mismatches	3; Indels
0;	Gaps	0;		
QY	1556	GGAGGGGCGCGGAGGG	1572	
DB	1	GGTGGGGGCGGACGG	17	
RESULT 938				
LOCUS	I53736			
DEFINITION	Sequence 1477 from patent US 5646042.			linear
ACCESSION	I53736			
VERSION	I53736.1	GI:2474939		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.			
TITLE	C-myb targeted ribozymes			
JOURNAL	Patent: US 5646042-A 1477 08-JUL-1997;			
FEATURES	Location/Qualifiers			
source	1. .17			
BASE COUNT	5 a	5 c	4 g	3 t
Query Match	0.8%;	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	82.4%;	Pred. NO. 7.1e+02;		
Matches	14;	Conservative	0; Mismatches	3; Indels
0;	Gaps	0;		
QY	1205	GGCACCATTCTCATCA	1221	
DB	1	GGCACCATTCTGGACAA	17	
RESULT 939				
LOCUS	I75308			
DEFINITION	Sequence 57 from patent US 5689052.			linear
ACCESSION	I75308			
VERSION	I75308.1	GI:3011449		

Search completed: December 23, 2003, 16:33:26
Job time : 34 secs

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Brown,S.Marie., Dean,D.Allen., Fromm,M.Ernest. and Sanders,P.Rigden.
TITLE Synthetic DNA sequences having enhanced expression in monocotyledonous plants and method for preparation thereof
JOURNAL Patent: US 5689052-A 57 18-NOV-1997;
FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
BASE COUNT 0 a 6 c 6 g 5 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred.No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1225 GGTCGTGGCTCGTCT 1241
||| ||||| |||||
Db 1 GCGCTGGCTCGTCT 17
RESULT 940
AB068835/c
LOCUS
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-CW-203-2 at 1p36.
ACCESSION AB068835
VERSION AB068835.1 GI:15129639
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K., Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H., Morohashi,A., Chira,M., Nakagawara,A., Liu,S., Hoshi,M., Hori,A. and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 17)
AUTHORS Hori,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Hori, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:hori@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
source Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature 1..17
/note="reverse primer for human STS sts-CW-203-2 at 1p36 sts-CW-203-2 obtained from clones B24G6, B27H21, 6K9, B8E14, B367J3, B352L16, B50N1, B122B1, B171J2, Human BAC library RPCI-11"
BASE COUNT 3 a 9 c 4 g 1 t
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred.No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1541 AGCCGGGGGGGGGGGG 1557
||| ||||| |||||
Db 17 AGCCTTGGGGGGGGGTGG 1

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:37:04 ; Search time 27 Seconds
(without alignments)
2.042 Million cell updates/sec

Title: us-10-001-844-3
Perfect score: 1576
Sequence: 1 gcgagcgacgcagcagggga.....caggggcgcggagggggcc 1576

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 998 seqs, 17490 residues

Total number of hits satisfying chosen parameters: 1996

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 145 summaries

Database : rnpb.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	1.9	30	1	US-10-001-844-6
2	27	1.7	27	1	US-09-992-665-289
3	24	1.5	24	1	US-08-462-386D-43
4	24	1.5	24	1	US-08-954-771-43
5	24	1.5	24	1	US-09-736-476-43
6	23.4	1.5	33	1	US-10-147-463-30
7	22	1.4	24	1	US-09-992-665-288
8	22	1.4	29	1	US-09-883-848A-37
9	22	1.4	29	1	US-10-164-282-19
10	22	1.4	30	1	US-09-828-034-7
11	21	1.3	21	1	US-10-001-844-4
12	20.6	1.3	27	1	US-10-108-969-4
13	20	1.3	20	1	US-10-001-844-10
14	20	1.3	20	1	US-10-001-844-11
15	20	1.3	20	1	US-10-001-844-12
16	20	1.3	20	1	US-10-001-844-13
17	20	1.3	20	1	US-10-001-844-14
18	20	1.3	20	1	US-10-001-844-15
19	20	1.3	20	1	US-10-001-844-16
20	20	1.3	20	1	US-10-001-844-17
21	20	1.3	20	1	US-10-001-844-18
22	20	1.3	20	1	US-10-001-844-19
23	20	1.3	20	1	US-10-001-844-20
24	20	1.3	20	1	US-10-001-844-21
25	20	1.3	20	1	US-10-001-844-22
26	20	1.3	20	1	US-10-001-844-23
27	20	1.3	20	1	US-10-001-844-24
28	20	1.3	20	1	US-10-001-844-25
29	20	1.3	20	1	US-10-001-844-26
30	20	1.3	20	1	US-10-001-844-27
31	20	1.3	20	1	US-10-001-844-28
32	20	1.3	20	1	US-10-001-844-29
33	20	1.3	20	1	US-10-001-844-30

1	US-10-001-844-31	Sequence 31, Appl
2	US-10-001-844-32	Sequence 32, Appl
3	US-10-001-844-33	Sequence 33, Appl
4	US-10-001-844-34	Sequence 34, Appl
5	US-10-001-844-35	Sequence 35, Appl
6	US-10-001-844-36	Sequence 36, Appl
7	US-10-001-844-37	Sequence 37, Appl
8	US-10-001-844-38	Sequence 38, Appl
9	US-10-001-844-39	Sequence 39, Appl
10	US-10-001-844-40	Sequence 40, Appl
11	US-10-001-844-41	Sequence 41, Appl
12	US-10-001-844-42	Sequence 42, Appl
13	US-10-001-844-43	Sequence 43, Appl
14	US-10-001-844-44	Sequence 44, Appl
15	US-10-001-844-45	Sequence 45, Appl
16	US-10-001-844-46	Sequence 46, Appl
17	US-10-001-844-47	Sequence 47, Appl
18	US-10-001-844-48	Sequence 48, Appl
19	US-10-001-844-49	Sequence 49, Appl
20	US-09-825-155-5	Sequence 5, Appl
21	US-09-825-155-9	Sequence 9, Appl
22	US-10-098-263B-66408	Sequence 66408, A
23	US-10-147-463-21	Sequence 21, Appl
24	US-09-825-155-6	Sequence 6, Appl
25	US-10-150-429B-7	Sequence 7, Appl
26	US-09-992-665-157	Sequence 157, App
27	US-10-098-263B-48877	Sequence 48877, A
28	US-09-788-038-31	Sequence 31, Appl
29	US-09-837-621-31	Sequence 31, Appl
30	US-10-378-437-12	Sequence 12, Appl
31	US-10-372-696-31	Sequence 31, Appl
32	US-10-278-455-12	Sequence 12, Appl
33	US-10-001-844-5	Sequence 5, Appl
34	US-10-188-869-21	Sequence 21, Appl
35	US-09-992-665-284	Sequence 284, App
36	US-08-787-862-23	Sequence 23, Appl
37	US-10-100-608B-12	Sequence 12, Appl
38	US-09-798-058-13	Sequence 13, Appl
39	US-09-828-034-10	Sequence 10, Appl
40	US-09-788-038-32	Sequence 32, Appl
41	US-09-837-621-35	Sequence 35, Appl
42	US-10-372-696-32	Sequence 32, Appl
43	US-09-791-406-46	Sequence 46, App
44	US-09-888-326-410	Sequence 410, App
45	US-09-776-479-243	Sequence 243, App
46	US-09-915-814-105	Sequence 105, App
47	US-08-851-871-26	Sequence 26, Appl
48	US-10-112-653-235	Sequence 235, App
49	US-10-017-995-243	Sequence 243, App
50	US-09-984-183-22	Sequence 22, Appl
51	US-09-848-754A-870	Sequence 870, App
52	US-09-500-700-68	Sequence 68, Appl
53	US-10-314-405-45	Sequence 45, Appl
54	US-10-126-355-60	Sequence 60, Appl
55	US-10-125-181-8	Sequence 8, Appl
56	US-10-122-434-7	Sequence 7, Appl
57	US-09-969-373-3868	Sequence 3868, Ap
58	US-09-920-033-22	Sequence 22, Appl
59	US-10-388-263-554	Sequence 554, App
60	US-10-052-390B-12	Sequence 12, Appl
61	US-10-053-645A-28	Sequence 28, Appl
62	US-10-305-810-43	Sequence 43, Appl
63	US-10-147-196-22	Sequence 22, Appl
64	US-09-887-145-29	Sequence 29, Appl
65	US-09-866-108-10651	Sequence 10651, A
66	US-09-866-108-10652	Sequence 2143, Ap
67	US-09-848-754A-2143	Sequence 3086, Ap
68	US-09-238-700-2801	Sequence 2801, Ap

```

107 14.4 0.9 17 1 US-10-156-306-5214 Sequence 5214, Ap
108 14.4 0.9 17 1 US-10-156-306-6011 Sequence 6011, Ap
109 14.4 0.9 17 1 US-10-156-306-6012 Sequence 6012, Ap
110 14.4 0.9 18 1 US-09-918-1868-99 Sequence 99, Appl
111 14.4 0.9 18 1 US-09-961-077-1165 Sequence 1165, Ap
112 14.4 0.9 20 1 US-09-791-243-11 Sequence 11, Appl
113 14.2 0.9 19 1 US-09-910-087-12 Sequence 12, Appl
114 14.2 0.9 19 1 US-09-938-795A-18 Sequence 18, Appl
115 14.2 0.9 19 1 US-09-791-190A-16 Sequence 16, Appl
116 14.2 0.9 19 1 US-10-244-647-9 Sequence 9, Appl
117 14.2 0.9 19 1 US-10-244-647-655 Sequence 655, Ap
118 14.2 0.9 20 1 US-09-752-983-42 Sequence 42, Appl
119 14.2 0.9 20 1 US-09-800-631-11 Sequence 11, Appl
120 14.2 0.9 20 1 US-09-780-172-32 Sequence 32, Appl
121 14.2 0.9 20 1 US-09-870-002-20 Sequence 20, Appl
122 14.2 0.9 20 1 US-09-865-866-68 Sequence 68, Appl
123 14.2 0.9 20 1 US-09-922-146-25 Sequence 25, Appl
124 14.2 0.9 20 1 US-10-388-263-746 Sequence 746, Ap
125 14.2 0.9 20 1 US-10-006-191-91 Sequence 91, Appl
126 14.2 0.9 20 1 US-10-006-191-111 Sequence 111, Ap
127 14.2 0.9 20 1 US-09-961-756-45 Sequence 45, Appl
128 14.2 0.9 20 1 US-09-851-871-154 Sequence 154, Ap
129 14.2 0.9 20 1 US-10-363-798-15 Sequence 15, Appl
130 14.2 0.9 20 1 US-10-005-344-42 Sequence 42, Appl
131 14.2 0.9 20 1 US-10-232-334-42 Sequence 42, Appl
132 14.2 0.9 20 1 US-10-293-783-11 Sequence 11, Appl
133 14.2 0.9 30 1 US-09-828-034-7 Sequence 7, Appl
134 14 0.9 15 1 US-09-757-100B-37 Sequence 37, Appl
135 14 0.9 15 1 US-10-440-850-167 Sequence 167, Ap
136 14 0.9 16 1 US-09-870-956-17 Sequence 17, Appl
137 14 0.9 17 1 US-09-780-533A-1789 Sequence 1789, Ap
138 14 0.9 17 1 US-09-780-533A-2337 Sequence 2337, Ap
139 14 0.9 18 1 US-08-911-824-77 Sequence 77, Appl
140 14 0.9 18 1 US-09-374-046A-201 Sequence 201, Ap
141 14 0.9 19 1 US-10-309-690-1 Sequence 1, Appl
142 14 0.9 20 1 US-10-001-844-40 Sequence 40, Appl
143 14 0.9 20 1 US-09-757-100B-17 Sequence 17, Appl
144 14 0.9 20 1 US-09-888-615-131 Sequence 131, Ap
145 14 0.9 20 1 US-10-430-196-5 Sequence 5, Appl

```

ALIGNMENTS

```

RESULT 1
US-10-001-844-6
; Sequence 6, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-001-844-6

```

```

Query Match 1.9%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 691 TATCCACTGCTCGGTGAAGCAGAGAACTC 720
Db 1 TATCCACTGCTCGGTGAAGCAGAGAACTC 30

```

```

RESULT 2
US-09-992-665-289/c
; Sequence 289, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 289
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-289
Query Match 1.7%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 11; Mismatches 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 755 TCGGCCACGGTGCACCTGGAGCAGGC 781
Db 27 TCGGCCACGGTGCACCTGGAGCAGGC 1

RESULT 3
US-08-462-386D-43
; Sequence 43, Application US/08462386D
; Publication No. US20030186357A1
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Tissue Pattern-Inducing
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,386D
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-006CP3
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-462-386D-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAAGATGCC 547
DB 1 ACCGAGGGCTGGGACGAAGATGCC 24

RESULT 4

US-08-954-771-43
Sequence 43, Application US/08954771
Publication No. US20030054437A1
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,771
FILING DATE: 20-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 04-MAY-1995
PRIOR APPLICATION DATA: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-954-771-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAAGATGCC 547
DB 1 ACCGAGGGCTGGGACGAAGATGCC 24

RESULT 5

US-09-736-476-43
Sequence 43, Application US/09736476
Publication No. US20030190696A1
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
APPLICANT: Bumcrot, David A.
APPLICANT: Marti-Gorostiza, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/736,476
FILING DATE: 13-DEC-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-736-476-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAAGATGCC 547
DB 1 ACCGAGGGCTGGGACGAAGATGCC 24

RESULT 6

```
US-10-147-463-30
; Sequence 30, Application US/10147463
; Publication No. US20030059838A1
; GENERAL INFORMATION:
; APPLICANT: ARIYASU, Toshio
; NAKAMURA, Shuji
; ORITA, Kunzo
; TITLE OF INVENTION: HEDGEHOG PROTEIN
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/147,463
; FILING DATE: 17-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/617,545
; FILING DATE: 14-Jul-2000
; APPLICATION NUMBER: 09/063,778
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 98-
; FILING DATE: 14-APR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: ARIYASU-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-35281
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-147-463-30

Query Match 1.5%; Score 23.4; DB 1; Length 33;
Best Local Similarity 81.8%; Pred. No. 63;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 208 CTCGGGACTGCGTGGCGACCGGCGAGGGGTT 240
DB 1 CCCGGGAATTCATTCCGGACCGGCGAGGGGTT 33

RESULT 7
US-09-992-665-288
; Sequence 288, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaia Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 24

US-10-147-463-30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-288

Query Match 1.4%; Score 22; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGGCGAGATGT 172
DB 3 GATGCTGCTGCTGGCGAGATGT 24

RESULT 8
US-09-883-848A-37/c
; Sequence 37, Application US/09883848A
; Publication No. US20030022819A1
; GENERAL INFORMATION:
; APPLICANT: Ling, L.
; APPLICANT: Sanicola-Nadel, M.
; TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
; FILE REFERENCE: CIBT-P01-119
; CURRENT APPLICATION NUMBER: US/09/883,848A
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/211,919
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-883-848A-37

Query Match 1.4%; Score 22; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TCGGACCGGCGAGGGGTTTCG 242
DB 22 TCGGACCGGCGAGGGGTTTCG 1

RESULT 9
US-10-164-282-19/c
; Sequence 19, Application US/10164282
; Publication No. US20030166543A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al.
; TITLE OF INVENTION: FUNCTIONAL ANTAGONISTS OF HEDGEHOG ACTIVITY
; FILE REFERENCE: CIBT-P02-113
; CURRENT APPLICATION NUMBER: US/10/164,282
; CURRENT FILING DATE: 2002-05-05
; PRIOR APPLICATION NUMBER: 09/890,975
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 19
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-282-19

Query Match 1.4%; Score 22; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TCGGACCGGCGAGGGGTTTCG 242
```


Db 22 TCGGACCGGGGAGGGGGTTCG 1
|||||

RESULT 10

US-09-828-034-7/c
; Sequence 7, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 30
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA

US-09-828-034-7
Query Match 1.4%; Score 22; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 82;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1546 GGGGGCGGGGAGGGGGCGGGAGCGGGC 1575
|||||

Db 30 GGGGGCGGGGCGGGGGCGGGCGGGCGGGC 1
|||||

RESULT 11

US-10-001-844-4
; Sequence 4, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer

US-10-001-844-4

Query Match 1.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 655 CGGCTTCGACTGGGTGTACTA 675
|||||

Db 1 CGGCTTCGACTGGGTGTACTA 21
|||||

RESULT 12

US-10-108-969-4
; Sequence 4, Application US/10108969
; Publication No. US20030198959A1
; GENERAL INFORMATION:
; APPLICANT: Kurnit, David M.

; TITLE OF INVENTION: Methods and Compositions for Analysis of Urine Samples in the D
; TITLE OF INVENTION: and Treatment of Kidney Diseases
; FILE REFERENCE: 65988-0001
; CURRENT APPLICATION NUMBER: US/10/108,969
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Indian hedgehog forward primer.
US-10-108-969-4

Query Match 1.3%; Score 20.6; DB 1; Length 27;
Best Local Similarity 85.2%; Pred. No. 1e+02; 4; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CAATTACACCCCGACATCATATTAA 411
|||||

Db 1 CAATTACATCCAGACATCATCTTCAA 27
|||||

RESULT 13

US-10-001-844-10/c
; Sequence 10, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-001-844-10

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GAGGGAGAGAGCGAGCGGGC 34
|||||

Db 20 GAGGGAGAGAGCGAGCGGGC 1
|||||

RESULT 14

US-10-001-844-11/c
; Sequence 11, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

```
US-10-001-844-11
Query Match          1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 CGCACAGGCACACCCGCC 89
Db 20 CGCACAGGCACACCCGCC 1

RESULT 15
US-10-001-844-12/c
; Sequence 12, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-12

Query Match          1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 TCGCGCCCGGACCCGCGG 117
Db 20 TCGCGCCCGGACCCGCGG 1

RESULT 16
US-10-001-844-13/c
; Sequence 13, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-13

Query Match          1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 133 CATCAGTCCATGGCGGAGA 152
Db 20 CATCAGTCCATGGCGGAGA 1

RESULT 17
US-10-001-844-14/c
; Sequence 14, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-14

Query Match          1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 135 TCAGTTCCATGGCGGAGTG 154
Db 20 TCAGTTCCATGGCGGAGTG 1

RESULT 18
US-10-001-844-15/c
; Sequence 15, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-15

Query Match          1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 AGTTCCATGGCGGAGTGCT 156
Db 20 AGTTCCATGGCGGAGTGCT 1

RESULT 19
US-10-001-844-16/c
; Sequence 16, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 20
```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-16

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 TTCCATGGCGGAGATGCTGC 158
Db 20 TTCCATGGCGGAGATGCTGC 1

RESULT 20
US-10-001-844-17/c
/ Sequence 17, Application US/10001844
/ Publication No. US20030105041A1
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
/ FILE REFERENCE: ISPH-0617
/ CURRENT APPLICATION NUMBER: US/10/001,844
/ CURRENT FILING DATE: 2001-11-16
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-17

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 CCATGGCGGAGATGCTGCTG 160
Db 20 CCATGGCGGAGATGCTGCTG 1

RESULT 21
US-10-001-844-18/c
/ Sequence 18, Application US/10001844
/ Publication No. US20030105041A1
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
/ FILE REFERENCE: ISPH-0617
/ CURRENT APPLICATION NUMBER: US/10/001,844
/ CURRENT FILING DATE: 2001-11-16
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-18

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 ATGGCGGAGATGCTGCTGCT 162
Db 20 ATGGCGGAGATGCTGCTGCT 1

RESULT 22
US-10-001-844-19/c
/ Sequence 19, Application US/10001844
/ Publication No. US20030105041A1
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
/ FILE REFERENCE: ISPH-0617
/ CURRENT APPLICATION NUMBER: US/10/001,844
/ CURRENT FILING DATE: 2001-11-16
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 19
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-19

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 GGGCGAGATGCTGCTGCTGG 164
Db 20 GGGCGAGATGCTGCTGCTGG 1

RESULT 23
US-10-001-844-20/c
/ Sequence 20, Application US/10001844
/ Publication No. US20030105041A1
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
/ FILE REFERENCE: ISPH-0617
/ CURRENT APPLICATION NUMBER: US/10/001,844
/ CURRENT FILING DATE: 2001-11-16
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-20

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 GCGAGATGCTGCTGCTGCG 166
Db 20 GCGAGATGCTGCTGCTGCG 1

RESULT 24
US-10-001-844-21/c
/ Sequence 21, Application US/10001844
/ Publication No. US20030105041A1
/ GENERAL INFORMATION:
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
/ FILE REFERENCE: ISPH-0617
/ CURRENT APPLICATION NUMBER: US/10/001,844
/ CURRENT FILING DATE: 2001-11-16
```

; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-21

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GAGATGCTGCTGGCGAG 168
|||
DB 20 GAGATGCTGCTGGCGAG 1

RESULT 25
US-10-001-844-22/c
; Sequence 22, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-22

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 GATGCTGCTGGCGAGAT 170
|||
DB 20 GATGCTGCTGGCGAGAT 1

RESULT 26
US-10-001-844-23/c
; Sequence 23, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-23

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 153 TGCTGCTGCTGGCGAGATGT 172
|||
DB 20 TGCTGCTGCTGGCGAGATGT 1

RESULT 27
US-10-001-844-24/c
; Sequence 24, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-24

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 CTGCTGCTGGCGAGATGTCT 174
|||
DB 20 CTGCTGCTGGCGAGATGTCT 1

RESULT 28
US-10-001-844-25/c
; Sequence 25, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-25

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 TGCTGCTGCTGGCGAGTGTG 217
|||
DB 20 TGCTGCTGCTGGCGAGTGTG 1

RESULT 29
US-10-001-844-26/c
; Sequence 26, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett

; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-26

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 CGGAGATCTCCAGAACTC 360
Db 20 CGGAGATCTCCAGAACTC 1

RESULT 30
US-10-001-844-27/c
; Sequence 27, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-27

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 432 CGGACAGGCTGATGACTCAG 451
Db 20 CGGACAGGCTGATGACTCAG 1

RESULT 31
US-10-001-844-28/c
; Sequence 28, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-28

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 501 GCCCAGGAGTGAACTGCGG 520
Db 20 GCCCAGGAGTGAACTGCGG 1

RESULT 32
US-10-001-844-29/c
; Sequence 29, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-29

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 556 AGAGGAGTCTCTGCACTACG 575
Db 20 AGAGGAGTCTCTGCACTACG 1

RESULT 33
US-10-001-844-30/c
; Sequence 30, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-30

Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 607 CCGCGACCGCAGCAAGTACG 626
Db 20 CCGCGACCGCAGCAAGTACG 1

RESULT 34
US-10-001-844-31/c
; Sequence 31, Application US/10001844

```
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-31

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      666 GGGTGACTACGAGTCCAG 685
DB      20 GGGTGACTACGAGTCCAG 1

RESULT 35
US-10-001-844-32/c
; Sequence 32, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-32

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      721 GGTGGCGGCCAAATCGGGAG 740
DB      20 GGTGGCGGCCAAATCGGGAG 1

RESULT 36
US-10-001-844-33/c
; Sequence 33, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-33

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      907 CTACGTGATCGAGCGCGG 926
DB      20 CTACGTGATCGAGCGCGG 1

; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-34/c
; Sequence 34, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-34

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      864 TCCTCACTTCTCGACGCG 883
DB      20 TCCTCACTTCTCGACGCG 1

RESULT 38
US-10-001-844-35/c
; Sequence 35, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-35

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      970 GCTGCTGAAGGACCTGAGCC 809
DB      20 GCTGCTGAAGGACCTGAGCC 1
```

```
RESULT 39
US-10-001-844-36/c
; Sequence 36, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-36
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 947 CTCACCGGCGGCACCTGCT 966
DB 20 CTCACCGGCGGCACCTGCT 1

RESULT 40
US-10-001-844-37/c
; Sequence 37, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-37
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 947 CTCACCGGCGGCACCTGCT 966
DB 20 CTCACCGGCGGCACCTGCT 1

RESULT 41
US-10-001-844-38/c
; Sequence 38, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-38
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1052 CCTCGGCGCGCTGTCCGACG 1071
DB 20 CCTCGGCGCGCTGTCCGACG 1

RESULT 42
US-10-001-844-39/c
; Sequence 39, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-39
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1099 CGTGGTGGCGGCGGTGACG 1118
DB 20 CGTGGTGGCGGCGGTGACG 1

RESULT 43
US-10-001-844-40/c
; Sequence 40, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-40
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1141 CGCTGTGCACAGCGTGACCC 1160
 Db 20 CGCTGTGCACAGCGTGACCC 1

RESULT 44

US-10-001-844-41/c
 ; Sequence 41, Application US/10001844
 ; Publication No. US20030105041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
 ; FILE REFERENCE: ISPH-0617
 ; CURRENT APPLICATION NUMBER: US/10/001,844
 ; CURRENT FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 41
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-001-844-41

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1187 GCGCGCTCAGCGCCAGGG 1206
 Db 20 GCGCGCTCAGCGCCAGGG 1

RESULT 45

US-10-001-844-42/c
 ; Sequence 42, Application US/10001844
 ; Publication No. US20030105041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
 ; FILE REFERENCE: ISPH-0617
 ; CURRENT APPLICATION NUMBER: US/10/001,844
 ; CURRENT FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 42
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-001-844-42

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1233 CCTGTGTACGGGTATC 1252
 Db 20 CCTGTGTACGGGTATC 1

RESULT 46

US-10-001-844-43/c
 ; Sequence 43, Application US/10001844
 ; Publication No. US20030105041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION

; FILE REFERENCE: ISPH-0617
 ; CURRENT APPLICATION NUMBER: US/10/001,844
 ; CURRENT FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-001-844-43

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1271 CACCGGGCCTTCGGCCCTT 1290
 Db 20 CACCGGGCCTTCGGCCCTT 1

RESULT 47

US-10-001-844-44/c
 ; Sequence 44, Application US/10001844
 ; Publication No. US20030105041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
 ; FILE REFERENCE: ISPH-0617
 ; CURRENT APPLICATION NUMBER: US/10/001,844
 ; CURRENT FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 44
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-001-844-44

Query Match 1.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1308 TCCTGCTGCACTGGCGCC 1327
 Db 20 TCCTGCTGCACTGGCGCC 1

RESULT 48

US-10-001-844-45/c
 ; Sequence 45, Application US/10001844
 ; Publication No. US20030105041A1
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
 ; FILE REFERENCE: ISPH-0617
 ; CURRENT APPLICATION NUMBER: US/10/001,844
 ; CURRENT FILING DATE: 2001-11-16
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 45
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-10-001-844-45


```
Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1350 ACAGCGCGCGGGGACCGC 1369
Db 20 ACAGCGCGCGGGGACCGC 1

RESULT 49
US-10-001-844-46/c
; Sequence 46, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-46

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1407 GTGCTGCCGACGCTCCGGT 1426
Db 20 GTGCTGCCGACGCTCCGGT 1

RESULT 50
US-10-001-844-47/c
; Sequence 47, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-47

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1466 CTCTACCAATAGGCACCTG 1485
Db 20 CTCTACCAATAGGCACCTG 1

RESULT 51
US-10-001-844-48/c
; Sequence 48, Application US/10001844
; Publication No. US20030105041A1
```

```
GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-48

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1512 CGCTGGGCATGGCGGTCAAG 1531
Db 20 CGCTGGGCATGGCGGTCAAG 1

RESULT 52
US-10-001-844-49/c
; Sequence 49, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-49

Query Match      1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1521 TGGCGGTCAAGTCCAGCTGA 1540
Db 20 TGGCGGTCAAGTCCAGCTGA 1

RESULT 53
US-09-825-155-5
; Sequence 5, Application US/09825155
; Publication No. US20030100032A1
; GENERAL INFORMATION:
; APPLICANT: Alcala, Ariel Ruiz
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 1049-1-008N
; CURRENT APPLICATION NUMBER: US/09/825,155
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 09/102,491
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/050,286
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
```

SEQ ID NO 5
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-825-155-5

Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 GAAGATCTCAGAAATCC 361
DB 1 GAAGATCTCAGAAATCC 19

RESULT 54

US-09-825-155-9
Sequence 9, Application US/09825155
Publication No. US20030100032A1
GENERAL INFORMATION:
APPLICANT: Altaba, Ariel Ruiz
TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND TREATMENT
FILE REFERENCE: 1049-1-008N
CURRENT APPLICATION NUMBER: US/09/825,155
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 09/102,491
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/050,286
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-825-155-9

Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 AGATGCTGCTGCTAGTCC 185
DB 1 AGATGCTGCTGCTAGTCC 19

RESULT 55

US-10-098-263B-66408
Sequence 66408, Application US/10098263B
Publication No. US2003010410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 66408
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-66408

Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.7e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 886 CGACGGCCCAAGAGTCTTCTAC 910
DB 1 CGACGACCAAGTAGGTCTTCGAC 25

RESULT 56

US-10-147-463-21
Sequence 21, Application US/10147463
Publication No. US20030059838A1
GENERAL INFORMATION:
APPLICANT: ARIYASU, Toshio
ORITA, Kunzo
TITLE OF INVENTION: HEDGEHOG PROTEIN
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/147,463
FILING DATE: 17-May-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/617,545
FILING DATE: 14-Jul-2000
APPLICATION NUMBER: 09/063,778
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 98-
FILING DATE: 14-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: ARIYASU-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-35281
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-147-463-21

Query Match 1.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 656 GGCTTCGACTGGGTGCTACTA 675
DB 1 GGCTTCGACTGGGTGCTACTA 20

RESULT 57

US-09-825-155-6/c
Sequence 6, Application US/09825155
Publication No. US20030100032A1
GENERAL INFORMATION:
APPLICANT: Altaba, Ariel Ruiz
TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND TREATMENT
FILE REFERENCE: 1049-1-008N

```
/ CURRENT APPLICATION NUMBER: US/09/825,155
/ CURRENT FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 09/102,491
/ PRIOR FILING DATE: 1998-06-22
/ PRIOR APPLICATION NUMBER: 60/050,286
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-825-155-6

Query Match      1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      559 GGAGTCTCTGCACTACGA 576
Db      18 GGAGTCTCTGCACTACGA 1

RESULT 58
US-10-150-429B-7
/ Sequence 7, Application US/10150429B
/ Publication No. US20030175383A1
/ GENERAL INFORMATION:
/ APPLICANT: Bojsen, Kirsten
/ APPLICANT: Poulsen, Charlotte Horsmans
/ APPLICANT: See, Jorn Borch
/ TITLE OF INVENTION: METHOD OF IMPROVING DOUGH AND BREAD QUALITY
/ FILE REFERENCE: Y0020078
/ CURRENT APPLICATION NUMBER: US/10/150,429B
/ CURRENT FILING DATE: 2002-05-17
/ PRIOR APPLICATION NUMBER: US 60/347,007
/ PRIOR FILING DATE: 2002-01-09
/ PRIOR APPLICATION NUMBER: GB 0112226.6
/ PRIOR FILING DATE: 2001-05-18
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 7
/ LENGTH: 21
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (1)..(21)
/ OTHER INFORMATION: Lipase primer JOM3
US-10-150-429B-7

Query Match      1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1020 GCTCGGGGCGCCCTTCGGGG 1040
Db      1 GCTCGTGTGCTTCGGGG 21

RESULT 59
US-09-992-665-157
/ Sequence 157, Application US/09992665
/ Publication No. US20030092009A1
/ GENERAL INFORMATION:
/ APPLICANT: Kata Palm
/ TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
/ TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
/ FILE REFERENCE: CMINES.002A
/ CURRENT APPLICATION NUMBER: US/09/992,665
/ CURRENT FILING DATE: 2001-11-13

/ CURRENT APPLICATION NUMBER: 60/249,508
/ PRIOR FILING DATE: 2000-11-16
/ NUMBER OF SEQ ID NOS: 380
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 157
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Probe
US-09-992-665-157

Query Match      1.1%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      195 CGCTGCTGGTATGCTCGGACTGG 218
Db      1 CACTGCTGGTCTGCTGAGGACTGG 24

RESULT 60
US-10-098-263B-48877
/ Sequence 48877, Application US/10098263B
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Mittman, Michael
/ TITLE OF INVENTION: Human Microarray
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098,263B
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/275,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48877
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263B-48877

Query Match      1.1%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      61 AAGAGAGAGCGCACACGACAC 84
Db      2 AAGACAGAGACACACACATAC 25

RESULT 61
US-09-788-038-31/c
/ Sequence 31, Application US/09788038
/ Patent No. US20020072055A1
/ GENERAL INFORMATION:
/ APPLICANT: Jones, Douglas H.
/ TITLE OF INVENTION: An Iterative and Regenerative DNA
/ TITLE OF INVENTION: Sequencing Method
/ NUMBER OF SEQUENCES: 41
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: LAHIVE & COCKFIELD, LLP
/ STREET: 28 State Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/788,038
```



```

RESULT 66
US-10-001-844-5/c
; Sequence 5, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-001-844-5

Query Match 1.1%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0;

Qy 729 CCAATCGGAGGCTGC 745
Db 17 CCAATCGGAGGCTGC 1

RESULT 67
US-10-188-869-21/c
; Sequence 21, Application US/10188869
; Publication No. US20030148306A1
; GENERAL INFORMATION:
; APPLICANT: LAVALLIE, EDWARD
; APPLICANT: RACIE, LISA
; APPLICANT: DIBLASIO, ELIZABETH
; APPLICANT: AGOSTINO, MICHAEL
; TITLE OF INVENTION: AGGRECANASE MOLECULES
; FILE REFERENCE: 08702.0092-00000
; CURRENT APPLICATION NUMBER: US/10/188,869
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 60/349,133
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/303,051
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-869-21

Query Match 1.1%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;

Qy 912 TGATCGAGCGGGGCGG 931
Db 21 TGAGCGAGCGGGGCGG 2

RESULT 68
US-09-992-665-284/c
; Sequence 284, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kala Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A

```

; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-284

Query Match 1.1%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1303 CGCGCTCTCTGCTGCATCG 1322
Db 20 CGCGCTCTCTGCTGCATCG 1

RESULT 69

US-09-797-862-23/c
; Sequence 23, Application US/09797862
; Patent No. US20020102276A1
; GENERAL INFORMATION:
; APPLICANT: PEAK, IAN RICHARD ANSELM
; APPLICANT: JENNINGS, MICHAEL PAUL
; APPLICANT: MOXON, E, RICHARD
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 085064/0134
; CURRENT APPLICATION NUMBER: US/09/797,862
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for PCR
US-09-797-862-23

Query Match 1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 329 GGAAGGTTGAAGGGAAG 346
Db 18 GGAAGGTTGAAGGGAAG 1

RESULT 70

US-10-100-608B-12/c
; Sequence 12, Application US/10100608B
; Publication No. US20030104412A1
; GENERAL INFORMATION:
; APPLICANT: Heiskala, Marja
; TITLE OF INVENTION: REG-LIKE PROTEIN
; FILE REFERENCE: CDS-261
; CURRENT APPLICATION NUMBER: US/10/100,608B
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/276,414
; PRIOR FILING DATE: 2002-03-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Primer
US-10-100-608B-12

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1249 CATCAGGAGCAGCAGCTG 1266
Db 18 CATCAGGAGCAGCAGCTG 1

RESULT 71

US-09-798-058-13
; Sequence 13, Application US/09798058
; Patent No. US20020098523A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Wilton, Alison Jane
; APPLICANT: Smith, Stephen
; APPLICANT: Main, Sarah Helen
; TITLE OF INVENTION: Human antibodies against eotaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-798-058-13

Query Match 1.0%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 2.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 763 GGTGCACCTGGAGCAGGG 780
Db 4 GGTGCTCTGGAGCAGGG 21

RESULT 72

US-09-828-034-10/c
; Sequence 10, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-10

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1364 GACCGCGGCGCGCGCGCGC 1384
Db 21 GCGCGCGCGCGCGCGCGC 1

RESULT 73

US-09-788-038-32
; Sequence 32, Application US/09788038
; Patent No. US20020072055A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA
; Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/788,038
; FILING DATE: 16-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/226,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: UIZ-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-788-038-32
Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1307 CTCCTGGTGGTGGTGGTGGC 1327
Db 1 CTCCTGGTGGTGGTGGTGGC 21

RESULT 74

US-09-788-038-35/c
; Sequence 35, Application US/09788038
; Patent No. US20020072055A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA
; Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/788,038
; FILING DATE: 16-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/226,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: UIZ-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-788-038-35

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1307 CTCCTGGTGGTGGTGGTGGC 1327
Db 22 CTCCTGGTGGTGGTGGTGGC 2

RESULT 75

US-09-837-621-32
; Sequence 32, Application US/09837621
; Publication No. US20030044784A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA Sequencing
; Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/837,621
; FILING DATE: 17-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/035,183
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:

```

/ NAME: Hanley, Elizabeth A.
/ REGISTRATION NUMBER: 33,505
/ REFERENCE/DOCKET NUMBER: UIZ-022CF
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 742-4214
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-837-621-32

```

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1307 CTCCTGGCTGCAC TGGCGCC 1327
|||
Db 1 CTCCTGGCTGGAC TGGCGCAC 21

```

RESULT 76
US-09-837-621-35/c
; Sequence 35, Application US/09837621
; Publication No. US20030044784A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA Sequencing

```

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

REF ID: A6793
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/837,621
FILING DATE: 17-Apr-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA: 09/035,183
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanley, Elizabeth A.
 REGISTRATION NUMBER: 33,505
 REFERENCE/DOCKET NUMBER: UIZ-0225CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)227-7400
 TELEFAX: (617)742-4214
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 35:
 9-837-621-35

Qy	1307	CTCCTGGCTGCAC	TGGCGCCC	1327
D β	22	CTCCTGGCTGGAC	TGGCGCAC	2

```

RESULT 77
US-10-372-696-32
: Sequence 32, Application US/10372696
: Publication No. US20030175780A1
: GENERAL INFORMATION:
: APPLICANT: Jones, Douglas H.
: TITLE OF INVENTION: An Iterative and Regenerative DNA
: Sequencing Method

```

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/372,696
FILING DATE: 24-Feb-2003

CLASSIFICATION: 150
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/742,755A
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanley, Elizabeth A.
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: UIZ-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 10-372-696-32

```
Query Match      1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1307 CTCCTGGCTGCACTGGCGCCC 1327
||| ||| ||| ||| ||| |||
pb 1 CTCCTCGCTGGACTGGCGCAC 21

```

, RESULT 78
, US-10-372-696-35/c
, ; Sequence 35, Application US/10372696
, ; Publication No. US20030175780A1
, ; GENERAL INFORMATION:
, ; APPLICANT: Jones, Douglas H.
, ; TITLE OF INVENTION: An Iterative and Regenerative DNA
, ; Sequencing Method
, ; NUMBER OF SEQUENCES: 41
, ; CORRESPONDENCE ADDRESS:
, ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
, ; STREET: 28 State Street
, ; CITY: Boston
, ;

```

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston


```

US-09-888-326-410
; Sequence 410, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 410
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphodiester backbone
US-09-888-326-410
Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1368 GCGGGGGCGCGCGCGAG 1386
Db 2 GCGGGCGCGCGCGCGCG 20

RESULT 81
US-09-776-479-243
; Sequence 243, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-243
Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1368 GCGGGGGCGCGCGCGAG 1386
Db 2 GCGGGCGCGCGCGCGCG 20

RESULT 82
US-09-915-814-105
; Sequence 105, Application US/09915814
; Publication No. US20030096771A1
; Publication No. US20030096771A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0587
; CURRENT APPLICATION NUMBER: US/09/915,814
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 105
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-814-105

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 481 CATCTCGGTGATCAACACG 499
Db 1 CATCTCGGTGATGTTCCAG 19

RESULT 83
US-09-851-871-26/c
; Sequence 26, Application US/09851871
; Publication No. US20030176374A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Karras, James G.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; FILE REFERENCE: Modulation of the Expression of B7 Protein
; CURRENT APPLICATION NUMBER: US/09/851,871
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-851-871-26

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 898 GAAGGTCTTCTACGTGTC 916
Db 19 GAGGTCTTCTACGTGAC 1

RESULT 84
US-10-112-653-235
; Sequence 235, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Beig, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
```

```
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060 (AMS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 235
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-235

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGGCGGGCGG 1386
Db 2 GCGGGGCGGGCGGGCGGG 20

RESULT 85
US-10-017-995-243
; Sequence 243, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 243
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-243

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGGCGGGCGG 1386
Db 2 GCGGGGCGGGCGGGCGGG 20

RESULT 86
US-09-984-183-22
; Sequence 22, Application US/09984183
; Patent No. US20020142983A1
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, BABITA
; APPLICANT: LONGENECKER, MICHAEL B.
; TITLE OF INVENTION: MUC-1 ANTAGONISTS AND METHODS OF TREATING IMMUNE
; FILE REFERENCE: DISORDERS
; FILE REFERENCE: 042881/0130
; CURRENT APPLICATION NUMBER: US/09/984,183
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/457,354
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/111,973
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 30
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-984-183-22

Query Match          1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AAATCGGAGGCTGCTTC 749
Db 3 ATATCGAGAGGCTGCTTC 21
```

```
RESULT 87
US-09-848-754A-870
; Sequence 870, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: M8900-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 870
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-870
```

```
Query Match          1.0%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 31 GCGGAGCGGAGCGGAG 47
Db 1 GCGGAGCGGAGCGGAG 17
```

```
RESULT 88
US-09-500-700-68
; Sequence 68, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter S.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPI1160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR FILING DATE: 1997-05-27
; PRIOR FILING DATE: US 08/863,813
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 18
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (GCG)6 probe
US-09-500-700-68
```

```
Query Match          1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1368 GCGGCGGCGGCGGCGC 1384
Db 1 GCGGCGGCGGCGGCGC 17
```

```
RESULT 89
US-10-314-405-45
; Sequence 45, Application US/10314405
; Publication No. US20030108940A1
; GENERAL INFORMATION:
; APPLICANT: Hidetoshi, Inoko
; APPLICANT: Gen, Tamiya
; APPLICANT: Yasunari, Matsuzaka
; TITLE OF INVENTION: NOVEL POLYMORPHIC MICROSATELLITE MARKERS IN THE HUMAN MHC CLASS
; FILE REFERENCE: 06501-069001
; CURRENT APPLICATION NUMBER: US/10/314,405
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/713,616
; PRIOR FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-314-405-45
```

```
Query Match          1.0%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1368 GCGGCGGCGGCGGCGC 1384
Db 1 GCGGCGGCGGCGGCGC 17
```

```
RESULT 90
US-10-126-355-60
; Sequence 60, Application US/10126355
; Publication No. US20030198965A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTEROID
; TITLE OF INVENTION: 11-BETA DEHYDROGENASE 1 EXPRESSION
; FILE REFERENCE: R1S-0428
; CURRENT APPLICATION NUMBER: US/10/126,355
; CURRENT FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-126-355-60
```

```
Query Match          1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1470 ACCAAATAGGCACCTGGCTC 1489
| | | | | | | | | | | | | | | | | |
```

Db 1 ATCAGAGGAGCTGGCTC 20

RESULT 91

US-10-125-181-8
; Sequence 8, Application US/10125181
; Publication No. US20020187954A1

GENERAL INFORMATION:

; APPLICANT: WRIGHT, Jim A.

; APPLICANT: YOUNG, Aiping H.

; APPLICANT: LEE, Yoon S.

; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE

; TITLE OF INVENTION: OLIGONUCLEOTIDE

; TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL

; FILE REFERENCE: 032396-046

; CURRENT APPLICATION NUMBER: US/10/125,181

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/295,593

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,791

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-23

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Human

US-10-125-181-8

Query Match

Best Local Similarity 1.0%; Score 15.2; DB 1; Length 20;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1540 AAGCCGGGGCGGGGGGAG 1559

Db 1 ACGTCGAGGGCGGGGGGAG 20

RESULT 92

US-10-122-434-7/c

; Sequence 7, Application US/10122434

; Publication No. US20030078402A1

GENERAL INFORMATION:

; APPLICANT: LEOP G.J. FRENKEN

; APPLICANT: CORNELIS P.E. VAN DER LOGT

; TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODY FRAGMENTS

; FILE REFERENCE: 60113/266062 - T3076(C)

; CURRENT APPLICATION NUMBER: US/10/122,434

; CURRENT FILING DATE: 2002-04-16

; PRIOR APPLICATION NUMBER: 09/487,253

; PRIOR FILING DATE: 2000-01-19

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: MS Word

; SEQ ID NO 7

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: PRIMER

US-10-122-434-7

Query Match

Best Local Similarity 1.0%; Score 15.2; DB 1; Length 20;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 769 CCTGGAGCGGGCGGACCA 788

Db 20 CCTGGAGCGGGCGGACCA 1

RESULT 93

US-09-969-373-3868

; Sequence 3868, Application US/09969373

; Patent No. US20020133852A1

GENERAL INFORMATION:

; APPLICANT: Effertz, Roger J.

; APPLICANT: Hauge, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; CURRENT FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 3868

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Glycine max

US-09-969-373-3868

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 19;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 AGCGAGGAGAGCGGAG 29

Db 1 AACGAGGAGAGAGAGAG 18

RESULT 94

US-09-920-033-22/c

; Sequence 22, Application US/09920033

; Publication No. US20030087853A1

GENERAL INFORMATION:

; APPLICANT: Rosanne M. Crooke

; APPLICANT: Mark J. Graham

; TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION

; FILE REFERENCE: ISPH-0592

; CURRENT APPLICATION NUMBER: US/09/920,033

; CURRENT FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 123

; SEQ ID NO 22

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-09-920-033-22

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 20;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGCGGAG 168

Db 19 GCTGCTGCTGCTGCGGG 2

RESULT 95

US-10-388-263-554/c

; Sequence 554, Application US/10388263

; Publication No. US20030228597A1

GENERAL INFORMATION:

; APPLICANT: Cowsett, Lex M.

; APPLICANT: Baker, Brenda F.

; APPLICANT: McNeill, John

; APPLICANT: Freier, Susan M.

; APPLICANT: Sasmor, Henri M.

; APPLICANT: Brooks, Douglas G.

; APPLICANT: Ohashi, Cara

; APPLICANT: Wyatt, Jacqueline R.

; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 554
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-554

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGGCGAG 168
| | | | | | | | | | | | | | | | | | | | | |
Db 19 GCTGCTGCTGCTGGCGGG 2

RESULT 96

US-10-052-390B-12/c
; Sequence 12, Application US/10052390B
; Publication No. US20030148970A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon H.
; APPLICANT: Vaisburg, Arkadii
; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavioie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-004US1
; CURRENT APPLICATION NUMBER: US/10/052,390B
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-390B-12

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1405 AGGTGCTGCGGCGCTCC 1422
| | | | | | | | | | | | | | | | | | | | | |
Db 18 AGGTGCTGCTGCGCGTGC 1

RESULT 97

US-10-051-819B-12/c
; Sequence 12, Application US/10051819B
; Publication No. US20030152557A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffery M.
; APPLICANT: Bonfils, Claire
; APPLICANT: Li, Zuomei
; APPLICANT: Woo, Soon
; APPLICANT: Vaisburg, Arkadii

; APPLICANT: Delorme, Daniel
; APPLICANT: Fournel, Marielle
; APPLICANT: Lavioie, Rico
; TITLE OF INVENTION: Methods for Specifically Inhibiting Histone Deacetylase-4
; FILE REFERENCE: MET-002US1
; CURRENT APPLICATION NUMBER: US/10/051,819B
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 60/261,674
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-051-819B-12

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1405 AGGTGCTGCGGCGCTCC 1422
| | | | | | | | | | | | | | | | | | | | | |
Db 18 AGGTGCTGCGGCGCTGC 1

RESULT 98

US-10-053-645A-28
; Sequence 28, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CEE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-28

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1371 GCGGCGGCGGCGGCGAG 1388
| | | | | | | | | | | | | | | | | | | | | |
Db 2 GCGGCGGCGGCGGCGAG 19

RESULT 99

US-10-305-810-43
; Sequence 43, Application US/10305810
; Publication No. US20030176385A1
; GENERAL INFORMATION:
; APPLICANT: Ju, Jingfang
; APPLICANT: Huang, Chunli
; APPLICANT: Zhong, Haihong
; APPLICANT: Simons, Jan Fredrik
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Chant, John S.
; APPLICANT: Peyman, John A.
; APPLICANT: Smithson, Glennda

APPLICANT: Millet, Isabelle
TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN EXPRESSION
FILE REFERENCE: 21402-501
CURRENT APPLICATION NUMBER: US/10/305,810
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/334,148
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/336,572
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/625,634
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/192,838
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/194,256
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: 09/957,187
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/233,798
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/970,813
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/182,637
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 60/240,316
PRIOR FILING DATE: 2000-10-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 47
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 43
LENGTH: 20
TYPE: DNA
ORGANISM: IL-8-AS1
US-10-305-810-43

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 118 GGACGCTCGGAGTCAT 135
Db 3 GGCCAGCTTGGAGTCAT 20

RESULT 100

US-10-147-196-22/c
Sequence 22, Application US/10147196
Publication No. US20030215943A1
GENERAL INFORMATION:
APPLICANT: Rosanne M. Crooke
APPLICANT: Mark J. Graham
TITLE OF INVENTION: ANTISENSE MODULATION OF APOLIPOPROTEIN B EXPRESSION
FILE REFERENCE: ISPH-0664
CURRENT APPLICATION NUMBER: US/10/147,196
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 124
SEQ ID NO 22
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-147-196-22

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 151 GATGCTGCTGCTGCGGAG 168
Db 19 GCTGCTGCTGCTGCGGAG 2

RESULT 101

US-09-887-145-29/c
Sequence 29, Application US/09887145
Publication No. US20030082139A1
GENERAL INFORMATION:
APPLICANT: Kim, Seung U
TITLE OF INVENTION: Immortalized human microglia cell and continuous cell line
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft Word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,145
FILING DATE: 22-Jun-2001
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: UBC-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-887-145-29

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 118 GGACGCTCGGAGTCAT 135
Db 18 GGCCAGCTTGGAGTCAT 1

RESULT 102

US-09-866-108-10651/c
Sequence 10651, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wenaheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30

; ORGANISM: Homo sapiens
US-09-848-754A-3086

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 32 GCGAGCCGCGGCGAG 47
Db 1 GGAGAGCCGCGGCGAG 16

RESULT 106

US-10-238-700-2801
; Sequence 2801, Application US/10238700
; Publication No. US2003015321A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2801
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-2801

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1369 CGGCGCGCGCGCGCGC 1384
Db 1 CGGCGCGCGCGCGCGC 16

RESULT 107

US-10-156-306-5214
; Sequence 5214, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5214
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-5214

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1133 CTGCGCGCGCGCTGTC 1148
Db 1 CGCGCGCGCGCGCGC 16

RESULT 108

US-10-156-306-6011
; Sequence 6011, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6011
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6011

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1132 CCTGCGCGCGCTGTC 1147
Db 2 CCGCGCGCGCGCGCGC 17

RESULT 109

US-10-156-306-6012
; Sequence 6012, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6012
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-6012

Query Match 0.9%; Score 14.4; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 3e+02;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1135 GCGCGCGCGCTGTCAC 1150
Db 2 GCGCGCGCGCGCGCGC 17

RESULT 110

US-09-918-186A-99/c
; Sequence 99, Application US/09918186A
; Patent No. US20020137708A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0585
; CURRENT APPLICATION NUMBER: US/09/918,186A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/496,694
; PRIOR FILING DATE: 2000-02-02

;
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 99
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-186A-99

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GCGGGCGGGCGGCGCA 1385
Db 18 GGTGGCGGGCGGCGCA 3

RESULT 111
US-09-961-077-1165/c
; Sequence 1165, Application US/09961077
; Publication No. US20030014775A1
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; Edington, Brent E.
; McSwiggen, James A.
; Merlo, Patricia Ann Owens
; Guo, Lining
; Skokut, Thomas A.
; Young, Scott A.
; Folkerts, Otto
; Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; MODULATION OF GENE EXPRESSION
; IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,077
; FILING DATE: 21-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/679,645
; FILING DATE: July 12, 1996
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

;
; INFORMATION FOR SEQ ID NO: 1165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1165:
US-09-961-077-1165

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1368 GCGGGCGGGCGGCGG 1383
Db 18 GCGGGCGGGCGGCGG 3

RESULT 112
US-09-791-243-11/c
; Sequence 11, Application US/09791243
; Patent No. US20020147164A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Rothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOHESIN-1 EXPRESSION
; FILE REFERENCE: RTS-0095
; CURRENT APPLICATION NUMBER: US/09/791,243
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-243-11

Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 4.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 GCGGAGCGGAGCGGAG 47
Db 19 GCGGAGCGGAGCGGAG 4

RESULT 113
US-09-910-087-12/c
; Sequence 12, Application US/09910087
; Patent No. US20020055480A1
; GENERAL INFORMATION:
; APPLICANT: Koopman, Peter
; Goodfellow, Peter
; TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
; USE IN THE REGENERATION OF BONE OR CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/910,087

;; FILING DATE: 20-Jul-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU PM9714
;; FILING DATE: 29-NOV-1994
;; APPLICATION NUMBER: AU PM9835
;; FILING DATE: 05-DEC-1994
;; APPLICATION NUMBER: PCT/AU95/00799
;; FILING DATE: 29-NOV-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Digiglio, Frank S.
;; REGISTRATION NUMBER: 31,346
;; REFERENCE/DOCKET NUMBER: 10981
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 516-742-4343
;; TELEFAX: 516-742-4366
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-910-087-12

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GCTCTACAGCGACTTCTC 868
DB 19 GTTCTTACCGACTTCTC 1

RESULT 114
US-09-938-795A-18
; Sequence 18, Application US/09938795A
; Publication No. US20030045688A1
; GENERAL INFORMATION:
; APPLICANT: CHU, CHARLES CHIYUAN
; APPLICANT: CHAVAN, SANGEETA S.
; APPLICANT: MASON, JAMES M.
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN
; FILE REFERENCE: LJ-9000-US
; CURRENT APPLICATION NUMBER: US/09/938,795A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227,818
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-938-795A-18

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1515 TGGGCATGGCGGTCAAGTC 1533
DB 1 TGGAGACGGCGGTCAAGTC 19

RESULT 115
US-09-791-190A-16
; Sequence 16, Application US/09791190A
; Publication No. US20030104372A1

;; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: Amadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Nyren, Pal
; TITLE OF INVENTION: Allele Specific Primer Extension Assay
; FILE REFERENCE: Docket 14259
; CURRENT APPLICATION NUMBER: US/09/791,190A
; CURRENT FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: Primer
US-09-791-190A-16

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1418 GCTCGGGTGGGGGGCCA 1436
DB 1 GCTCGTGGTGCAGGGCCA 19

RESULT 116
US-10-244-647-9
; Sequence 9, Application US/10244647
; Publication No. US20030206887A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: Morrissey, David
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
; FILE REFERENCE: 400/060 (MBH02-1000)
; CURRENT APPLICATION NUMBER: US/10/244,647
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: PCT US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
US-10-244-647-9

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 4e+02;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 173 CTGCTGCTAGTCTCTGCTCT 191
DB 1 CUGUGCUAUGCCUUAUCU 19

RESULT 117
US-10-244-647-655/c

```
/ Sequence 655, Application US/10244647
/ Publication No. US20030206887A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceutical, Inc.
/ APPLICANT: Morrissey, David
/ APPLICANT: McSwiggen, James
/ APPLICANT: Beigelman, Leonid
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis B Virus (HBV)
/ FILE REFERENCE: 400/060 (MBH02-1000)
/ CURRENT APPLICATION NUMBER: US/10/244,647
/ CURRENT FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/393,924
/ PRIOR FILING DATE: 2002-07-03
/ PRIOR APPLICATION NUMBER: PCT US02/09187
/ PRIOR FILING DATE: 2002-03-26
/ PRIOR APPLICATION NUMBER: US 60/296,876
/ PRIOR FILING DATE: 2001-06-08
/ NUMBER OF SEQ ID NOS: 1524
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 655
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-244-647-655

Query Match      0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 173 CTGCTGCTAGTCTCTCTCT 191
DB 19 CTGCTGCTATGCTCTATCT 1

RESULT 118
US-09-752-983-42/c
/ Sequence 42, Application US/09752983
/ Patent No. US20010016575A1
/ GENERAL INFORMATION:
/ APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
/ APPLICANT: Graham, Brett P. Monia
/ TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
/ TITLE OF INVENTION: EXPRESSION
/ NUMBER OF SEQUENCES: 271
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Jane Massey Licata
/ STREET: 66 East Main Street
/ CITY: Marlton
/ STATE: NJ
/ COUNTRY: U.S.A.
/ ZIP: 08053
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
/ COMPUTER: IBM PC
/ OPERATING SYSTEM: WINDOWS 95
/ SOFTWARE: WORDPERFECT 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/752,983
/ FILING DATE: 02-Jan-2001
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/280,805
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Licata, Jane Massey
/ REGISTRATION NUMBER: 32,257
/ REFERENCE/DOCKET NUMBER: ISPH-0346
/ TELECOMMUNICATION INFORMATION:
```

```
/ TELEPHONE: 609-810-1515
/ TELEFAX: 609-810-1454
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Single
/ TOPOLOGY: Linear
/ ANTI-SENSE: Yes
/ US-09-752-983-42

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 144 TGGCGGAGATGCTGCTGCT 162
DB 20 TGACCGAGATCTGCTGCT 2

RESULT 119
US-09-800-631-11/c
/ Sequence 11, Application US/09800631
/ Patent No. US20020082228A1
/ GENERAL INFORMATION:
/ APPLICANT: Hong Zhang
/ APPLICANT: Jacqueline Wyatt
/ TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EXI
/ FILE REFERENCE: ISPH-0544
/ CURRENT APPLICATION NUMBER: US/09/800,631
/ CURRENT FILING DATE: 2001-03-07
/ PRIOR APPLICATION NUMBER: US/09/657,346
/ PRIOR FILING DATE: 2000-09-07
/ NUMBER OF SEQ ID NOS: 175
/ SEQ ID NO 11
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PCR Primer
US-09-800-631-11

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 170 TGTCTGCTGCTAGTCTCTCG 188
DB 20 TGCTGCAGCTCGTCTCG 2

RESULT 120
US-09-780-172-32
/ Sequence 32, Application US/09780172
/ Patent No. US20020147163A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert McKay
/ APPLICANT: Susan M. Freier
/ APPLICANT: Jacqueline Wyatt
/ TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
/ FILE REFERENCE: RTS-0159
/ CURRENT APPLICATION NUMBER: US/09/780,172
/ CURRENT FILING DATE: 2001-02-08
/ NUMBER OF SEQ ID NOS: 96
/ SEQ ID NO 32
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-780-172-32

Query Match      0.9%; Score 14.2; DB 1; Length 20;
```

Best Local Similarity 84.2%; Pred. No. 4.4e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 3;

QY 390 ACAACCCGACATCATATT 408
Db 2 AAATCCCTGACATCATATT 20

RESULT 121

US-09-870-002-20/c
; Sequence 20, Application US/09870002
; Publication No. US20030013670A1
; GENERAL INFORMATION:
; APPLICANT: Monia, B. P., Cowser, L. M. and Manoharan, M.
; TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of ras
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1 for WINDOWS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/870,002
; FILING DATE: 30-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/575,554
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0463
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (856) 810-1515
; TELEFAX: (856) 810-1454
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 20
US-09-870-002-20

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGCGCGCGCGGAG 1386
Db 19 GCGGGCGCGCGCGGAG 1

RESULT 122

US-09-865-866-68
; Sequence 68, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173

; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-68

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 329 GGAAGGTATGAAGGGAAGA 347
Db 1 GGAAGGTTCACAGGGAAGA 19

RESULT 123

US-09-922-146-25/c
; Sequence 25, Application US/09922146
; Publication No. US20030083285A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RFS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-922-146-25

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1298 GCGACGCGCTCCTGGCTG 1316
Db 20 GTGGCGCGCTCCTGGCTG 2

RESULT 124

US-10-388-263-746/c
; Sequence 746, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Samor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 746
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-388-263-745

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 170 TGTCTGCTAGTCTCTCG 188
||||| ||| ||| ||| |||
DB 20 TGTCTGCAGCTGCTCTCG 2

RESULT 125

US-10-006-191-91/c
; Sequence 91, Application US/10006191
; Publication No. US2003014223A1

;
; GENERAL INFORMATION:

APPLICANT: William Gaarde

APPLICANT: Andrew T. Watt

;
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION

;
; FILE REFERENCE: RTS-0274

;
; CURRENT APPLICATION NUMBER: US/10/006,191

;
; CURRENT FILING DATE: 2001-12-10

;
; NUMBER OF SEQ ID NOS: 153

;
; SEQ ID NO 91

;
; LENGTH: 20

;
; TYPE: DNA

;
; ORGANISM: Artificial Sequence

;
; FEATURE:

;
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-006-191-91

Query Match

Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GCAGCCAGCGAGGAGAGA 24
||||| ||| ||| ||| |||
DB 19 GAAGCCAGAGAGTGAGAGA 1

RESULT 126

US-10-006-191-111

;
; Sequence 111, Application US/10006191

;
; Publication No. US2003014223A1

;
; GENERAL INFORMATION:

APPLICANT: William Gaarde

APPLICANT: Andrew T. Watt

;
; TITLE OF INVENTION: ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION

;
; FILE REFERENCE: RTS-0274

;
; CURRENT APPLICATION NUMBER: US/10/006,191

;
; CURRENT FILING DATE: 2001-12-10

;
; NUMBER OF SEQ ID NOS: 153

;
; SEQ ID NO 111

;
; LENGTH: 20

;
; TYPE: DNA

;
; ORGANISM: Artificial Sequence

;
; FEATURE:

;
; OTHER INFORMATION: Antisense Oligonucleotide

US-10-006-191-111

Query Match

Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1451 TGGTACTCGCAGCTGCTCT 1469
||||| ||| ||| ||| |||
DB 2 TGGTATTGCAGCTGCTTT 20

RESULT 127

US-09-961-756-45/c

;
; Sequence 45, Application US/09961756
; Publication No. US20030170253A1

;
; GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: OLOFSSON, Birgitta

APPLICANT: ALITALO, Kari

APPLICANT: PAJUSOLA, Katri

;
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

;
; DNA CODING THEREFOR

;
; NUMBER OF SEQUENCES: 57

;
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.

STREET: 1200 G Street, N.W., Suite 700

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

;
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

;
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/961,756

FILING DATE: 25-Sep-2001

CLASSIFICATION: 435

;
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/609,443B

FILING DATE: 01-MAR-1996

APPLICATION NUMBER: US 08/397,651

FILING DATE: 01-MAR-1995

APPLICATION NUMBER: US 08/469,427

FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/569,063

FILING DATE: 06-DEC-1995

;
; ATTORNEY/AGENT INFORMATION:

NAME: EVANS, Joseph D

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 1064/41979CF4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844

;
; INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

;
; MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-09-961-756-45

Query Match

Best Local Similarity 0.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1331 CGCAGCGACCGCGCGGG 1349
||||| ||| ||| ||| |||
DB 19 CGCAGCTACCTGGCGGGG 1

RESULT 128

US-09-851-871-154/c

;
; Sequence 154, Application US/09851871

;
; Publication No. US20030176374A1

;
; GENERAL INFORMATION:

APPLICANT: Bennett, Clarence Frank

APPLICANT: Vickers, Timothy A.

APPLICANT: Karrias, James G.

;
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the

;
; Modulation of the Expression of B7 Protein

;
; FILE REFERENCE: ISPH-0543

;
; CURRENT APPLICATION NUMBER: US/09/851,871

; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: PCT/US00/14471
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/326,186
; PRIOR FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 154
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-851-871-154

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 898 GAAGGTCTTCTAGTGATC 916
||||| ||||| ||||| |||||
Db 19 GAAGGTCTTCTCTGAGC 1

RESULT 129

US-10-363-798-15/c
; Sequence 15, Application US/10363798
; Publication No. US20030180280A1
; GENERAL INFORMATION:
; APPLICANT: Kong, Xiangyin
; APPLICANT: Xiao, Shangxi
; APPLICANT: Zhao, Guoping
; APPLICANT: Yu, Chuan
; APPLICANT: Hu, Landian
; TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA
; TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED
; FILE REFERENCE: 9548.78USWO
; CURRENT APPLICATION NUMBER: US/10/363,798
; CURRENT FILING DATE: 2003-03-05
; PRIOR APPLICATION NUMBER: CN 00125042.6
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-363-798-15

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 853 CTACAGGAGCTTCCTCACT 871
||||| ||||| ||||| |||||
Db 20 CAACAGGAGATCCTCAT 2

RESULT 130

US-10-005-344-42/c
; Sequence 42, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Koller

; APPLICANT: Mingyi Chiang
; APPLICANT: Mario Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-42

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 144 TGGCGGAGATCTCTCTGCT 162
||||| ||||| ||||| |||||
Db 20 TGACCGAGATCTCTCTGCT 2

RESULT 131

US-10-222-334-42/c
; Sequence 42, Application US/10222334
; Publication No. US20030073116A1
; GENERAL INFORMATION:
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Gallia
; APPLICANT: Tsai, Han-Mou
; TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
; FILE REFERENCE: UM-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/312,834
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-222-334-42

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1393 CCTAACCGCTCCAGGTGCT 1411
||||| ||||| ||||| |||||
Db 20 CCTAGCCTCTCAGGTGT 2

RESULT 132

US-10-293-783-11/c
; Sequence 11, Application US/10293783
; Publication No. US20030130222A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST EX
; FILE REFERENCE: ISPH-0544
; CURRENT APPLICATION NUMBER: US/10/293,783
; CURRENT FILING DATE: 2002-11-13

```

; PRIOR APPLICATION NUMBER: US/09/800,631
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US/09/657,346
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-0293-783-11

```

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%;
Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels

```

RESULT 133
US-09-828-034-7
; Sequence 7, Application US/09828034
; Patent No. US20020054771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 30
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
US-09-828-034-7

```

```
Query Match          0.9%; Score 14.2; DB 1; Length 30;
Best Local Similarity 70.4%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```

RESULT 134
US-09-757-100B-37
; Sequence 37, Application US/09757100B
; Patent No. US20010034329A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
;
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense
US-09-757-100B-37

```

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels

```

RESULT 135
US-10-440-850-167
; Sequence 167, Application US/10440850
; Publication No. US20030207837A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for
; IMMUNIZATION OF ANIMALS WITH IMMUNE RESPONSES
; FILE REFERENCE: 250/130 (MBH000-900-A)
; CURRENT APPLICATION NUMBER: US/10/440,950
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/650,012
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 08/585,684
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: US 60/000,951
; PRIOR FILING DATE: 1995-07-07
; PRIOR APPLICATION NUMBER: US 09/038,073
; PRIOR FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 2295
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-440-850-167

```

Query Match	0.9%	Score 14;	DB 1;	Length 15;
Best Local Similarity	64.3%	Pred. No. 2.6e+02;		
Matches 9;	Conservative	5;	Mismatches 0;	Indels 0;
			Gaps 0;	

```

RESULT 136
US-09-870-956-17
; Sequence 17, Application US/09870956
; Patent No. US20020127669A1
; GENERAL INFORMATION:
; APPLICANT: Knipp, Gregory T.
; APPLICANT: Herrera-Ruiz, Dea
; APPLICANT: Rutgers, The State University
; TITLE OF INVENTION: No. US20020127669A1el
; TITLE OF INVENTION: Histidine Transporter
; FILE REFERENCE: Rutgers 00-0126
; CURRENT APPLICATION NUMBER: US/09/870,956
; CURRENT FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/7208,061
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 56

```

; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 17
 ; LENGTH: 16
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-09-870-956-17

Query Match 0.9%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 491 ATGAACCAAGTGGCC 504
 DB 1 ATGAACCAAGTGGCC 14

RESULT 137
 US-09-780-533A-1789
 ; Sequence 1789, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH800, 878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 1789
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-09-780-533A-1789

Query Match 0.9%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1373 GCGCGCGCGGCAG 1386
 DB 2 GCGCGCGCGGCAG 15

RESULT 138
 US-09-780-533A-2337
 ; Sequence 2337, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haerberli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH800, 878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2337
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens

US-09-780-533A-2337

Query Match 0.9%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1373 GCGCGCGCGGCAG 1386
 DB 3 GCGCGCGCGGCAG 16

RESULT 139
 US-08-911-824-77/c
 ; Sequence 77, Application US/08911824
 ; Publication No. US20030004323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Hackett, John R., Jr.
 ; APPLICANT: Yamaguchi, Julie
 ; APPLICANT: Golden, Alan M.
 ; APPLICANT: Brennan, Catherine A.
 ; APPLICANT: Hickman, Robert K.
 ; APPLICANT: Devare, Sushil G.
 ; TITLE OF INVENTION: NOVEL ANTIGEN CONSTRUCTS USEFUL IN THE
 ; FILE REFERENCE: 6165 US 01
 ; CURRENT APPLICATION NUMBER: US/08/911,824
 ; CURRENT FILING DATE: 1997-08-15
 ; NUMBER OF SEQ ID NOS: 121
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 77
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Human Immunodeficiency Virus
 ; FEATURE:
 ; OTHER INFORMATION: HIV-1 Group O (env25R) PCR reverse primer
 US-08-911-824-77

Query Match 0.9%; Score 14; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 3.8e+02;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 764 GTGCACCTGGAGCAGG 779
 DB 16 GYGACCTGGAGTAGG 1

RESULT 140
 US-09-374-046A-201
 ; Sequence 201, Application US/09374046A
 ; Publication No. US20030096951A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John M.
 ; APPLICANT: Lavallie, Edward R.
 ; APPLICANT: Collins-Racie, Lisa A.
 ; APPLICANT: Evans, Cheryl
 ; APPLICANT: Merberg, David
 ; APPLICANT: Treacy, Maurice
 ; APPLICANT: Agostino, Michael J.
 ; APPLICANT: Steininger II, Robert J.
 ; APPLICANT: Spaulding, Vikki
 ; APPLICANT: Wong, Gordon G.
 ; APPLICANT: Clark, Hilary
 ; APPLICANT: Fachtel, Kim
 ; APPLICANT: Genetics Institute, Inc.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 ; FILE REFERENCE: GI 6075-83A
 ; CURRENT APPLICATION NUMBER: US/09/374,046A
 ; CURRENT FILING DATE: 1999-08-13
 ; NUMBER OF SEQ ID NOS: 240
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 201

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-374-046A-201

Query Match 0.9%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 785 ACCAAGCTGGTGAA 798
Db 2 ACCAAGCTGGTGAA 15

RESULT 141

US-10-309-690-1
; Sequence 1, Application US/10309690
; Publication No. US20030138831A1
; GENERAL INFORMATION:
; APPLICANT: Kwagh, Jae-Gyu
; APPLICANT: Macklin, John J.
; APPLICANT: Mitsis, Paul G.
; APPLICANT: Ulmer, Kevin M.
; TITLE OF INVENTION: METHOD FOR SEQUENCING AND CHARACTERIZING POLYMERIC
; TITLE OF INVENTION: BIOMOLECULES USING APTAMERS AND A METHOD FOR PRODUCING
; TITLE OF INVENTION: APTAMERS
; FILE REFERENCE: PL/2CIP
; CURRENT APPLICATION NUMBER: US/10/309,690
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/578,634
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/135,863
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...19
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: n is any one of
; OTHER INFORMATION: 5', a, t or c
US-10-309-690-1

Query Match 0.9%; Score 14; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 4.3e+02;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1552 CGGGGAGGGCGCGGGAG 1570
Db 1 CGGGGAGGACGGGCGAG 19

RESULT 142

US-10-001-844-40
; Sequence 40, Application US/10001844
; Publication No. US20030105041A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHH EXPRESSION
; FILE REFERENCE: ISPH-0617
; CURRENT APPLICATION NUMBER: US/10/001,844
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-844-40

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1141 CGCTGTGCACAGCG 1154
Db 7 CGCTGTGCACAGCG 20

RESULT 143

US-09-757-100B-17
; Sequence 17, Application US/09757100B
; Patent No. US20010034329A1
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; APPLICANT: Nero, Pamela S.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0533
; CURRENT APPLICATION NUMBER: US/09/757,100B
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/377,310
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/US00/18999
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-17

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 191 TCCTCGCTGCTGCT 204
Db 3 TCCTCGCTGCTGCT 16

RESULT 144

US-09-888-615-131
; Sequence 131, Application US/09888615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CHENEPEEL, SEAN
; APPLICANT: CHARYDCZAK, GLEN
; APPLICANT: MANNING, GERALD
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 131

Search completed: December 23, 2003, 16:37:33
Job time : 29 secs

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SNP
US-09-888-615-131

Query Match          0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 4.7e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1458 CGCAGCTGCTCTACCA 1473
Db 1 CGCACCTGCTCYACCA 16

RESULT 145
US-10-430-196-5/C
; Sequence 5, Application US/10430196
; Publication No. US20030194738A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/430,196
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517A
; FILING DATE: 07-Aug-2001
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-430-196-5

Query Match          0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1351 CAGCGCGCGCGGG 1364
Db 16 CAGCGCGCGCGGG 3
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:38:23 ; Search time 4 Seconds
(without alignments)

1.902 Million cell updates/sec

Title: us-10-001-844-3

Perfect score: 1576

Sequence: 1 gcaggagcagcgaggga.....gaaggcgcgaggaggggcc 1576

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 119 seqs, 2414 residues

Total number of hits satisfying chosen parameters: 238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 137 summaries

Database : rst.seq*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22	1.4	31	1	A2853311
C 2	21	1.3	29	1	A2764536
C 3	19.6	1.2	26	1	A2604431
C 4	19.2	1.2	25	1	A1762378
C 5	19	1.2	27	1	A2604434
C 6	19	1.2	27	1	A2649949
C 7	18.6	1.2	25	1	A2861588
C 8	17.6	1.1	24	1	A2486765
C 9	17.6	1.1	24	1	A2597705
C 10	17.6	1.1	24	1	A2861766
C 11	17.2	1.1	23	1	A2447239
C 12	17.2	1.1	24	1	A2375584
C 13	17.2	1.1	24	1	A2764494
C 14	16.8	1.1	21	1	A2871389
C 15	16.2	1.0	21	1	A2583408
C 16	16.2	1.0	21	1	A2819539
C 17	16.2	1.0	22	1	A2447246
C 18	16.2	1.0	22	1	A2764516
C 19	16.2	1.0	23	1	A2324328
C 20	16.2	1.0	23	1	A2764518
C 21	15.8	1.0	20	1	A2345513
C 22	15.6	1.0	22	1	A2326022
C 23	15.6	1.0	22	1	A2331687
C 24	15.6	1.0	22	1	A2338780
C 25	15.6	1.0	22	1	A2344385
C 26	15.6	1.0	22	1	A2346734
C 27	15.6	1.0	22	1	A2351203
C 28	15.6	1.0	22	1	A2353898
C 29	15.6	1.0	22	1	A2358103
C 30	15.6	1.0	22	1	A2427736
C 31	15.6	1.0	22	1	A2437946
C 32	15.6	1.0	22	1	A2438244
C 33	15.6	1.0	22	1	A2438934
C 34	15.6	1.0	22	1	A2441517
C 35	15.6	1.0	22	1	A2456332
C 36	15.6	1.0	22	1	A2458425
C 37	15.6	1.0	22	1	A2462694
C 38	15.6	1.0	22	1	A2483835
C 39	15.6	1.0	22	1	A2486750
C 40	15.6	1.0	22	1	A2581190
C 41	15.6	1.0	22	1	A2584757
C 42	15.6	1.0	22	1	A2590321
C 43	15.6	1.0	22	1	A2597625
C 44	15.6	1.0	22	1	A2602985
C 45	15.6	1.0	22	1	A2642084
C 46	15.6	1.0	22	1	A2642494
C 47	15.6	1.0	22	1	A2647408
C 48	15.6	1.0	22	1	A2766712
C 49	15.6	1.0	22	1	A2767823
C 50	15.6	1.0	22	1	A2775873
C 51	15.6	1.0	22	1	A2779302
C 52	15.6	1.0	22	1	A2781352
C 53	15.6	1.0	22	1	A2789340
C 54	15.6	1.0	22	1	A2805250
C 55	15.6	1.0	22	1	A2806801
C 56	15.6	1.0	22	1	A2807363
C 57	15.6	1.0	22	1	A2808089
C 58	15.6	1.0	22	1	A2814991
C 59	15.6	1.0	22	1	A2817117
C 60	15.6	1.0	22	1	A2826596
C 61	15.6	1.0	22	1	A2864279
C 62	15.6	1.0	22	1	A2875718
C 63	15.6	1.0	22	1	A2941907
C 64	15.6	1.0	22	1	TA327H04P
C 65	15.6	1.0	22	1	TA389D09P
C 66	15.6	1.0	22	1	TA45B04P
C 67	15.2	1.0	20	1	A2345438
C 68	15.2	1.0	20	1	A2426899
C 69	15.2	1.0	20	1	A2645269
C 70	15.2	1.0	20	1	A2823365
C 71	15.2	1.0	21	1	A2345794
C 72	14.8	0.9	19	1	A2427731
C 73	14.8	0.9	19	1	A2447248
C 74	14.8	0.9	19	1	A2854647
C 75	14.8	0.9	21	1	A2967472
C 76	14.4	0.9	25	1	A2861588
C 77	14.2	0.9	19	1	AA9878744
C 78	14.2	0.9	19	1	AA9505094
C 79	14.2	0.9	19	1	A2305212
C 80	14.2	0.9	19	1	A2345894
C 81	14.2	0.9	19	1	A2410166
C 82	14.2	0.9	19	1	A2427750
C 83	14.2	0.9	19	1	A2493581
C 84	14.2	0.9	19	1	A2760597
C 85	14.2	0.9	19	1	A2813861
C 86	14.2	0.9	19	1	A2861832
C 87	14.2	0.9	19	1	A2983014
C 88	14.2	0.9	20	1	A2328703
C 89	14.2	0.9	20	1	A2512326
C 90	14.2	0.9	20	1	A2579495
C 91	14.2	0.9	20	1	A2659755
C 92	14.2	0.9	20	1	A2861615
C 93	14.2	0.9	20	1	A2969440
C 94	14	0.9	16	1	AI154875
C 95	13.8	0.9	19	1	AA953971
C 96	13.8	0.9	19	1	A2491644
C 97	12.8	0.8	16	1	AI1648507
C 98	12.8	0.8	25	1	BQ593528
C 99	12.8	0.8	25	1	AI762378
C 100	12.4	0.8	17	1	AW247673
C 101	12.4	0.8	17	1	AW247673
C 102	12.2	0.8	17	1	BM396258
C 103	12.2	0.8	17	1	BM399757
C 104	12.2	0.8	17	1	BM400820
C 105	12	0.8	29	1	A2764536
C 106	11.8	0.7	15	1	BM396431

ACCESSION:AZ441517
ACCESSION:AZ456332
ACCESSION:AZ458425
ACCESSION:AZ462694
ACCESSION:AZ483835
ACCESSION:AZ486750
ACCESSION:AZ581190
ACCESSION:AZ584757
ACCESSION:AZ590321
ACCESSION:AZ597625
ACCESSION:AZ602985
ACCESSION:AZ642084
ACCESSION:AZ642494
ACCESSION:AZ647408
ACCESSION:AZ766712
ACCESSION:AZ767823
ACCESSION:AZ775873
ACCESSION:AZ779302
ACCESSION:AZ781352
ACCESSION:AZ789340
ACCESSION:AZ805250
ACCESSION:AZ806801
ACCESSION:AZ807363
ACCESSION:AZ808089
ACCESSION:AZ814991
ACCESSION:AZ817117
ACCESSION:AZ826596
ACCESSION:AZ864279
ACCESSION:AZ875718
ACCESSION:AZ941907
ACCESSION:AL497313
ACCESSION:AL498971
ACCESSION:AL453917
ACCESSION:AZ345438
ACCESSION:AZ426899
ACCESSION:AZ645269
ACCESSION:AZ823365
ACCESSION:AZ8345794
ACCESSION:AZ427731
ACCESSION:AZ447248
ACCESSION:AZ854647
ACCESSION:AZ967472
ACCESSION:AA878744
ACCESSION:AA9505094
ACCESSION:AZ305212
ACCESSION:AZ345894
ACCESSION:AZ410166
ACCESSION:AZ427750
ACCESSION:AZ493581
ACCESSION:AZ760597
ACCESSION:AZ813861
ACCESSION:AZ861832
ACCESSION:AZ983014
ACCESSION:AZ28703
ACCESSION:AZ512326
ACCESSION:AZ579495
ACCESSION:AZ659755
ACCESSION:AZ861615
ACCESSION:AZ969440
ACCESSION:AI154875
ACCESSION:AA953971
ACCESSION:AZ491644
ACCESSION:AI1648507
ACCESSION:BQ593528
ACCESSION:AI762378
ACCESSION:AW247673
ACCESSION:BM396258
ACCESSION:BM399757
ACCESSION:BM400820
ACCESSION:AZ764536
ACCESSION:BM396431

```

107 11.8 0.7 15 1 BQ588758
108 11.8 0.7 16 1 A1274782
109 11.6 0.7 26 1 ACCESSION: A1274782
110 11.4 0.7 23 1 ACCESSION: A2604431
111 11.4 0.7 13 1 ACCESSION: BM399929
112 11.4 0.7 15 1 ACCESSION: BM398494
113 11.4 0.7 16 1 ACCESSION: BM398873
114 11.4 0.7 21 1 ACCESSION: A2967472
115 11.2 0.7 16 1 ACCESSION: A1357296
116 11.2 0.7 16 1 ACCESSION: A1569544
117 11.2 0.7 16 1 ACCESSION: BM400746
118 11.2 0.7 16 1 ACCESSION: BQ590688
119 11.2 0.7 25 1 ACCESSION: A2861766
120 10.8 0.7 27 1 ACCESSION: A2604434
121 10.8 0.7 15 1 ACCESSION: BM396472
122 10.8 0.7 23 1 ACCESSION: A2447239
123 10.8 0.7 24 1 ACCESSION: A2764518
124 10.8 0.7 24 1 ACCESSION: A2486765
125 10.8 0.7 24 1 ACCESSION: A2597705
126 10.8 0.7 24 1 ACCESSION: A2375584
127 10.8 0.7 24 1 ACCESSION: A2764494
128 10.8 0.7 31 1 ACCESSION: A2649949
129 10.6 0.7 23 1 ACCESSION: A2853311
130 10.4 0.7 13 1 ACCESSION: A2324328
131 10.4 0.7 13 1 ACCESSION: A2918967
132 10.4 0.7 13 1 ACCESSION: BM396557
133 10.4 0.7 13 1 ACCESSION: BM399557
134 10 0.6 10 1 ACCESSION: BM399961
135 10 0.6 10 1 ACCESSION: BM396011
136 10 0.6 10 1 ACCESSION: BM398849
137 10 0.6 12 1 ACCESSION: BM398341
138 10 0.6 13 1 ACCESSION: BM399950

```

ALIGNMENTS

```

RESULT 1
A2853311/c 31 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0156L23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0156L23 F, genomic survey sequence.
ACCESSION A2853311
VERSION A2853311.1 GI:13041297
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: L column: 23
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 31.
FEATURES
Location/Qualifiers
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"

```

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0156L23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|GB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 0 a 30 c 0 g 1 t
Query Match 1.4%; Score 22; DB 1; Length 31;
Best Local Similarity 83.3%; Pred. No. 3.8;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1545 GCGGGCGCGGGGAGGGCGCGGGAGGGGG 1574
DB 31 GCGGGCGCGGGGAGGGCGCGGGAGGGGG 2
RESULT 2
A2764536 29 bp DNA linear GSS 16-FEB-2001
LOCUS IM0560A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0560A24 R, genomic survey sequence.
ACCESSION A2764536
VERSION A2764536.1 GI:12879599
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 29)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: A column: 24
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES
Location/Qualifiers
1..29
/organism="Mus musculus"
/mol_type="genomic DNA"

```

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560A24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|9b|A129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      1 c      2 g      0 t
Query Match      1.3%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1545 GGGGGCGGGGAGGGCGGGGAGGGG 1573
      |||||
Db 1 GGGGGGGGGGGGGGGGGGGGGGGGGGG 29

```

```

RESULT 3
AZ604431/c
LOCUS      26 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      1M0425114F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0425114 F, genomic survey sequence.
ACCESSION      AZ604431
VERSION      AZ604431.1
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0425 row: 1 column: 14
Seq primer: CGTGTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
FEATURES
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"

```

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0425114"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|9b|A129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a      24 c      2 g      0 t
Query Match      1.2%; Score 19.6; DB 1; Length 26;
Best Local Similarity 84.6%; Pred. No. 7.6;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 1548 GGGCGGGGGGAGGGCGGGGAGGGG 1573
      |||||
Db 26 GGGCGGGGGGGGGGGGGGGGGGGGGGG 1

```

```

RESULT 4
AT1762378/c
LOCUS      25 bp      mRNA      linear      EST 21-DEC-1999
DEFINITION      W1544f10.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2394091.3
similar to IR:Q69340 Q69340 ORF1, ORF2, AND ORF3. ;contains TARI.t2
TARI repetitive element ; mRNA sequence.
ACCESSION      AT1762378
VERSION      AT1762378.1
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 2471 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..25
/organism="Homo sapiens"
/mol_type="mRNA"

```

/db_xref="taxon:9606"
 /clone="IMAGE:2394091"
 /tissue_type="colon tumor, RER+"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Col6"
 /notes="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Col6 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1057416-1061255, and 1144584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 1 a 19 c 5 g 0 t

Query Match 1.2%; Score 19.2; DB 1; Length 25;
 Best Local Similarity 87.5%; Pred. No. 8.3;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGAGGGAGGGGCC 1576
 |||||
 Db 25 GGGGTGGGGCGGGCGGGCGGGGCC 2

RESULT 5
 AZ604434/c
 LOCUS
 DEFINITION 1M0425118F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0425118 F, genomic survey sequence.

ACCESSION AZ604434
 VERSION AZ604434.1 GI:11726624
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0425 row: 1 column: 18
 Seq primer: CGTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES
 source
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0425118"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114 gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor-mouse DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 26 c 0 g 1 t

Query Match 1.2%; Score 19; DB 1; Length 27;
 Best Local Similarity 81.5%; Pred. No. 11;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1546 GGGGGCGGGAGGGCGGGCGGGAGGG 1572
 |||||
 Db 27 GGGGGCGGGAGGGCGGGCGGGAGGG 1

RESULT 6
 AZ649949/c
 LOCUS

DEFINITION 1M0519P18R Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0519P18 R, genomic survey sequence.

ACCESSION AZ649949
 VERSION AZ649949.1 GI:11783942
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0519 row: P column: 18
 Seq primer: CACACGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES
 source
 1..27
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0519P18"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /note="Vector: pMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 26 c 0 g 1 t

Query Match 1.2%; Score 19; DB 1; Length 27;
Best Local Similarity 81.5%; Pred. No. 11;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1547 GGGGCCGGGGAGGGCGGGGAGGGG 1573

Db 27 GGGGGGGGGAGGGCGGGGAGGGG 1

RESULT 7
AZ861588/c
LOCUS 25 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0168J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0168J04 F, genomic survey sequence.

ACCESSION AZ861588
VERSION AZ861588.1 GI:13058058
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 25)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0168 row: J column: 04

Seq primer: CGTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0168J04"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 3 g 0 t

Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1547 GGGGCCGGGGAGGGCGGGGAGGGG 1571

Db 25 GGGGGGGGGAGGGCGGGGAGGGG 1

RESULT 8
AZ486765/c

LOCUS 24 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0315D09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315D09 F, genomic survey sequence.

ACCESSION AZ486765
VERSION AZ486765.1 GI:10653860
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 24)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 09

Seq primer: CGTGTAAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D09"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 1 g 0 t

Query Match 1.1%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1545 GGGGGGGCGGGGAGGGCGCGGG 1568

Db 24 GGGGGGGCGGGGAGGGCGCGGG 1

RESULT 9

AZ597705/c

LOCUS

DEFINITION AZ597705 24 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0411G07 R, genomic survey sequence.

ACCESSION AZ597705

VERSION AZ597705.1 GI:11719895

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0411 row: G column: 07

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24
/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC1M0411G07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 1 g 0 t

Query Match 1.1%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1545 GGGGGGGCGGGGAGGGCGCGGG 1568

Db 24 GGGGGGGCGGGGAGGGCGCGGG 1

RESULT 10

AZ861766/c

LOCUS

DEFINITION AZ861766 25 bp DNA linear GSS 21-FEB-2001
clone UUGC2M0168K19 R, genomic survey sequence.

ACCESSION AZ861766

VERSION AZ861766.1 GI:13058414

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 25)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: K column: 19

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1..25
/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UUGC2M0168K19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 24 c 1 g 0 t

Query Match 1.1%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Cy 1545 GGGGGCGGGGGGGGGGGGGGGGG 1568
|||||
Db 25 GGGGGCGGGGGGGGGGGGGGGGG 2

RESULT 11

AZ447239 23 bp DNA linear GSS 04-OCT-2000
LOCUS
DEFINITION
IM0244M18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244M18 F, genomic survey sequence.

ACCESSION AZ447239

VERSION A2447239.1 GI:10599026

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 23)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0244 row: M column: 18

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0244M18"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 22 g 0 t

Query Match 1.1%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1553 GGGGGAGGGGGGGGGGGGGGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGGGGGG 22

RESULT 12

AZ375584/c 24 bp DNA linear GSS 02-OCT-2000
LOCUS
DEFINITION
IM0129F04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0129F04 F, genomic survey sequence.

ACCESSION AZ375584

VERSION A2375584.1 GI:10489284

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 24)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: F column: 04

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1..24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0129F04"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 1 g 0 t

Query Match 1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1553 GGGGAGGGCGGGCGGGAGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGGGGG 1

RESULT 13

AZ764494/c

LOCUS

DEFINITION AZ764494 24 bp DNA linear GSS 16-FEB-2001
M0560E06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560E06 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

1 (bases 1 to 24)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: E column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. 24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0560E06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 23 c 1 g 0 t

Query Match 1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1553 GGGGAGGGCGGGCGGGAGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGGGGG 1

RESULT 14

AZ871389/c

LOCUS

DEFINITION AZ871389 21 bp DNA linear GSS 21-FEB-2001
2M0184A1F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0184A14 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0184 row: A column: 14

Seq primer: CTTGTAAACGACGCCGCT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. 21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0184A14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 2 g 0 t

Query Match 1.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1545 GGGGGCCGGGGAGGGGCG 1564
|||||
Db 20 GGGGGCCGGGGAGGGGCGG 1

RESULT 15
AZ583408/c
LOCUS 21 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0378N23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0378N23 F, genomic survey sequence.

ACCESSION AZ583408
VERSION GI:11703261
KEYWORDS GSS
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0378 row: N column: 23
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source 1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0378N23"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 20 c 1 t

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGCGGGAGGGG 1573
|||||
Db 21 GGGGGAGGGGCGGGAGGGG 1

RESULT 16
AZ819539/c
LOCUS 21 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0091A17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0091A17 F, genomic survey sequence.

ACCESSION AZ819539
VERSION GI:12989447
KEYWORDS GSS
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: A column: 17
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source 1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A17"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 2 g 0 t

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCCGGGGAGGGGGCGC 1565
||||| ||||| ||||| ||||| |||||
DB 21 GGGGGGGGGGGGGGGGGGGGGC 1

RESULT 17

AZ447246/c

LOCUS

DEFINITION IM0244E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244E23 F, genomic survey sequence.

ACCESSION AZ447246

VERSION AZ447246.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0244 row: E column: 23

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0244E23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G[4732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 0 g 1 t

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1554 GGGGAGGGCGCGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
DB 22 GGGGGGGGGGGGGGGGGGGG 2

RESULT 18

AZ764516/c

LOCUS

DEFINITION IM0560112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560112 R, genomic survey sequence.

ACCESSION AZ764516

VERSION AZ764516.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: I column: 12

Seq primer: CACACGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560112"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 1 g 0 t

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1554 GGGAGGGGGCGGGAGGGGG 1574
|||||
Db 22 GGGGGGGGGCGGGGGGGG 2

RESULT 19
AZ324328
LOCUS AZ324328 23 bp DNA linear GSS 29-SEP-2000
DEFINITION IM004616F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M004616 F, genomic survey sequence.

ACCESSION AZ324328

VERSION AZ324328.1 GI:10379937

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: B column: 16
Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23

FEATURES
source
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M004616"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 8 c 10 g 3 t

Query Match 1.0%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1367 CGCGGGGGCGGGCGGGCGG 1387
|||||
Db 1 CGCGGTGGCGGGCGGTCA 21

RESULT 20
AZ764518/c
LOCUS AZ764518 23 bp DNA linear GSS 16-FEB-2001
DEFINITION IM0560L1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560L1 R, genomic survey sequence.

ACCESSION AZ764518

VERSION AZ764518.1 GI:12879563

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: L column: 11
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23

FEATURES
source
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560L1"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 1 g

Query Match 1.0%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1553 GGGGAGGGGGGGGGGGGGGGG 1573
|||||
Db 21 GGGGGGGGGGGGGGGGGGGG 1

RESULT 21
AZ345513/c
LOCUS 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0080J04 F, genomic survey sequence.

ACCESSION AZ345513
VERSION 1 GI:10424750
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 3 a 13 c 0 g 4 t

Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 235 GGGTTCCGGAAGAGGAGG 253
|||||
Db 20 GGGGTTAGGAAGGGGAGG 2

RESULT 22
AZ326022/c
LOCUS 22 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0048K03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0048K03 R, genomic survey sequence.

ACCESSION AZ326022
VERSION 1 GI:10383291
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0048 row: K column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0048K03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGAGGGCGCGGGAGGGG 1574
|||||
Db 22 GGGGGGGGGGGGGGGGGGG 1

RESULT 23

A2331687

LOCUS A2331687 22 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0059117R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0059117 R, genomic survey sequence.

ACCESSION

A2331687

VERSION

A2331687.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: 1 column: 17

Seq primer: CACACGGAAACAGTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0059117"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGAGGGCGCGGGAGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGG 22

RESULT 24

A2338780

LOCUS

A2338780 22 bp DNA linear GSS 29-SEP-2000

DEFINITION

IM0070C06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0070C06 F, genomic survey sequence.

ACCESSION

A2338780

VERSION

A2338780.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0070 row: C column: 06

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0070C06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGCGGGAGGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGGGG 22

RESULT 25
AZ344385 22 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0078D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0078D23 F, genomic survey sequence.

ACCESSION AZ344385
VERSION AZ344385.1 GI:10423563
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: D column: 23
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0078D23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGCGGGAGGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGGGG 22

RESULT 26
AZ346734 22 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0082B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0082B09 F, genomic survey sequence.

ACCESSION AZ346734
VERSION AZ346734.1 GI:10425971
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: B column: 09
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source 1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0082B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGCGGGAGGGG 1574
|||||
Db 22 GGGGGGGGGGGGGGGGGGGG 1

RESULT 27

AZ351203 22 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0089C07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0089C07 F, genomic survey sequence.

ACCESSION AZ351203

VERSION 1

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0089 row: C column: 07

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0089C07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGCGGGAGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGGG 22

RESULT 28

AZ353898 22 bp DNA linear GSS 02-OCT-2000
LOCUS 1M0092P24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0092P24 R, genomic survey sequence.

ACCESSION AZ353898

VERSION 1

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0092 row: P column: 24

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0092P24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGCGGGAGGGG 1574
|||||
Db 22 GGGGGAGGGCGCGGGAGGGG 1

RESULT 29

AZ358103

LOCUS

DEFINITION AZ358103 22 bp DNA linear GSS 02-OCT-2000
1M0100P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0100P09 F, genomic survey sequence.

ACCESSION

AZ358103

VERSION

AZ358103.1

KEYWORDS

GI:10471803

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: P column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: Plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0100P09"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGCGGGAGGGG 1574
|||||
Db 1 GGGGGAGGGCGCGGGAGGGG 22

RESULT 30

AZ427736/c

LOCUS

DEFINITION AZ427736 22 bp DNA linear GSS 03-OCT-2000
1M0209121R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0209121 R, genomic survey sequence.

ACCESSION

AZ427736

VERSION

AZ427736.1

KEYWORDS

GI:10551749

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0209 row: I column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0209121"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G[14732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGCGGGGAGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGG 1

RESULT 31
AZ437946
LOCUS
DEFINITION 22 bp DNA linear GSS 03-OCT-2000
1M0226N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0226N07 R, genomic survey sequence.

ACCESSION
AZ437946

VERSION
AZ437946.1 GI:10561959

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0226 row: N column: 07

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0226N07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G[14732114|gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 g 0 c

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGCGGGGAGGGG 1574

Db 1 GGGGGGGGGGGGGGGGGGG 22

RESULT 32
AZ438244
LOCUS
DEFINITION 22 bp DNA linear GSS 03-OCT-2000
1M0228A16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0228A16 F, genomic survey sequence.

ACCESSION
AZ438244

VERSION
AZ438244.1 GI:10562257

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0228 row: A column: 16

Seq primer: CGTGTAAACAGCGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0228A16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||

Db 1 GGGGGGGGGGGGGGGGGGGGG 22

RESULT 33
AZ438934/c
LOCUS
DEFINITION
1M0229J13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0229J13 F, genomic survey sequence.

ACCESSION
A2438934
VERSION
A2438934.1 GI:10562947
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0229 row: J column: 13
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0229J13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||

Db 22 GGGGGGGGGGGGGGGGGGGGG 1

RESULT 34
AZ441517/c
LOCUS
DEFINITION
1M0233016F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0233016 F, genomic survey sequence.

ACCESSION
A2441517
VERSION
A2441517.1 GI:10565530
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0233 row: O column: 16
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers

FEATURES
source
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0233016"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GCGGGAGGGCGCGGGAGGGGG 1574
|||||
Db 22 GCGGGGGGGGGGGGGGGGGGGGG 1

RESULT 35

AZ456332/c

LOCUS

DEFINITION 1M0259A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0259A10 F, genomic survey sequence.

ACCESSION

AZ456332

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0259 row: A column: 10

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0259A10"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42hv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GCGGGAGGGCGCGGGAGGGGG 1574
|||||
Db 22 GCGGGGGGGGGGGGGGGGGGGGG 1

RESULT 36

AZ458425/c

LOCUS

DEFINITION 1M0262E02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0262E02 R, genomic survey sequence.

ACCESSION

AZ458425

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0262 row: E column: 02

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0262E02"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGGAGGGGG 1574
 ||||| ||||| ||||| ||||| |||||
 Db 22 GGGGGAGGGCGGGGAGGGGG 1

RESULT 37
 AZ462694/c
 LOCUS
 DEFINITION 22 bp DNA linear GSS 04-OCT-2000
 1M0271G1OF Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0271G10 F, genomic survey sequence.

ACCESSION AZ462694
 VERSION AZ462694.1 GI:10620819
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0271 row: G column: 10
 Seq primer: CGTTGTAAACGAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
 source
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0271G10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGGAGGGGG 1574
 ||||| ||||| ||||| ||||| |||||
 Db 22 GGGGGAGGGCGGGGAGGGGG 1

RESULT 38
 AZ483835/c
 LOCUS
 DEFINITION 22 bp DNA linear GSS 05-OCT-2000
 1M0310H06F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0310H06 F, genomic survey sequence.

ACCESSION AZ483835
 VERSION AZ483835.1 GI:10648411
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0310 row: H column: 06
 Seq primer: CGTTGTAAACGAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.

FEATURES
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCLM0310H06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCLM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGGGCGGGAGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGG 1

RESULT 39
LOCUS AZ486750 22 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0315103F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0315103 F, genomic survey sequence.

ACCESSION AZ486750
VERSION AZ486750.1 GI:10653830

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: I column: 03

Seq primer: CTTTATAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0315103"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGGGCGGGAGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGG 1

RESULT 40
LOCUS AZ581190 22 bp DNA linear GSS 13-DEC-2000
DEFINITION IM0369E16R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0369E16 R, genomic survey sequence.

ACCESSION AZ581190
VERSION AZ581190.1 GI:11695955

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0369 row: E column: 16

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

FEATURES

source

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0369E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGCGCGGGAGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGG 22

RESULT 41

AZ584757/c

LOCUS

DEFINITION IM0389D12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0389D12 R, genomic survey sequence.

ACCESSION AZ584757

VERSION AZ584757.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0389 row: D column: 12

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0389D12"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGCGCGGGAGGGG 1574
|||||
Db 22 GGGGGGGGGGGGGGGGGGG 1

RESULT 42

AZ590321

LOCUS

DEFINITION

IM0393C23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0393C23 R, genomic survey sequence.

ACCESSION AZ590321

VERSION AZ590321.1

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0399 row: C column: 23

Seq primer: CACACGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

FEATURES

source

1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0393C23"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1553 GGGGAGGGCGCGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 1 GGGGGGGGGGGGGGGGGGGGGGG 22

RESULT 43
AZ597625/c
LOCUS
DEFINITION
clone UUGC1M0411P07 R, genomic survey sequence.

ACCESSION
AZ597625
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0411 row: p column: 07
Seq primer: CACACGAGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0411P07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1553 GGGGAGGGCGCGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 22 GGGGGGGGGGGGGGGGGGGGGG 1

RESULT 44
AZ602985/c
LOCUS
DEFINITION
clone UUGC1M0422F06 F, genomic survey sequence.

ACCESSION
AZ602985
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0422 row: F column: 06
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1. .22

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0422F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGGGGGGGGGGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGGGG 1

RESULT 45
AZ642084/c

LOCUS AZ642084 22 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0504N21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0504N21 R, genomic survey sequence.

ACCESSION AZ642084

VERSION AZ642084.1 GI:11768367

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0504 row: N column: 21

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0504N21"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGGGGGGGGGGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGGGG 1

RESULT 46
AZ642494/c

LOCUS AZ642494 22 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0505J06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0505J06 R, genomic survey sequence.

ACCESSION AZ642494

VERSION AZ642494.1 GI:11769156

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE DUNN, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0505 row: J column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

FEATURES

source

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0505J06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGGGCGGGAGGGGG 1574
|||||
DB 22 GGGGGGGGGGGGGGGGGGG 1

RESULT 47

AZ647408

LOCUS

DEFINITION IM0513H19R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0513H19 R, genomic survey sequence.

ACCESSION

AZ647408

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0513 row: H column: 19

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0513H19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 8 c 5 g

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 587 GTGGACATCACCGTCTGACC 608
|||||
DB 1 GTGTGCATCACCATGCTGACC 22

RESULT 48

AZ766712/c

LOCUS

DEFINITION IM0564A03R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0564A03 R, genomic survey sequence.

ACCESSION

AZ766712

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: A column: 03

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC1M0564A03"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 1 a 21 c 0 g 0 t
 Query Match 1.0%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 30;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGCGGGAGGGGG 1574
 ||||| ||||| ||||| ||||| |||||
 Db 22 GGGGGAGGGCGCGGGAGGGGG 1

RESULT 49
 AZ767823/c
 LOCUS 22 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0567K20F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0567K20 F, genomic survey sequence.

ACCESSION AZ767823
 VERSION AZ767823.1 GI:12886316
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0567 row: K column: 20
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES
 source 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0567K20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t
 Query Match 1.0%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 30;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGCGGGAGGGGG 1574
 ||||| ||||| ||||| ||||| |||||
 Db 22 GGGGGAGGGCGCGGGAGGGGG 1

RESULT 50
 AZ775873/c
 LOCUS 22 bp DNA linear GSS 16-FEB-2001
 DEFINITION 2M0009B07F Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0009B07 F, genomic survey sequence.

ACCESSION AZ775873
 VERSION AZ775873.1 GI:12902863
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0009 row: B column: 07
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers

FEATURES
 source 1..22
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCLM0009B07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCLM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGGCGGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 22 GGGGGAGGGGGCGGGGAGGGGG 1

RESULT 51
AZ779302/c
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0015K01R Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UUGC2M0015K01 R, genomic survey sequence.

ACCESSION AZ779302
VERSION AZ779302.1 GI:12909819
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0015 row: K column: 01
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source

1. .22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0015K01"
/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGGCGGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 22 GGGGGAGGGGGCGGGGAGGGGG 1

RESULT 52
AZ781352
LOCUS 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0019B10R Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UUGC2M0019B10 R, genomic survey sequence.

ACCESSION AZ781352
VERSION AZ781352.1 GI:12913959
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0019 row: B column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.

FEATURES
source

1. .22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0019B10"
/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGGGGAGGGG 1574
|||||
Db 1 GGGGGGGGGGGGGGGGGGG 22

RESULT 53
AZ789340/c
LOCUS
DEFINITION 22 bp DNA linear GSS 16-FEB-2001
clone UUGC2M0037C03 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: C column: 03
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers

1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0037C03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES
source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGGAGGGCGGGGAGGGG 1574
|||||
Db 22 GGGGGGGGGGGGGGGGGGG 1

RESULT 54
AZ805250/c
LOCUS
DEFINITION 22 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0066K02 R, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 22)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: K column: 02
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 22.

Location/Qualifiers

1. 22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0066K02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

FEATURES
source

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGGCGCGGAGGGGG 1574

Db 22 GGGGGGGGGGGGGGGGGGGGG 1

RESULT 55

AZ806801

LOCUS 2M0069A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0069A10 F, genomic survey sequence.

ACCESSION AZ806801

VERSION AZ806801.1 GI:12970514

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0069 row: A column: 10

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0069A10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGAGGGGCGCGGAGGGGG 1574

Db 1 GGGGGGGGGGGGGGGGGGGGG 22

RESULT 56

AZ807363/c

LOCUS 2M0070I07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0070I07 F, genomic survey sequence.

ACCESSION AZ807363

VERSION AZ807363.1 GI:12971635

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0070 row: I column: 07

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0070I07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGGGGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 22 GGGGGGGGGGGGGGGGGGGGG 1

RESULT 57
AZ808089/c
LOCUS AZ808089 22 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0071K19F Mouse 10kb plasmid UGCM library Mus musculus genomic
clone UGCM2M0071K19 F, genomic survey sequence.

ACCESSION AZ808089
VERSION AZ808089.1 GI:12973085
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0071 row: K column: 19

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0071K19"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGGGGGGGAGGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 22 GGGGGGGGGGGGGGGGGGGGG 1

RESULT 58

AZ814991/c

LOCUS AZ814991 22 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0083A05F Mouse 10kb plasmid UGCM library Mus musculus genomic

clone UGCM2M0083A05 F, genomic survey sequence.

ACCESSION AZ814991

VERSION AZ814991.1 GI:12984899

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0083 row: A column: 05

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0083A05"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCM library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGAGGGG 1574
|||||
Db 22 GGGGGGGGGGGGGGGGGG 1

RESULT 59

AZ817117/c

LOCUS

DEFINITION 2M0086012F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086012 F, genomic survey sequence.

ACCESSION

AZ817117

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0086 row: 0 column: 12

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0086012"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1553 GGGGGAGGGCGGGAGGGG 1574
|||||
Db 22 GGGGGGGGGGGGGGGGGG 1

RESULT 60

AZ826596

LOCUS

DEFINITION 2M0102M15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0102M15 F, genomic survey sequence.

ACCESSION

AZ826596

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0102 row: M column: 15

Seq primer: CGTTGTAACACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0102M15"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 c 22 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGAGCGCGCGGAGGGG 1574
|||||
Db 1 GGGGCGGGGGGGGGGGGG 22

RESULT 61

AZ864279/c

LOCUS

DEFINITION 2M0173118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0173118 R, genomic survey sequence.

ACCESSION AZ864279.1 GI:13063421

VERSION 1

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 22)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: 1 column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0173118"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGAGCGCGCGGAGGGG 1574
|||||
Db 22 GGGGCGGGGGGGGGGGGG 1

RESULT 62

AZ875718/c

LOCUS

DEFINITION 2M0190619F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0190619 F, genomic survey sequence.

ACCESSION AZ875718

VERSION 1

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 22)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: 6 column: 19
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
1..22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0190619"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 21 c 1 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1552 CGGGGAGGGCGGGGAGGGG 1573
||||| ||||| ||||| ||||| |||||
Db 22 CGGGGAGGGCGGGGAGGGG 1

RESULT 63

AZ941907/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .22

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0201A19"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone_libs="Mouse 10kb plasmid UUC2M library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource"

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 0 g 0 t

Query Match 1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1553 GGGGAGGGCGGGGAGGGG 1574
||||| ||||| ||||| ||||| |||||
Db 22 GGGGAGGGCGGGGAGGGG 1

RESULT 64

TA327H04P

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

/clone="327h04"

Location/Qualifiers

1. .22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

Location/Qualifiers

1. .22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

Location/Qualifiers

1. .22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

Location/Qualifiers

1. .22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

Location/Qualifiers

1. .22

/organism="Trypanosoma brucei"

/mol_type="genomic DNA"

/strain="TREU927"

/db_xref="taxon:5691"

Location/Qualifiers

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G[14732114]gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 1 g 0 t

Query Match 1.0%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 29;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1554 GGGGAGGGCGGGGAGGGG 1573
 ||||| ||||| ||||| ||||| |||||
 Db 20 GGGGGGGGGGGGGGGGGGG 1

RESULT 68
 AZ426899/c
 LOCUS
 DEFINITION IMC208A08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0208A08 R, Genomic survey sequence.

ACCESSION AZ426899
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0208 row: A column: 08
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 source
 1..20
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0208A08"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (G[14732114]gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 19 c 1 g 0 t

Query Match 1.0%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 29;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGGGG 1564
 ||||| ||||| ||||| ||||| |||||
 Db 20 GGGGGGGGGGGGGGGGGGG 1

RESULT 69
 AZ645269/c

LOCUS
 DEFINITION AZ645269 Mouse 20 bp DNA linear GSS 14-DEC-2000
 clone UUGC1M0510B10 R, Genomic survey sequence.

ACCESSION AZ645269
 VERSION
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 20)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0510 row: B column: 10
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES
 source
 1..20
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0510B10"
 /sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone lib="Mouse 10kb plasmid UGCM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [G14732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 1 c 20 g 0 t
 Query Match 1.0%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 32;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGGGGGGGGGGGGGGGGGG 1564
 ||||| ||||| ||||| |||||
 Db 2 GGGGGGGGGGGGGGGGGGGGGG 21

RESULT 72
 AZ427731/c
 LOCUS
 DEFINITION
 1M0209G19R Mouse 10kb plasmid UGCM library Mus musculus genomic
 clone UGCM0209G19 R, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D.,Weiss,R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0209 row: G column: 19
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0209G19"
 /sex="Male"

/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone lib="Mouse 10kb plasmid UGCM library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [G14732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 1 g 0 t
 Query Match 0.9%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 31;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1545 GGGGGGGGGGGGGGGGGGGGGG 1562
 ||||| ||||| ||||| |||||
 Db 19 GGGGGGGGGGGGGGGGGGGGGG 2

RESULT 73
 AZ447248/c
 LOCUS
 DEFINITION
 1M0244H23F Mouse 10kb plasmid UGCM library Mus musculus genomic
 clone UGCM0244H23 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
 ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D.,Weiss,R.

TITLE
 JOURNAL
 COMMENT
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0244 row: H column: 23
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 1. .19
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCM0244H23"
 /sex="Male"

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 19 g 0 t
 Query Match 0.9%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 38;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1553 GGGGAGGGGGCGCGGAG 1570
 |||||
 Db 4 GGGGGGGGGCGCGGGG 21

RESULT 76
 AZ861588
 LOCUS 25 bp DNA linear GSS 21-FEB-2001
 DEFINITION 2M0168704F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0168704 F, genomic survey sequence.
 ACCESSION AZ861588
 VERSION AZ861588.1 GI:13058058
 KEYWORDS GSS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 25)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.,
 and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0168 Row: J Column: 04
 Seq primer: CCGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 25.
 Location/Qualifiers
 1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0168704"
 /sex="Male"

FEATURES
 source
 1. .25
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0168704"
 /sex="Male"

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: pWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 22 c 3 g 0 t
 Query Match 0.9%; Score 14.4; DB 1; Length 25;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 82 CACCCCGCGCGCCTACTCGGCC 105
 |||||
 Db 2 CCCCCGCGCGCGCGGCC 25

RESULT 77
 AA878744/c
 LOCUS 19 bp mRNA linear EST 25-MAR-1998
 DEFINITION c855a08.s1 NCI CGAP L15 Homo sapiens cDNA clone IMAGE:1437110 3',
 similar to TR:067633 Q67633 ECO Q PROTEIN. [1]; contains TARI.t2
 TARI repetitive element; mRNA sequence.
 ACCESSION AA878744
 VERSION AA878744.1 GI:2987709
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 19)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@nci.nih.gov
 unknown library type
 trace considered overall poor quality
 Seq primer: -40m13 fwd. ET from Amerham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1437110"
 /tissue_type="hepatic adenoma"
 /lab host="DH10B"
 /clone lib="NCI CGAP L15"
 /notes="Organ: liver; Vector: pCMV-SPORT4; Site: 1; Salt;
 Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 0.8 kb."
 16 c 1 g 2 t

BASE COUNT 0 a 16 c 1 g 2 t
 Query Match 0.9%; Score 14.2; DB 1; Length 19;
 Best Local Similarity 84.2%; Pred. No. 40;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY      1370 GGGGGCGCGCGCGCGCAG 1388
Db      19 GGGGGCGCGCGCGCGCAG 1

RESULT 78
AA995094
LOCUS
DEFINITION
  AA995094 19 bp mRNA linear EST 27-AUG-1998
  similar to TR:Q69566 Q69566; contains TAR1.t2 MER35 repetitive
  element; mRNA sequence.
ACCESSION
  AA995094
VERSION
  AA995094.1 GI:3181583
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1. (bases 1 to 19)
  NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: ccapsb-remail.nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CCGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1087 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
  Location/Qualifiers
    1..19
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:1635040"
      /lab_host="DH10B"
      /clone_lib="NCI_CGAP_Kid3"
      /note="Organ: Kidney; Vector: pRTT3D-Pac (Pharmacia) with
      a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
      strand cDNA was primed with a Not I - oligo(dT) primer,
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not
      I and Eco RI sites of the modified pRTT3 vector. mRNA
      source: 2 pooled kidneys. Library went through one round
      of normalization. Library constructed by Bento Soares and
      M. Fatima Bonaldo. "
BASE COUNT      8 a      1 g      0 t
                10 c
Query Match      0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      70 CGCACACACACACACCGC 88
Db      1 CACACACACACACACG 19

RESULT 79
AA995094
LOCUS
DEFINITION
  AA995094 19 bp DNA linear GSS 29-SEP-2000
  IM0005115R Mouse 10kb plasmid UUC1M library Mus musculus genomic
  clone UUC1M0005115 R, genomic survey sequence.
ACCESSION
  AA995094

```

```

VERSION
  AZ305212.1 GI:10342003
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1. (bases 1 to 19)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
  M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
  and Wright, D., Weiss, R.,
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished
COMMENT
  Contact: Robert B. Weiss
  University of Utah
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0005 row: 1 column: 15
  Seq primer: CACACAGGAACACGATGACC
  Class: plasmid ends
  High quality sequence stop: 19.
FEATURES
  Location/Qualifiers
    1..19
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUC1M0005115"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."
BASE COUNT      0 a      1 g      0 t
                18 c
Query Match      0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1544 CGCGGGCGCGCGCGGAGGG 1562
Db      19 CGCGGGCGCGCGCGGAGGG 1

RESULT 80
AA345894/c
LOCUS
DEFINITION
  AA345894 19 bp DNA linear GSS 29-SEP-2000
  IM0080C24R Mouse 10kb plasmid UUC1M library Mus musculus genomic
  clone UUC1M0080C24 R, genomic survey sequence.
ACCESSION
  AA345894

```

```

VERSION      AZ345894.1  GI:10425131
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 19)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0080 row: C column: 24
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.

FEATURES     Location/Qualifiers
              1..19
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M080C24"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a 18 c 1 g 0 t
              Query Match      0.9%; Score 14.2; DB 1; Length 19;
              Best Local Similarity 84.2%; Pred. No. 40;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCCCGGGGGGGGGG 1563
      ||||| ||||| |||||
Db 19 GGGGGGGGGGGGGGGGGG 1

RESULT 81
AZ410166/c
AZ410166 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0182J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0182J17 F, genomic survey sequence.
ACCESSION AZ410166

VERSION      AZ410166.1  GI:10534179
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 19)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0182 row: J column: 17
              Seq primer: CGTGTGAAAACGACGCCACT
              Class: plasmid ends
              High quality sequence stop: 19.

FEATURES     Location/Qualifiers
              1..19
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0182J17"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   4 a 5 c 2 g 8 t
              Query Match      0.9%; Score 14.2; DB 1; Length 19;
              Best Local Similarity 84.2%; Pred. No. 40;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 332 AGGTATGAGGGAAGATCT 350
      ||||| ||||| |||||
Db 19 AGTTAAGAGGGAAGATCT 1

RESULT 82
AZ427750/c
AZ427750 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0209N19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0209N19 R, genomic survey sequence.
ACCESSION AZ427750

```

VERSION AZ427750.1 GI:10551763
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0209 row: N column: 19

Seq primer: CACACAGAACACCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG1M0328A24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUCG1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 t

Query Match 0.9%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 40;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1554 GGGGAGGGGGCGGGAGGG 1572

Db 19 GGGGGGGGGGGCGGGGGGG 1

RESULT 83

AZ493581/c

LOCUS 19 bp DNA linear GSS 05-OCT-2000

DEFINITION IM0328A24F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0328A24 F, genomic survey sequence.

ACCESSION AZ493581

VERSION AZ493581.1 GI:10667400

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0328 row: A column: 24

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. 19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUCG1M0328A24"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUCG1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 t

Query Match 0.9%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 40;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1553 GGGGAGGGGGCGGGAGGG 1571

Db 19 GGGGGGGGGGGCGGGGGGG 1

RESULT 84

AZ760597/c

LOCUS 19 bp DNA linear GSS 16-FEB-2001

DEFINITION IM0554N21F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0554N21 F, genomic survey sequence.

ACCESSION AZ760597


```

VERSION      AZ760597.1  GI:12868613
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 19)
              Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0554 row: N column: 21
              Seq primer: CGTTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 19.
FEATURES     source
              1..19
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC1M0554N21"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a      0 g      1 t
              Query Match      0.9%; Score 14.2; DB 1; Length 19;
              Best Local Similarity 84.2%; Pred. No. 40;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1555 GGGAGGGCGCGGAGGGG 1573
Db      |||||
        |||||
        19 GGGAGGGGGGGGGGGGGG 1
RESULT 85
AZ813861/c
LOCUS      2M0081A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0081A01 R, genomic survey sequence.
ACCESSION AZ813861

VERSION      AZ813861.1  GI:12983865
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 19)
              Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0081 row: A column: 01
              Seq primer: CACACAGGAACACGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.
FEATURES     source
              1..19
              /organism="Mus musculus"
              /mol_type="genomic DNA"
              /strain="C57BL/6J"
              /db_xref="taxon:10090"
              /clone="UUGC2M0081A01"
              /sex="Male"
              /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
              /clone_lib="Mouse 10kb plasmid UUGC1M library"
              /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a      18 c      1 g      0 t
              Query Match      0.9%; Score 14.2; DB 1; Length 19;
              Best Local Similarity 84.2%; Pred. No. 40;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1545 GGGGGCGCGGGGAGGGG 1563
Db      |||||
        |||||
        19 GGGGGGGGGGGGGGGGG 1
RESULT 86
AZ861832
LOCUS      AZ861832
DEFINITION 2M0168H21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0168H21 R, genomic survey sequence.
ACCESSION AZ861832

```

```

VERSION      AZ861832.1  GI:13058546
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE
1 (bases 1 to 19)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: H column: 21
Seq primer: CACACAGGAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0168H21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      0 a      2 c      17 g      0 t
Query Match      0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1547 GGGGCGGGGGGGGGGGCGC 1565
      |||||
Db 1 GGGGGGGGGGGGGGGGGCGC 19

RESULT 87
AZ983014/c
LOCUS      AZ983014
DEFINITION 2M0264H02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0264H02 F, genomic survey sequence.
ACCESSION  AZ983014

```

```

VERSION      AZ983014.1  GI:13854241
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE
1 (bases 1 to 19)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: H column: 02
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1. 19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0264H02"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT      0 a      9 c      1 g      9 t
Query Match      0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 AGCGAGGGGAGAGAGCGGAGC 30
      |||||
Db 19 AGAGAGAGAGAGAGAGAGC 1

RESULT 88
AZ328703
LOCUS      AZ328703
DEFINITION 1M052A07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0052A07 R, genomic survey sequence.
ACCESSION  AZ328703

```

```

VERSION      AZ328703.1  GI:10388697
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished
JOURNAL
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0052 row: A column: 07
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
FEATURES     source
              1..20
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0052A07"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a 1 c 19 g 0 t

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.44;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1544 CGGGGGCGGGCGGGGAGGG 1562
      |||||
      1 CGGGGGCGGGCGGGGAGGG 19

Db

RESULT 89
AZ512326/c
LOCUS
DEFINITION 1M0357118R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0357118 R, genomic survey sequence.
ACCESSION AZ512326

VERSION      AZ512326.1  GI:10693642
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D.,Weiss,R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished
JOURNAL
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0357 row: I column: 18
              Seq primer: CACACAGGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
FEATURES     source
              1..20
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0357118"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a 18 c 0 g 2 t

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred.No.44;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1554 GGGGAGGGCGGGCGGGGAGGG 1572
      |||||
      20 GGGGAGGGCGGGCGGGGAGGG 2

Db

RESULT 90
AZ579495
LOCUS
DEFINITION 1M0367C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0367C13 F, genomic survey sequence.
ACCESSION AZ579495

```



```

VERSION      AZ659755.1  GI:11796901
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0367 row: C column: 13
              Seq primer: CGTGTAAACGACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
FEATURES     source
              1..20
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0537F22"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   1 a      2 c      17 g      0 t
              Query Match      0.9%; Score 14.2; DB 1; Length 20;
              Best Local Similarity 84.2%; Pred. No. 44;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1546  GGGGCGCGGGGAGGGGCG 1564
Db  1  GCGGGGGGGGGAGGGGCG 19

RESULT 91
AZ659755/c
LOCUS    20 bp      DNA      linear      GSS 21-FEB-2001
DEFINITION  2M0168C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0537F22 F, genomic survey sequence.
ACCESSION  AZ659755

```

```

VERSION      AZ861615.1  GI:13058112
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0168 row: C column: 23
              Seq primer: CGTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
FEATURES     source
              1..20
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0168C23"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a      3 c      17 g      0 t
              Query Match      0.9%; Score 14.2; DB 1; Length 20;
              Best Local Similarity 84.2%; Pred. No. 44;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1542 GCCGGGGGCGCGGGGAGG 1560
Db   2 GCCGGGGGCGCGGGGGGG 20

RESULT 93
AZ869440/c
LOCUS      20 bp DNA linear GSS 27-APR-2001
DEFINITION 2M024012F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
              clone UUGC2M024012 F, genomic survey sequence.
ACCESSION  AZ869440

VERSION      AZ969440.1  GI:13840667
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 20)
              Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0242 row: O column: 12
              Seq primer: CGTGTAAACGACGCCAGT
              Class: plasmid ends
              High quality sequence stop: 20.
              Location/Qualifiers
FEATURES     source
              1..20
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M024012"
                /sex="Female"
                /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC2M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (female) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   0 a      19 c      0 g      1 t
              Query Match      0.9%; Score 14.2; DB 1; Length 20;
              Best Local Similarity 84.2%; Pred. No. 44;
              Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1553 GGGGGGCGCGGGGGAGG 1571
Db   19 GGGGGGCGCGGGGGGGG 1

RESULT 94
A1154875/c
LOCUS      A1154875 16 bp mRNA linear EST 30-SEP-1998
DEFINITION ud80f04.r1 Soares mammary gland NMLMG Mus musculus cDNA clone
              IMAGE:1477183 5' Similar to TR:O14557 O14557 F25965_1 ; mRNA
              sequence.

```

```

ACCESSION      AI154875
VERSION         AI154875.1  GI:3683344
KEYWORDS       EST.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus

REFERENCE
AUTHORS        Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
               Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
               Schellenberg,K., Stepien,M., Tan,F., Underwood,K., Moore,B.,
               Theising,B., Wylie,F., Lennon,G., Soares,B., Wilson,R. and
               Waterston,R.
TITLE          The WashU-HMI Mouse EST Project
JOURNAL        Unpublished
COMMENT        Contact: Marra M/Mouse EST Project
               WashU-HMI Mouse EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu
               This clone is available royalty-free through LLNL ; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               MGI:925539
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 16
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1477183"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p773 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      5 a 4 c 6 g 1 t
Query Match      0.9%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 GCTTTGGCCATCTC 486
Db 14 GCTTTGGCCATCTC 1

RESULT 95
AA953971/c
LOCUS           19 bp  mRNA  linear  EST 07-JUL-1998
DEFINITION      o88h01.e1 NCI CGAP Kids Homo sapiens cDNA clones IMAGE:1573297 3',
               similar to TR:Q00484 Q00484 MINI-COLLAGEN PRECURSOR ; contains
               element MSRI repetitive element ;, mRNA sequence.
ACCESSION       AA953971.1  GI:3116889
VERSION         AA953971.1
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

JOURNAL COMMENT
Contact: Robert Strausberg, Ph.D.
Email: c9pbbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 485 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1573297"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Kids"
/notes="Organ: kidney; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AAGTGAAGAATTCGGCGCGCAATATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT      0 a 15 c 0 t
Query Match      0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1545 GGGGGGCGGGGGGAGGG 1561
Db 19 GGGGGGCGGGGGGAGGG 3

RESULT 96
AA491644/c
LOCUS           19 bp  DNA  linear  GSS 05-OCT-2000
DEFINITION      IM0325A20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
               clone UUGCIM0325A20 F, genomic survey sequence.
ACCESSION       AA491644
VERSION         AA491644.1  GI:10663543
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

```

Insert Length: 10000 Std Error: 0.00
 Place: 0325 row: A column: 20
 Seq primer: CGTGTAAACAGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0325A20"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: FWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnates/). The DNA was hydrotynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 2 c 9 g 8 t

Query Match 0.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. NO. 47;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 72 CACACGCACACACCGC 88
 Db 19 CACACGCACACACCGC 3

RESULT 97

AI648507/c

LOCUS

DEFINITION t254c09.x1 NCI CGAP Ov35 Homo sapiens cDNA clone IMAGE:2292400 3' similar to TR:000599 000599 CON1.; mRNA sequence.

ACCESSION AI648507.1 GI:4729341

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

FEATURES

source

1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2292400"
 /tissue_type="tumor, 5 pooled (see description)"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Ov35"
 /notes="Organ: Ovary; Vector: pCMV-SPORT6; Site 1: Sali; Site 2: NotI; This library represents the normally version of NCI CGAP Ov23. Cloned unidirectionally. Primer: Oligo dt. Average insert size 0.86 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Constructed by Life Technologies."

BASE COUNT 0 a 13 c 3 g 0 t

Query Match 0.8%; Score 12.8; DB 1; Length 16;
 Best Local Similarity 87.5%; Pred. NO. 51;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1550 GCCGGGGGAGGGGGCGC 1565
 Db 16 GCCGGGGGAGGGGGCGC 1

RESULT 98

BO593528/c

LOCUS

DEFINITION S015925-024-026-123-SP6 MP1Z-ADIS-024-developing root Beta vulgaris cDNA clone 024-026-123 5-PRIME, mRNA sequence.

ACCESSION BO593528

VERSION EST.

KEYWORDS Beta vulgaris

SOURCE Beta vulgaris

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Contact: Weissshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215082851

Email: weissshaar@mpiz-koeln.mpg.de

Insert Length: 17 Std Error: 0.00

Plate: 26 row: I column: 23

Seq primer: SP6; CATACGATTAGTGACACTATAG.

Location/Qualifiers

1..17

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:193326"

/db_xref="taxon:161934"

/clone="024-026-123"

/tissue_type="developing root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-developing root"

/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatztucht AG Einbeck, Germany, contact:
b.schulz@ws.de; cloning sites Sali-NoI, primer sites and
orientation:

SP6-Sali-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet project
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 0 a 8 c 1 g 8 t

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 57;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CGAGGAGAGAGCGAG 29
|||||
DB 16 CGAGAGAGAGAGAG 1

RESULT 99
LOCUS A1762378 25 bp mRNA linear EST 21-DEC-1999
DEFINITION w54f10.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2394091 3'
similar to TR:Q93340 Q93340 ORF1, ORF2, AND ORF3. ;contains TAR1.t2
TAR1 repetitive element ;, mRNA sequence.

ACCESSION A1762378.1 GI:5178045
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 2471 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES
Source

1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2394091"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Col6"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 1 a 19 c 0 t

Query Match 0.8%; Score 12.8; DB 1; Length 25;

Best Local Similarity 70.8%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 88 CGCGCGCACCTCGCGCCCGGACCC 111
|||||
DB 1 CGGCCCCCGCGCGCCCGGACCC 24

RESULT 100
LOCUS AW247673

DEFINITION 2820207.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820207 5',
mRNA sequence.

ACCESSION AW247673
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Other_ESis: 2820207.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: trace file contained 17 contiguous distinct peaks
following vector sequence.

Plate: LLCM3 row: J column: 16.

FEATURES
Location/Qualifiers

1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820207"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_7"
/note="Organ: lung; Vector: pOT87; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dr priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 1 a 8 c 6 g

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 67;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1003 GCCCGAGGCGCTCT 1016
|||||
DB 2 GCCCGAGGCGCTCT 15

RESULT 101
AW247673/c

LOCUS
DEFINITION 2820207.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820207 5',
17 bp mRNA linear EST 07-JAN-2000
mrna sequence.

ACCESSION
VERSION AW247673
KEYWORDS AW247673.1 GI:6590666
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
1 (bases 1 to 17)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Other_ESTS: 2820207.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTP/DNP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbr/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
<http://www.genome.washington.edu/LowQuality> Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 17 contiguous distinct peaks
following vector sequence.
Plate: L10W3 row: J column: 16.

FEATURES
source

1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:2820207"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site:1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected 500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 1 a 8 c 6 g 2 t

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 67;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1167 AGGAGCGCGCGGC 1180

Db 15 AGGAGCGCTCGGC 2

RESULT 102
BM396258/c

LOCUS
DEFINITION 5009-0-19-G03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
17 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
VERSION BM396258
KEYWORDS BM396258.1 GI:18196311
SOURCE EST.
ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
AUTHORS

1 (bases 1 to 17)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished

CONTACT: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source

1. .17
Location/Qualifiers
/organism="Tetrahymena thermophila"
/mol_type="mrna"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 2 a 4 c 8 g 3 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1433 GCCACCGCGGCTCCCA 1449

Db 17 GCCACCGCGTGACTCCA 1

RESULT 103
BM399757/c

LOCUS
DEFINITION 5009-0-60-HJ2.t.1 Chilcoat/Turkewitz cDNA (large fraction)
17 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION
VERSION BM399757
KEYWORDS BM399757.1 GI:18199810
SOURCE EST.

ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
1 (bases 1 to 17)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished

CONTACT: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3

FEATURES
source

1. .17
Location/Qualifiers
/organism="Tetrahymena thermophila"
/mol_type="mrna"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 2 a 5 c 7 g 3 t

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 72;

UNCLASSIFIED

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3

Location/Qualifiers

1. .15
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

1 a 4 c 8 g 2 t

BASE COUNT

Query Match 0.7%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 67;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1434 CCACCGCGGCATCC 1448

Db 15 CCACCGCGGCAGCC 1

RESULT 107

LOCUS

DEFINITION B0588758 15 bp mRNA linear EST 06-DEC-2002
E012534-024-014-P24-SP6 MP12-ADIS-024-storage root Beta vulgaris
cDNA clone 024-014-P24 5-PRIME, mRNA sequence.

ACCESSION B0588758

VERSION B0588758.1 GI:26118341

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 15)

REFERENCE

AUTHORS

Herrig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lebrach, H.

and Radloff, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

CONTACT: Weishaar, B.

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@piz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 14 row: P column: 24

Seq primer: SP6; CATGATTAGTGACACTATAG.

Location/Qualifiers

1. .15

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line

)"

/db_xref="GABI:187217"

/db_xref="taxon:161934"

/clone="024-014-P24"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulzekws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-SalI-CCACCGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet project
, local PI: Dr. Katharina Schneider, coordinator: Prof.
Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

BASE COUNT 0 a 1 c 14 g 0 t

Query Match

Best Local Similarity 86.7%; Score 11.8; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1560 GGGCGGGAGGGGG 1574

Db 1 GGGCGGGGGGGGG 15

RESULT 108

LOCUS

DEFINITION A1274782/c 16 bp mRNA linear EST 21-DEC-1998

QY67H03.X1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:1986677.3,

similar to WP:F59E12.9 CE11534 ;contains element M81 repetitive

element ;, mRNA sequence.

ACCESSION A1274782

VERSION A1274782.1 GI:3897056

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

REFERENCE

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher Moskaiuk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1556 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1986677"

/tissue_type="well-differentiated endometrial

adenocarcinoma, 7 pooled tumors"

/lab_host="DH10B"

/clone_lib="NCI CGAP Utl1"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: oligo dt.

Average insert size 1.75 Kb. Life Technologies catalog #:

11538-014"

BASE COUNT 0 a 13 c 2 g 1 t

Query Match

Best Local Similarity 86.7%; Score 11.8; DB 1; Length 16;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 643 GCGGTGAGCGCGG 657

Db 15 GCGGGGGAGGCGCG 1


```

RESULT 109
LOCUS      AZ604431
DEFINITION 26 bp DNA linear GSS 13-DEC-2000
            1W043511AF Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0425114 F, genomic survey sequence.
ACCESSION  AZ604431
VERSION     AZ604431.1 GI:11726621
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 26)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
            Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.,
            and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT     Unpublished
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: rdunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0425 row: I column: 14
            Seq primer: CGTTGTAAACGACGCGCAGT
            Class: plasmid ends
            High quality sequence stop: 26.
FEATURES   source
            1..26
            Location/Qualifiers
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clones="UUGC1M0425114"
                /sex="Male"
                /lab_hosts="E. Coli strain XL10-Gold, Ti-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT  0 a 24 c 2 g 0 t
            Query Match 0.7%; Score 11.6; DB 1; Length 26;
            Best Local Similarity 65.4%; Pred. No. 1.4e+02;
            Matches 17; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Cy 85 CCGCGCGCGCACCTCGCGCGCGGACC 110
      |||||
Db 1 CCCCCCCCCCCCCCCCCCCCCCGGCC 26

```

```

RESULT 110
LOCUS      BM399929
DEFINITION 13 bp mRNA linear EST 17-JAN-2002
            5009-0-63-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM399929
VERSION     BM399929.1 GI:18199982
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
REFERENCE   1 (bases 1 to 13)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            J., and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished
            Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES   source
            1..13
            Location/Qualifiers
                /organism="Tetrahymena thermophila"
                /mol_type="mRNA"
                /strain="CU428.1"
                /db_xref="taxon:5911"
                /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                /note="Vector: Bluescript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT  2 a 3 c 7 g 1 t
            Query Match 0.7%; Score 11.4; DB 1; Length 13;
            Best Local Similarity 92.3%; Pred. No. 60;
            Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 716 AACCTCGTGGCGG 728
      |||||
Db 1 AACGCGGTGGCGG 13

RESULT 111
LOCUS      BM398494
DEFINITION 15 bp mRNA linear EST 17-JAN-2002
            5009-0-46-A03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM398494
VERSION     BM398494.1 GI:18198547
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
REFERENCE   1 (bases 1 to 15)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
            J., and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished
            Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES   source
            1..15
            Location/Qualifiers

```


KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2001457"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site: 1;
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
11 c 5 g 0 t

BASE COUNT 0 a 11 c 5 g 0 t

Query Match 0.7%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 95;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1361 GGGGACCGGGGGCG 1376
|||||
Db 16 GGGGCCCCGGGGGG 1

RESULT 115
AI569544/c
LOCUS
DEFINITION
t028d10.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2180371.3,
similar to TR:Q18444 Q18444 COSMID C34D4. ;contains MSRL.b2 MSRL
repetitive element ;, mRNA sequence.
AI569544
AI569544 GI:4532918
EST.
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 16)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1683 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLVA=No.
Location/Qualifiers
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2180371"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
1 a 14 c 0 g 1 t

BASE COUNT 1 a 14 c 0 g 1 t

Query Match 0.7%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 95;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1547 GGGGCGGGGGGAGGGG 1562
|||||
Db 16 GGGTGGGGGGGAGGGG 1

RESULT 116
BM400746/c
LOCUS
DEFINITION
5009-0-78-F05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
AI400746
AI400746 GI:18200799
EST.
SOURCE
ORGANISM
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 16)
AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
, J. and Klobutcher, L.
TITLE Unpublished
JOURNAL
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. .16
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
2 a 4 c 7 g 3 t

BASE COUNT 2 a 4 c 7 g 3 t

Query Match 0.7%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 95;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1434 CCACCGCGGGCATCCA 1449
Db 16 CCACCGCGGTGACTCCA 1

RESULT 117
BQ590688/c
LOCUS
DEFINITION
  BQ590688 16 bp mRNA linear EST 06-DEC-2002
  S013717-024-018-023-T7 MP1Z-ADIS-024-storage root Beta vulgaris
  cDNA clone 024-018-023 3-PRIME, mRNA sequence.
ACCESSION
  BQ590688
VERSION
  BQ590688.1 GI:26120271
KEYWORDS
  EST.
SOURCE
  Beta vulgaris
  Beta vulgaris
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
REFERENCE
  1 (bases 1 to 16)
  Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radelof,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
JOURNAL
  Plant J. 32 (5), 845-857 (2002)
COMMENT
  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@piz-koeln.mpg.de
  Insert Length: 16 Std Error: 0.00
  Plate: 18 row: 0 column: 23
  Seq primer: 17; GTAATACGACATCATATAGGCG.
FEATURES
  source
  1..16
  Location/Qualifiers
    /organism="Beta vulgaris"
    /mol_type="mRNA"
    /cultivar="KWS2320 (double haploid, monogerm breeding line
    )"
    /db_xref="GABI:189433"
    /db_xref="taxon:161934"
    /clone="024-018-023"
    /tissue_type="storage root"
    /lab_host="EMDH103"
    /clone_lib="MP1Z-ADIS-024-storage root"
    /note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI;
    cDNA library from sugar beet, library provided by KWS
    Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:
    b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
    orientation:
    SP6-Sall-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
    Sequencing granted in the context of the GABI-Beet project
    , local PI: Dr. Katharina Schneider, coordinator; Prof.
    Christian Jung; Sequence submission managed by
    RZPD/GABI-Primary database: http://gabi.rzpd.de"
  BASE COUNT
    0 a 16 c 0 g 0 t

  Query Match 0.7%; Score 11.2; DB 1; Length 16;
  Best Local Similarity 81.2%; Pred. No. 95;
  Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1547 GGGGCGGGGGAGGGG 1562
Db 16 GGGGCGGGGGGGGGG 1

RESULT 118
AZ861766
LOCUS
DEFINITION
  AZ861766 25 bp DNA linear GSS 21-FEB-2001
  2M0168K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0168K19 R, genomic survey sequence.
ACCESSION
  AZ861766

```

```

A2861766.1 GI:13058414
GSS.
Mus musculus (house mouse)
Mus musculus
REFERENCE
  1 (bases 1 to 25)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
  M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
  and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0168 row: K column: 19
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 25.
FEATURES
  source
  1..25
  Location/Qualifiers
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0168K19"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
  BASE COUNT
    0 a 24 c 1 g 0 t

  Query Match 0.7%; Score 11.2; DB 1; Length 25;
  Best Local Similarity 66.7%; Pred. No. 1.5e+02;
  Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 82 CACCGCGCGGCGACTTCGCGGCC 105
Db 1 CCGCGCGCGCGCGCGCGCGCG 24

RESULT 119
AZ604434
LOCUS
DEFINITION
  AZ604434 27 bp DNA linear GSS 13-DEC-2000
  1M0425I18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0425I18 F, genomic survey sequence.
ACCESSION
  AZ604434

```

```

VERSION      AZ604434.1  GI:11726624
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 27)
            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0425 row: I column: 18
            Seq primer: CGTTGTAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 27.
            Location/Qualifiers
FEATURES     source
            1..27
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone_lib="UUCIM0425118"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUCIM library"
            /notes="Vector: pKD2nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWB42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            BASE COUNT      0 a      26 c      0 g      1 t
            Query Match      0.78; Score 11; DB 1; Length 27;
            Best Local Similarity 63.0; Pred. No. 1.6e+02;
            Matches 17; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy      84  CCGCCCGCGGCGACTCGCGCCGAGC 110
            ||| ||| ||| ||| ||| ||| ||| |||
Db      1  CCCCCCCCCCCCCCTCCCCCCCCCCCC 27

RESULT 120
BM396472/c
LOCUS
DEFINITION
5009-0-21-C09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM396472

```

```

VERSION      BM396472.1  GI:18196525
KEYWORDS     EST.
SOURCE       Tetrahymena thermophila
ORGANISM     Tetrahymena thermophila
REFERENCE    Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
AUTHORS     Hymenostomatida; Tetrahymenina; Tetrahymena.
            1 (bases 1 to 15)
            Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
            J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
            plasmid inserts
JOURNAL     Unpublished
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
            Location/Qualifiers
FEATURES     source
            1..15
            /organism="Tetrahymena thermophila"
            /mol_type="mRNA"
            /strain="CU428.1"
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /note="Vector: Bluescript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
            BASE COUNT      1 a      4 c      7 g      3 t
            Query Match      0.78; Score 10.9; DB 1; Length 15;
            Best Local Similarity 85.7; Pred. No. 99;
            Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1434  CCACGCGGGCAGTC 1447
            ||| ||| ||| ||| ||| ||| ||| |||
Db      14  CCACGCGGGTCAGC 1

RESULT 121
AZ447239/c
LOCUS
DEFINITION
1M0244M18F Mouse 10kb plasmid UUCIM library Mus musculus genomic
clone UUCIM0244M18 F, genomic survey sequence.
ACCESSION
AZ447239
VERSION
AZ447239.1  GI:10599026
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0244 row: M column: 18
            Seq primer: CGTTGTAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.

```



```

FEATURES          source
1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315D09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      0 a 23 c 1 g 0 t

Query Match      0.7%; Score 10.8; DB 1; Length 24;
Best Local Similarity 68.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 84 CCGCGCGCGCGCACTCGCGCCC 105
      |||||
Db 1 CCCCCCCCCCCCCCGCGCCCC 22

RESULT 124
AZ597705
LOCUS      24 bp DNA linear GSS 13-DEC-2000
DEFINITION clone UUGC1M0411G07 R, genomic survey sequence.
ACCESSION AZ597705
VERSION    GI:11719895
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0411 row: G column: 07
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.

FEATURES          source
1. 24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0411G07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT      0 a 23 c 1 g 0 t

Query Match      0.7%; Score 10.8; DB 1; Length 24;
Best Local Similarity 68.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 84 CCGCGCGCGCGCACTCGCGCCC 105
      |||||
Db 2 CCCCCCCCCCCCCCGCGCCCC 23

RESULT 125
AZ375584
LOCUS      24 bp DNA linear GSS 02-OCT-2000
DEFINITION clone UUGC1M0125F04 F, genomic survey sequence.
ACCESSION AZ375584
VERSION    GI:10489284
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0129 row: F column: 04
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 24.

```



```

FEATURES
source
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0129F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a 23 c 1 g 0 t
Query Match      0.7%; Score 10.8; DB 1; Length 24;
Best Local Similarity 68.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 84 CCGCGCGCGCGCACTCGCGCCC 105
    |||||
DB 2 CCCCCCGCGCGCCCCCCCCCCC 23

RESULT 126
AZ764494
LOCUS      24 bp DNA linear GSS 16-FEB-2001
DEFINITION 1M0560306R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0560306 R, genomic survey sequence.
ACCESSION  AZ764494
VERSION     AZ764494.1 GI:12879515
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 24)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0560 row: E column: 06
            Seq primer: CACACGAGAACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.

FEATURES
source
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0129F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT      0 a 23 c 1 g 0 t
Query Match      0.7%; Score 10.8; DB 1; Length 24;
Best Local Similarity 68.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 84 CCGCGCGCGCGCACTCGCGCCC 105
    |||||
DB 2 CCCCCCGCGCGCCCCCCCCCCC 23

RESULT 127
AZ649949
LOCUS      27 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0519P18R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0519P18 R, genomic survey sequence.
ACCESSION  AZ649949
VERSION     AZ649949.1 GI:11783942
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 27)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL     Unpublished
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0519 row: P column: 18
            Seq primer: CACACGAGAACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 27.

```


FEATURES source

Location/Qualifiers

1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0519P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 26 c 0 g 1 t

Query Match 0.7%; Score 10.8; DB 1; Length 27;
Best Local Similarity 68.2%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 84 CCGCGCGCGCGCACTCGCGCCC 105
|||
Db 2 CCCCCCCCCCCCCCTCCCCCCC 23

RESULT 128

AZ853311
LOCUS 31 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0156L23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0156L23 F, genomic survey sequence.

ACCESSION AZ853311
VERSION AZ853311.1 GI:13041237
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 31)

REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0156 row: L column: 23
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 31.

FEATURES source

Location/Qualifiers

1. 31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0156L23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 30 c 0 g 1 t

Query Match 0.7%; Score 10.8; DB 1; Length 31;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 84 CCGCGCGCGCACTCGCGCGCGCGC 113
|||
Db 1 CCCCCCTCCCCCCCCCCCCCCCCCCC 30

RESULT 129

AZ324328
LOCUS 23 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0045B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0045B16 F, genomic survey sequence.

ACCESSION AZ324328
VERSION AZ324328.1 GI:10379937
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

REFERENCE 1 (bases 1 to 23)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0046 row: B column: 16
Seq primer: CGTGTAAACGACGCGCACT
Class: plasmid ends
High quality sequence stop: 23.

```

FEATURES
source
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0046B16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: FWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
2 a 8 c 10 g 3 t
BASE COUNT
2 a 8 c 10 g 3 t
Query Match 0.7%; Score 10.6; DB 1; Length 23;
Best Local Similarity 76.5%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 984 ACGACTCGCCACCGG 1000
|||||
Db 17 ACGCGCCGCCACCGG 1

RESULT 130
AA918967/c
LOCUS
DEFINITION
13 bp mRNA linear EST 10-JUN-1998
O182905.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1536152 3'
similar to TR:Q69566 Q69566 ; contains element PTR7 repetitive
element ;, mRNA sequence.
AA918967
AA918967.1 GI:3058857
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 1056 Std Error: 0.00
Seq primer: -40m13 fwd. Et from Amersham
High quality sequence stop: 1.

FEATURES
source
Location/Qualifiers
1..13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1536152"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kids"
/notes="Organ: Kidney; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AAGTGAAGAATTCGGCGGCAATATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
0 a 2 c 6 g 5 t
BASE COUNT
0 a 2 c 6 g 5 t
Query Match 0.7%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 73 ACACGCACACAC 84
|||||
Db 13 ACACGCACACAC 2

RESULT 131
BM396557
LOCUS
DEFINITION
13 bp mRNA linear EST 17-JAN-2002
5009-0-22-P07.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
BM396557
BM396557.1 GI:18196625
EST.
KEYWORDS
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 13)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
J., and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
1 a 4 c 6 g 2 t
BASE COUNT
1 a 4 c 6 g 2 t
Query Match 0.7%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1364 GACCGCGGGGC 1375
|||||
Db 1 GACCGCGGGGC 12

```

```

RESULT 132
BM396557/c
LOCUS
DEFINITION
5009-0-22-F07.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM396557
VERSION
BM396557.1 GI:18196625
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 13)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
1..13
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT
1 a 4 c 6 g 2 t
Query Match 0.7%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 90;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1433 GCCACCGCGGCG 1444
Db 12 GCCACCGCGGTC 1
RESULT 133
BM399961
LOCUS
DEFINITION
5009-0-63-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM399961
VERSION
BM399961.1 GI:18200014
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

```

```

FEATURES
source
Location/Qualifiers
1..14
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT
1 a 5 c 7 g 1 t
Query Match 0.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 1e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 717 ACTCGGTGGCGG 728
Db 3 ACCGGTGGCGG 14
RESULT 134
BM396011/c
LOCUS
DEFINITION
5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM396011
VERSION
BM396011.1 GI:18196064
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
source
Location/Qualifiers
1..10
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/notes="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT
0 a 4 c 5 g 1 t
Query Match 0.6%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1433 GCCACCGCGG 1442
Db 10 GCCACCGCGG 1
RESULT 135
BM398849/c
LOCUS
DEFINITION
5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM398849

```

BM398849.1 GI:18198902
 EST.
 Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE
 1 (bases 1 to 10)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
 ,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source
 1..10
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 0 a 4 c 5 g 1 t
 Query Match 0.6%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1433 GCCACCGCGG 1442
 |||||
 Db 10 GCCACCGCGG 1

RESULT 136
 BM398341/c
 LOCUS
 DEFINITION
 5009-0-44-D05.t.2 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION
 BM398341
 VERSION
 BM398341.1 GI:18198394
 SOURCE
 EST.
 Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE
 1 (bases 1 to 12)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
 ,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source
 1..12
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 1 a 4 c 6 g 1 t
 Query Match 0.6%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1433 GCCACCGCGG 1442
 |||||
 Db 10 GCCACCGCGG 1

RESULT 137
 BM399550/c
 LOCUS
 DEFINITION
 5009-0-59-C05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION
 BM399550
 VERSION
 BM399550.1 GI:18199603
 SOURCE
 EST.
 Tetrahymena thermophila
 Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 REFERENCE
 1 (bases 1 to 13)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
 ,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES
 source
 1..13
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 BASE COUNT 0 a 6 c 5 g 2 t
 Query Match 0.6%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1434 CCACCGCGG 1443
 |||||
 Db 13 CCACCGCGG 4

Search completed: December 23, 2003, 16:38:29
 Job time : 6 secs

PT Identifying two nucleotides which are separated by an interval in
PT double stranded nucleic acid using restriction endonuclease that
PT generates 5' overhang, template-directed ligation to labeled adaptors
PT and amplification -

XX
PS Example 2; Page 29; 59pp; English.

CC The invention relates to an iterative and regenerative method for
CC sequencing DNA. The method involves identifying two nucleotides which
CC are separated by an interval in double stranded (ds) nucleic acid using
CC restriction endonuclease that generates 5' overhang, template-directed
CC ligation to labeled adaptors and amplification. The method is useful
CC for identifying a first nucleotide n and a second nucleotide n+x in a
CC ds nucleic acid segment which is a genomic DNA, cDNA, a product of an
CC in vitro DNA amplification e.g., a polymerase chain reaction (PCR)
CC product or a product of a strand displacement amplification, or a
CC vector insert. It is also useful for sequencing an interval within a
CC ds nucleic acid segment in several of staggered ds molecules produced
CC from the double stranded nucleic acid segment. It is useful for
CC removing all or a part of a primer sequence from a primer extended
CC product and for automated sequencing of double-stranded DNA segments.
CC The present sequence is an adaptor oligonucleotide used to illustrate
CC the method of the invention.

SQ Sequence 24 BP; 4 A; 6 C; 11 G; 2 T; 1 other;

Query Match 1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1305 CGCTCCTGGTGCACCTGGGCCC 1327

Db 24 CACTCCTGGTGCACCTGGGCCC 2

Search completed: December 23, 2003, 16:34:55
Job time : 25 secs

DE Mouse RT-PCR primer Shh rp #1.
 XX Mouse; primer; ss; Hedgehog signalling pathway; T-cell mediated disease;
 KW T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate;
 KW ovary; T-cell activation; T-cell proliferation; lymphoma; carcinoma;
 KW autoimmune disease; inflammatory disease; proliferative disorder;
 KW viral infection; genetic immunodeficiency; neurodegenerative disease;
 KW myelodysplastic syndrome; ischaemic injury; toxin-induced disease;
 KW wasting disease; RT-PCR; reverse transcriptase; Shh; sonic hedgehog.
 XX
 OS Mus musculus.
 XX
 XX WO200280952-A2.
 PN
 XX 17-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-GB01666.
 PF
 XX 09-APR-2001; 2001GB-0008872.
 PR
 XX 09-APR-2001; 2001GB-0008873.
 PR
 XX (LORA-) LORANTIS LTD.
 PA
 XX Lamb JR, Hoyne GF, Dallman MJ, Champion BR;
 PI
 XX WPI; 2003-058470/05.
 DR
 XX
 XX Use of a modulator of Hedgehog signalling pathways for treating T-cell
 PT mediated disease or infection and diseases associated with increased or
 PT decreased T-cell apoptosis and T-cell proliferation -
 PT
 XX Example 10; Page 110; 154pp; English.
 PS
 XX The invention relates to use of a modulator of a Hedgehog signalling
 CC pathway or a modulator of a target of the pathway in the preparation of a
 CC medicament for treating T-cell mediated disease or infection or a disease
 CC or disorder associated with increased or decreased T-cell apoptosis and
 CC for modification of peripheral T-cell activation or proliferation or
 CC T-cell apoptosis, and for modulation of the Notch signalling pathway in
 CC immune cells. The modulator is useful for treating cancer of the breast,
 CC prostate or ovary, lymphomas and carcinomas, autoimmune diseases such as
 CC systemic lupus erythematosus, multiple sclerosis and diabetes,
 CC inflammatory diseases such as osteoarthritis and Crohn's disease,
 CC proliferative disorders such as atherosclerosis and psoriasis, viral
 CC infections such as AIDS and herpesviruses, genetic immunodeficiencies,
 CC neurodegenerative diseases such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as aplastic anaemia, ischaemic
 CC injuries such as myocardial infarction, toxin-induced diseases such as
 CC cirrhosis and wasting diseases such as cachexia. This sequence represents
 CC a reverse transcriptase PCR (RT-PCR) primer used in the scope of the
 CC invention.
 XX
 SQ Sequence 22 BP; 6 A; 5 C; 6 G; 5 T; 0 other;
 Query Match 1.1%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 1.9e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 661 CGACTGGGTCTACTACGAGTCC 682
 Db |||||
 22 CGACTGGGTCTACTATGATCC 1
 RESULT 67
 AAX01774/c
 ID AAX01774 standard; DNA; 24 BP.
 XX
 AC AAX01774;
 XX
 XX 09-APR-1999 (first entry)
 DT
 XX Human cystic fibrosis transmembrane conductance regulator oligo #29.

KW Cystic fibrosis transmembrane conductance regulator; sequencing;
 KW genetic identification; forensic analysis; genetic counselling;
 KW medical diagnostic; offset collection; multiplex automation; primer; ss.
 XX
 OS Synthetic.
 XX Homo sapiens.
 PN US5958671-A.
 XX
 PD 12-JAN-1999.
 XX
 XX 01-NOV-1996; 96US-0742755.
 PF
 XX 01-NOV-1996; 96US-0742755.
 PR
 XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX Jones DH;
 PI
 XX WPI; 1999-119868/10.
 DR
 XX Sequencing of double stranded nucleic acids - by an iterative and
 PT regenerative method which uses a restriction enzyme with a cleavage
 PT site separate from its recognition site
 XX
 PS Example 2; Column 52; 52pp; English.
 XX
 XX This sequence is an oligonucleotide used to describe a sequencing method
 CC which identifies the first and second nucleotides in double (ds)
 CC nucleic acid segments. The method can be used to sequence DNA, for
 CC example, in genetic identification, forensic analysis, genetic
 CC counselling or medical diagnostics. The method sequences in discrete
 CC intervals that start at one end of each DNA segment. The method
 CC overcomes problems inherent in other sequencing methods, such as the need
 CC for gel resolution of DNA fragments and the generation of artifacts
 CC caused by ss DNA secondary structures. It can be used to create offset
 CC collections of DNA segments, and sequence the segments in parallel, to
 CC provide continuous sequence information over long intervals. This method
 CC is also suitable for automation and multiplex automation to sequence
 CC large sets of segments.
 XX
 SQ Sequence 24 BP; 4 A; 6 C; 11 G; 2 T; 1 other;
 Query Match 1.1%; Score 17.2; DB 1; Length 24;
 Best Local Similarity 82.6%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1305 CGCTCTGGTGCACGTGGCGCC 1327
 Db |||||
 24 CACTCTGGTGCACGTGGCGAC 2
 RESULT 68
 AAA64229
 ID AAA64229 standard; DNA; 24 BP.
 XX
 AC AAA64229;
 XX
 XX 20-DEC-2000 (first entry)
 DT
 XX RACE PCR primer JAB73 for cDNA encoding SNORF25 receptor.
 DE
 XX
 XX SNORF25 receptor; steroid hormone disorder; epinephrine release disorder;
 KW gastrointestinal disorder; cardiovascular disorder; immune disorder;
 KW electrolyte balance disorder; respiratory disorder; endocrine disorder;
 KW musculoskeletal disorder; neuroendocrine disorder; cognitive disorder;
 KW memory disorder; somatosensory disorder; neurotransmission disorder;
 KW motor coordination disorder; sensory integration disorder; anorexia;
 KW motor integration disorder; dopaminergic function disorder; obesity;
 KW appetite disorder; somatosensory neurotransmission disorder; diabetes;
 KW olfaction disorder; autonomic nervous system disorder; pain; migraine;
 KW respiratory disorder; hypertension; psychotic behaviour; cancer;
 KW proliferative disease; wound healing; tissue regeneration;

CC agents that can modulate activity of cellular proteins involved in tissue
 CC proliferation and differentiation. Hedgehog proteins can also be used to
 CC expand a population of neural stem cells from a subject, then the cells
 CC are returned to the subject, specifically for treatment of Parkinson's or
 CC Alzheimer's diseases or spinal cord injury. Bigenic animals derived from
 CC (A) make it possible to activate otherwise silent transgenes in progeny
 CC from a simple cross since the transcription activator and the silent
 CC transgene are maintained in separate mouse lines, and abnormal expression
 CC is only induced in the bigenic animal. This eliminates the need for
 CC microinjection and genotypic screening for each experiment, and many
 CC bigenic embryos can be produced by cross-breeding.

XX Sequence 21 BP; 5 A; 6 C; 4 G; 6 T; 0 other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 557 GAGGAGTCTCTGCACTACGAG 577
 Db 21 GAGGAGTCTCTACACTATGAG 1

RESULT 64
 AAD52804
 ID AAD52804 standard; DNA; 21 BP.

XX AAD52804;
 AC
 DT 14-MAY-2003 (first entry)
 XX
 DE LipA gene sequencing PCR primer, JOM3.

XX Flour dough; baked product; noodle product; pasta product; cake; lipA;
 KW lipase; PCR; primer; ss.
 XX Unidentified.

XX WO200294123-A2.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-IB02792.

XX 18-MAY-2001; 2001GB-0012226.

XX 09-JAN-2002; 2002US-347007P.

XX (DANI-) DANISCO AS.

XX Bojlsen K, Poulsen CH, Soe JB;

XX WPI; 2003-120738/11.

XX Preparing flour dough for preparing baked products, by adding an enzyme
 PT that hydrolyses glycolipid and phospholipid, but not triglyceride
 PT and/or 1-monoglyceride, to dough components and mixing dough components

PS Disclosure; Page 106; 107pp; English.

XX The invention relates to a method of preparing flour dough for preparing
 CC baked products. The method involves adding an enzyme that hydrolyses
 CC glycolipid and phospholipid, but not triglyceride and/or 1-monoglyceride,
 CC to dough components and mixing dough components. The method is useful for
 CC preparing a flour dough which is useful for producing baked products,
 CC noodle products, pasta products and cakes. The invention also provides
 CC a method for improving the strength and machinability of doughs and the
 CC volume, softness and crumb structure of bread and other baked products.
 CC The present sequence is a PCR primer used to sequence lipase (lipA)
 CC gene. This primer is used to illustrate the method of the invention.

XX Sequence 21 BP; 0 A; 7 C; 9 G; 5 T; 0 other;

Query Match 1.1%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1020 GCTCGGGCGCGCTTCGGGG 1040
 Db 1 GCTCGTGTGCGCTTCGGGG 21

RESULT 65
 ABT03636
 ID ABT03636 standard; DNA; 25 BP.

XX ABT03636;
 AC
 DT 13-SEP-2002 (first entry)
 XX
 DE Human Hey-2 gene PCR primer SEQ ID NO: 157.

XX Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
 KW transcription factor; PCR; primer; ss.

XX Homo sapiens.

XX WO200240716-A2.

XX 23-MAY-2002.

XX 13-NOV-2001; 2001WO-US43461.

XX 16-NOV-2000; 2000US-249508P.

XX (CEMI-) CEMINES LLC.

XX Palm K;

XX WPI; 2002-537346/57.

XX Determining the presence of neoplastic molecular markers, by
 PT identifying the presence of markers in host test sample using array of
 PT neoplastic molecular marker specific reagents and analyzing the array
 PT of the reagents -

XX Example 1; Page 15; 41pp; English.

XX The present invention relates to a method for determining the presence of
 CC neoplastic molecular markers in a host, involving the use of neoplastic
 CC molecular marker specific reagents to detect such markers and analysing
 CC the array of reagents, allowing the identification of the neoplastic
 CC disease present. This can be used to determine the best treatment for
 CC cancers, in particular neural cell, lung and prostate tumours. The
 CC present sequence is a PCR primer useful for detecting the coding
 CC sequences of markers of the invention.

XX Sequence 25 BP; 4 A; 6 C; 9 G; 6 T; 0 other;

Query Match 1.1%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 195 CGCTGCTGTATGCTCGGACTGG 218
 Db 1 CACTGTGCTGCTGTGAGGACTGG 24

RESULT 66
 ABS55991/c
 ID ABS55991 standard; DNA; 22 BP.
 XX ABS55991;
 AC

XX 23-JAN-2003 (first entry)

XX PA (UUNY) UNIV NEW YORK STATE.
 XX PI Altaba ARI;
 XX DR WPI; 2001-366473/38.
 XX PT Detecting the onset or presence of skin cancer, particularly sporadic
 PT basal cell carcinoma, comprises measuring the level of Gli1 in the
 PT sample -
 XX
 XX Disclosure; Column 8; 2lpp; English.
 XX
 XX This invention relates to a method of detecting the onset or presence of
 CC sporadic basal cell carcinoma (BCC) in an animal. The method involves
 CC measuring the level of Gli1 in a sample of skin. Gli1 levels above basal
 CC or normal indicate the presence or onset of sporadic basal cell
 CC carcinoma. Gli1 is a zinc finger transcription factor down stream of
 CC secreted sonic hedgehog (shh) activation in a cascade of cytoplasmic
 CC signal transduction. Gli1 in turn can induce Shh expression in an
 CC auto regulatory manner. There are links between ectopic expression of the
 CC Gli1 gene and the development or onset of BCC. The method is useful for
 CC detecting the onset or presence of sporadic basal cell carcinoma.
 CC particularly in detecting skin cancer. The present sequence represents a
 CC PCR primer specific for human Shh cDNA. The primer is used in the method
 CC of the invention.
 XX
 XX SQ Sequence 18 BP; 4 A; 5 C; 5 G; 4 T; 0 other;
 Query Match 1.1%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 559 GGAGTCTCTGCACTACGA 576
 DB 18 GGAGTCTCTGCACTACGA 1
 RESULT 62
 AAA95383/c
 ID AAA95383 standard; DNA; 21 BP.
 XX AC AAA95383;
 XX DT 12-FEB-2001 (first entry)
 XX DE Rat Shh coding sequence PCR primer #2.
 XX KW Rat; Nurr1; tyrosine hydroxylase; catecholamine-related disease;
 XX KW Parkinson's disease; manic depression; schizophrenia; PCR primer; ss.
 XX OS Rattus norvegicus.
 XX XX WO200058451-A1.
 XX PD 05-OCT-2000.
 XX PF 21-MAR-2000; 2000WO-US07544.
 XX PR 26-MAR-1999; 99US-0277078.
 XX PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX PI Sakurada K, Palmer T, Gage FH;
 XX DR WPI; 2000-656165/63.
 XX XX Cell comprising exogenous nucleic acid inducing tyrosine hydroxylase
 PT expression useful for treating catecholamine-related diseases such as
 PT Parkinson's disease, manic depression and schizophrenia -
 XX
 XX Example 1; Page 20; 68pp; English.

CC The present invention describes the rat Nurr1 coding and protein
 CC sequences. The Nurr1 protein is involved in the induction of tyrosine
 CC hydroxylase expression in adult rat-derived hippocampal progenitor cells.
 CC The Nurr1 gene and protein can be used in the treatment of
 CC catecholamine-related diseases such as Parkinson's disease, manic
 CC depression and schizophrenia. They can also be used to induce tyrosine
 CC hydroxylase expression and identify tyrosine hydroxylase related
 CC deficiencies, which are linked to the same diseases. The present sequence
 CC is a PCR primer used in a method to differentiate adult neural progenitor
 CC cells.
 XX
 XX SQ Sequence 21 BP; 2 A; 7 C; 5 G; 7 T; 0 other;
 Query Match 1.1%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 1.5e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 604 TGACCGGACCGCAGCAAGTA 624
 DB 21 TGACCGGACCGCAGCAAGTA 1
 RESULT 63
 AAZ49111/c
 ID AAZ49111 standard; DNA; 21 BP.
 XX AC AAZ49111;
 XX DT 06-APR-2000 (first entry)
 XX DE PCR primer for mouse Shh gene.
 XX KW Upstream activating sequence; transgenic animal; regulatory DNA sequence;
 KW hedgehog gene; bigenic animal; transcriptional activating sequence;
 KW disease model; cancer; altered vascularisation; brain size regulation;
 KW autoimmune disease; tissue proliferation; Parkinson's disease; Shh;
 KW Alzheimer's disease; spinal cord injury; therapy; PCR primer; ss.
 XX OS Mus sp.
 XX XX WO9963052-A2.
 XX XX 09-DEC-1999.
 XX XX 03-JUN-1999; 99WO-US12417.
 XX PR 03-JUN-1998; 98US-0087899.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Rowitch DH, McMahon AP;
 XX XX WPI; 2000-105693/09.
 XX Transgenic animals useful as disease models, e.g. for cancer -
 XX Example 1; Page 20; 44pp; English.
 XX
 XX This sequence represents a PCR primer for the mouse Shh gene.
 CC The invention relates to a transgenic non-human animal (A) whose cells
 CC contain a non-viral regulatory DNA sequence (I) (e.g. an upstream
 CC activating sequence) linked to a recombinant hedgehog gene (II), which
 CC was introduced into the mammal, or its ancestor, at an embryonic stage.
 CC Bigenic animals (A'), derived from (A) by introducing a transcriptional
 CC activating sequence (TAS), are useful as models of disease, particularly
 CC cancer (of breast, skin, prostate, kidney, lung, or central nervous
 CC system, also primitive neuroectodermal tumours and medulloblastoma).
 CC Particularly they are used to assess the effect of misexpression of
 CC target genes on signalling pathways involving hedgehog proteins (HP)
 CC (e.g. altered vascularisation, regulation of brain size, density and
 CC cellular concentration etc.), and for assaying for a temporal requirement
 CC for HP in disease progression (particularly of cancers and autoimmune
 CC disease). The animals can be used to screen for potential therapeutic

CC producing neuroectoderm cells. It is also useful for producing
 CC differentiated or partially differentiated cells from neural ectoderm
 CC cells. The method can be also useful for maintaining neuroectoderm cells
 CC in vitro in homogeneous cell populations. It can also be used for
 CC producing genetically modified neuroectoderm cells. The cells can be used
 CC in the treatment of neuronal diseases, including Parkinson's disease,
 CC Huntington's disease, lysosomal storage diseases, multiple sclerosis,
 CC memory and behavioural disorders, and Alzheimer's disease. The method can
 CC also be used for preparation of tissue or organs for transplant. Neural
 CC crest cells produced by the method are useful for the treatment of spinal
 CC cord disorders and Schwann cells produced by the method are used for the
 CC treatment of multiple sclerosis.

XX Sequence 20 BP; 5 A; 2 C; 9 G; 4 T; 0 other;

Query Match 1.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 855 ACAGCGACTTCTCCTCCTTC 874
 Db 20 ACAGCGACTTCTCCTCCTTC 1

RESULT 59

AA15200
 ID AAX15200 standard; DNA; 24 BP.

XX AC AAX15200;

DT 25-MAR-2003 (updated)

DT 28-APR-1999 (first entry)

DE Central region sequence.

XX Double-stranded DNA; triple helix; quinoline; palindromic;
 KW quinazoline-based structure; hydrogen bonding; ds.

XX Synthetic.

XX WO9623777-A1.

XX 08-AUG-1996.

XX 29-JAN-1996; 96WO-US01473.

XX 01-FEB-1995; 95US-0384324.

XX (UYNE-) UNIV NEBRASKA.

XX Gold BI;

XX WPI; 1996-371338/37.

XX New substd. quinoline and quinazoline cpds. - are monomers for
 PT triple helix-forming oligo;nucleotide analogues useful e.g. for
 PT treating tumours or viral infection

XX Example 11; Page 57; 102pp; English.

XX The specification describes novel monomeric compositions which are
 CC substituted quinoline or quinazoline-based structures capable of
 CC hydrogen bonding specifically with interstrand purine-pyrimidine
 CC pairs in a double stranded Watson-Crick DNA molecule to form a
 CC triple-helix. The present sequence appears in the specification.
 CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 24 BP; 3 A; 9 C; 10 G; 2 T; 0 other;

Query Match 1.2%; Score 18.2; DB 1; Length 24;
 Best Local Similarity 87.0%; Pred. No. 1.5e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1001 GAGCCGAGCGTCCTCGGCGTC 1023
 Db 2 GAGCCGAGCGCGCTCGGCGTC 24

RESULT 60

AAV59458/c
 ID AAV59458 standard; DNA; 25 BP.

XX AAV59458;

DT 21-DEC-1998 (first entry)

DE Hedgehog protein derivative primer 2.

XX ds; Hedgehog protein; cancer; PCR; primer; amplification.

XX Synthetic.

XX JP10215867-A.

PD 18-AUG-1998.

XX 04-FEB-1997; 97JP-0021811.

XX 04-FEB-1997; 97JP-0021811.

XX (ASAG) ASAHI GLASS CO LTD.

XX WPI; 1998-499061/43.

XX Hedgehog protein derivative and gene encoding it - useful for
 PT prediction and diagnosis of various diseases e.g. lung cancer

XX Disclosure; Page 6; 7pp; Japanese.

XX The primers AAV59457-V59462 were used in the production of hedgehog a
 CC (hh) protein derivative may be used in the prediction and diagnosis of
 CC various diseases e.g. cancer.

XX Sequence 25 BP; 3 A; 9 C; 8 G; 5 T; 0 other;

Query Match 1.2%; Score 18.2; DB 1; Length 25;
 Best Local Similarity 87.0%; Pred. No. 1.5e+02;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 722 GTGCGGCCCAATCGGAGCGTG 744
 Db 24 GTGCGGCCCAATCGGAGCGTG 2

RESULT 61

AAH45474/c

ID AAH45474 standard; DNA; 18 BP.

XX AAH45474;

DT 07-SEP-2001 (first entry)

DE PCR primer Shh-D specific for human secreted sonic hedgehog cDNA.

XX Sporadic basal cell carcinoma; BCC; detection; Gli1; skin cancer;
 KW transcription factor; PCR primer; human; ss; sonic hedgehog; shh.

XX Homo sapiens.

XX US6238876-B1.

XX 29-MAY-2001.

XX 22-JUN-1998; 98US-0102491.

XX 20-JUN-1997; 97US-0050286.

be distinguished from adult cells in a blood specimen by (a) treating a blood specimen from a pregnant female to yield a mixture of cells comprising foetal cells and adult cells; (b) amplifying one or more mRNAs within the cells, the mRNAs being selectively expressed in target foetal cells to be distinguished but not expressed in adult blood cells; (c) performing in situ hybridisation on the cells under hybridising conditions suitable to maintain cell membranes in a substantially intact state and with a hybridisation medium comprising a detectably labelled probe complementary to the amplified mRNA that is selectively expressed in the target foetal cells but not expressed in adult blood cells; (d) removing the hybridisation medium and unhybridised probe from the mixture of cells to yield hybridised cells; and (e) detecting the labelled probe remaining in the hybridised cells; whereby cells in which the labelled probe is detected are identified as the target foetal cells; A second method for determining the presence of a target nucleotide sequence in individual foetal cells present in a cellular specimen is also provided. The methods (especially the second) is useful for detecting HIV, hepatitis viruses or herpes viruses in foetal cells, or for detecting chromosomal abnormalities in foetal cells. The present sequence represents a probe used for the detection of the Fragile X chromosome in amniocytes and in peripheral blood mononuclear cells.

Sequence 25 BP; 0 A; 9 C; 16 G; 0 U; 0 other;

Query Match 1.2%; Score 18.6; DB 1; Length 25;
 Best Local Similarity 84.0%; Pred. No. 1.4e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGGGGACGCGGGGCGCGGC 1381
 Db 1 CGCGGGGCGCGGGGCGCGGC 25

RESULT 57
 AAV62410
 ID AAV62410 standard; DNA; 20 BP.
 AC AAV62410;
 DT 02-FEB-1999 (first entry)
 DE Human Desert hedgehog gene sense PCR primer.
 XX Desert hedgehog; human; HUDHH; PCR; RACE; primer; ss.

XX Synthetic.
 OS Homo sapiens.
 XX EP874048-A2.
 XX 28-OCT-1998.
 XX 24-APR-1998; 98EP-0303187.
 XX 14-APR-1998; 98JP-0117873.
 XX 25-APR-1997; 97JP-0121578.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 FI Ariyasu T, Nakamura S, Orita K;
 DR WPI; 1998-544642/47.
 XX Human Desert hedgehog protein - and corresponding DNA and monoclonal antibody

PS Example 1-4; Page 10; 39pp; English.

CC This sense primer corresponds to nucleotides 460-479 of a cDNA clone (see AAV62396) coding for novel human Desert hedgehog protein (see AAW79596). It was used with an antisense primer (see AAV62411) in a first-step PCR amplification of human leukaemia plasma cell line ARH-77 (ATCC CRL-1621) cDNA in a modified PCR method of

CC 3'RACE. 2 Subsequent PCR amplifications (see AAV62423-26) yielded a cDNA clone (see AAV62399) encoding a C-terminal fragment (see AAW79599) of the novel human Desert hedgehog protein. Nucleotide sequences (see AAV62393-95) encoding mature and precursor forms (see AAW79593-95) of human Desert hedgehog are claimed. The Desert hedgehog DNA, protein and a claimed monoclonal antibody can be used in to elucidate hereditary morphological abnormalities in humans to establish their treatments and diagnoses.

XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 other;

Query Match 1.2%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.2e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 656 GCGTCGACTGGGTCTACTA 675
 Db 1 GCGTCGACTGGGTCTACTA 20

RESULT 59
 AAF87046/C
 ID AAF87046 standard; DNA; 20 BP.
 AC AAF87046;
 XX 18-SEP-2001 (first entry)
 DE PCR primer for Shh gene.
 XX PCR primer; neuroectoderm cell; cell production; Parkinson's disease; early primitive ectoderm-like cell; EPL cell; cell therapy;
 KW transgenic animal; gene therapy; neuronal disease; Huntington's disease;
 KW lysosomal storage disease; multiple sclerosis; memory disorder;
 KW behavioural disorder; Alzheimer's disease; organ transplant;
 KW spinal cord disorder; Shh; ss.

OS Unidentified.

XX WO200151611-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-AU000030.

XX 14-JAN-2000; 2000AU-0005098.

XX 20-APR-2000; 2000AU-0007045.

XX 27-APR-2000; 2000AU-0007143.

XX (BRES-) BRESAGEN LTD.

XX Rathjen PD, Rathjen J;

XX WPI; 2001-432908/46.

XX Producing neuroectoderm cells for treatment of Parkinson's and Alzheimer's and for transplantation comprises culturing early primitive ectoderm-like cells in conditioned medium -

PS Example 3; Page 41; 91pp; English.

CC This sequence represents a PCR primer for the Shh gene, used within the scope of the invention. The invention relates to a method for producing neuroectoderm cells (I) comprising: (a) providing a source of early primitive ectoderm-like (EPL) cells and a neural-inducing conditioned medium (CM) or extract of it; and (b) contacting the EPL cells with the CM or extract for a time sufficient to generate controlled differentiation to (I). The cells or partially differentiated progeny are useful in human, or animal cell therapy, transgenic animal production, human or animal gene therapy, the screening of pharmaceuticals that induce a biological response in neuroectoderm cells or their partially differentiated progeny and evaluation of biological molecules that direct differentiation of neural cells. The method is useful for

KW fluorescent; kit; detection; haemoglobin; rhesus; gamma globulin;
 NR; nitrogen reductase; ss.

OS Homo sapiens.

PN WO9402646-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US06828.

XX 17-JUL-1992; 92US-0915965.

XX (RERE-) RES DEV FOUND.

XX Aagari M, Blick M, Bresser J, Cubbage ML, Ju S;
 PI Prashad N;

XX WPI; 1994-048903/06.

XX Identifying foetal cells, conc. from maternal blood, using
 PT specific marker - e.g. surface antigen, before in situ
 PT hybridisation of target nucleic acid to detect viral infection,
 PT genetic abnormality, etc.

PS Disclosure; Page 73; 109pp; English.

XX Probes (AAQ55857-873) detect regions of 3 fragments of the HUMGLN
 CC gene (AAQ64058). Bases 1-91 correspond to bases 2179-2269 of HUMGLN,
 CC bases 92-314 are from 2393-2615 of HUMGLN and bases 315-443 are
 CC from 3502-3630 of HUMGLN.

CC The probes (AAQ55854-55) were used as control, positive and negative
 CC genetic testing probes. Probe (AAQ55856) was used to detect the fragile
 CC X condition (Example 14)

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 25 BP; 0 A; 9 C; 16 G; 0 U; 0 other;

Query Match 1.2%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 1.4e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGGGGACCGCGGGCGCGCGCGC 1381

Db 1 CGCGGGGCGCGCGGGCGCGCGCGC 25

RESULT 55

AAQ85271

ID AAQ85271 standard; DNA; 25 BP.

XX AAQ85271;

XX 25-MAR-2003 (updated)

DT 24-AUG-1995 (first entry)

XX Probe for Fragile X condition.

DE Prenatal diagnosis; fragile X; probe; ss.

XX Synthetic.

XX WO9503431-A1.

XX 02-FEB-1995.

XX 19-JUL-1994; 94WO-US08342.

XX 19-JUL-1993; 93US-0094710.

XX (APRO-) APROGENEX INC.

XX Bresser J, Weber WD, Ryusaki T, Prashad N, Cubbage ML, Blick M;

PI Aagari M, Poindexter BJ;

XX WPI; 1995-075255/10.

XX Identifying foetal cells in samples contg. maternal cells - used
 PT for monitoring foetus status, identifying sex or detecting
 PT genetic abnormalities or viral infection

XX Example; Page 75; 115pp; English.

XX In the example, Fragile X Chromosome is identified in amniocytes
 CC and in peripheral blood mononuclear cells. The 5' aminohexyl oligos
 CC is coupled to the fluorescent dye fluorescein. When an
 CC amplification of the CGG DNA fragment (of the X chromosome in
 CC XQ27.3) is present, there is an increase in the intensity of the
 CC signal.

CC (Updated on 25-MAR-2003 to correct PN field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 25 BP; 0 A; 9 C; 16 G; 0 U; 0 other;

Query Match 1.2%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 1.4e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGGGGACCGCGGGCGCGCGCGC 1381

Db 1 CGCGGGGCGCGGGCGCGCGCGC 25

RESULT 56

AAQ05267

ID AAX05267 standard; DNA; 25 BP.

XX AAX05267;

XX 14-APR-1999 (first entry)

XX Fragile X chromosome detecting probe.

XX Genetic testing; foetal cell; maternal; blood; pregnant; hybridisation;
 KW detection; HIV, hepatitis virus; herpes virus; chromosomal abnormality;
 KW probe; ss.

XX Synthetic.

OS Homo sapiens.

XX US5858649-A.

XX 12-JAN-1999.

XX 31-DEC-1996; 96US-0775609.

XX 17-JUL-1992; 92US-0915765.

PR 19-JUL-1993; 93US-0094710.

PR 19-JUL-1994; 94WO-US08342.

PR 17-JAN-1995; 95US-0374144.

PR 31-DEC-1996; 96US-0775609.

XX (APRO-) APROGENEX INC.

XX Aagari M, Blick M, Bresser J, Cubbage ML, Prashad N;

XX WPI; 1999-152096/13.

XX Method for distinguishing foetal cells from adult cells in blood -
 PT based on amplification and detection of mRNA selectively expressed
 PT in foetal cells

XX Example 4, 14; Column 49; 49pp; English.

PS The invention relates to a method of enriching foetal cells from
 CC maternal blood and for identifying such foetal cells. Foetal cells can

CC diseases involving cell proliferation or differentiation.

SQ Sequence 19 BP; 2 A; 6 C; 5 G; 6 T; 0 other;

Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 784 CACCAAGCTGGTGAAGGAC 802

Db 19 CACCAAGCTGGTGAAGGAC 1

RESULT 52

AAH45473

ID AAH45473 standard; DNA; 19 BP.

XX AC AAH45473;

DT 07-SEP-2001 (first entry)

XX PCR primer Shh-U2 specific for human secreted sonic hedgehog cDNA.

DE Sporadic basal cell carcinoma; BCC; detection; Gli1; skin cancer;
KW transcription factor; PCR primer; human; ss; sonic hedgehog; shh.

XX Homo sapiens.

OS US6238876-B1.

FN 29-MAY-2001.

XX 22-JUN-1998; 98US-0102491.

XX 20-JUN-1997; 97US-0050286.

XX (UUNY) UNIV NEW YORK STATE.

XX Altaba ARI;

XX WPI; 2001-366473/38.

XX Detecting the onset or presence of skin cancer, particularly sporadic
PT basal cell carcinoma, comprises measuring the level of Gli1 in the
PT sample -

XX Disclosure; Column 8; 2lpp; English.

XX This invention relates to a method of detecting the onset or presence of
CC sporadic basal cell carcinoma (BCC) in an animal. The method involves
CC measuring the level of Gli1 in a sample of skin. Gli1 levels above basal
CC or normal indicate the presence or onset of sporadic basal cell
CC carcinoma. Gli1 is a zinc finger transcription factor down stream of
CC secreted sonic hedgehog (shh) activation in a cascade of cytoplasmic
CC signal transduction. Gli1 in turn can induce Shh expression in an
CC auto regulatory manner. There are links between ectopic expression of the
CC Gli1 gene and the development or onset of BCC. The method is useful for
CC detecting the onset or presence of sporadic basal cell carcinoma,
CC particularly in detecting skin cancer. The present sequence represents a
CC PCR primer specific for human Shh cDNA. The primer is used in the
CC of the invention.

XX SQ Sequence 19 BP; 7 A; 6 C; 3 G; 3 T; 0 other;

Query Match 1.2%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 GAAGATCTCCAGAACTCC 361

Db 1 GAAGATCTCCAGAACTCC 19

RESULT 53

AAH45477

ID AAH45477 standard; DNA; 19 BP.

XX AC AAH45477;

DT 07-SEP-2001 (first entry)

XX PCR primer Shh-U1 specific for human secreted sonic hedgehog cDNA.

XX Sporadic basal cell carcinoma; BCC; detection; Gli1; skin cancer;
KW transcription factor; PCR primer; human; ss; sonic hedgehog; shh.

XX Homo sapiens.

XX US6238876-B1.

XX 29-MAY-2001.

XX 22-JUN-1998; 98US-0102491.

XX 20-JUN-1997; 97US-0050286.

XX (UUNY) UNIV NEW YORK STATE.

XX Altaba ARI;

XX WPI; 2001-366473/38.

XX Detecting the onset or presence of skin cancer, particularly sporadic
PT basal cell carcinoma, comprises measuring the level of Gli1 in the
PT sample -

XX Disclosure; Column 8; 2lpp; English.

XX This invention relates to a method of detecting the onset or presence of
CC sporadic basal cell carcinoma (BCC) in an animal. The method involves
CC measuring the level of Gli1 in a sample of skin. Gli1 levels above basal
CC or normal indicate the presence or onset of sporadic basal cell
CC carcinoma. Gli1 is a zinc finger transcription factor down stream of
CC secreted sonic hedgehog (shh) activation in a cascade of cytoplasmic
CC signal transduction. Gli1 in turn can induce Shh expression in an
CC auto regulatory manner. There are links between ectopic expression of the
CC Gli1 gene and the development or onset of BCC. The method is useful for
CC detecting the onset or presence of sporadic basal cell carcinoma,
CC particularly in detecting skin cancer. The present sequence represents a
CC PCR primer specific for human Shh cDNA. The primer is used in the
CC generation of a human Shh cDNA specific probe, which is used in the
CC course of the invention.

XX SQ Sequence 19 BP; 3 A; 5 C; 5 G; 6 T; 0 other;

Query Match 1.2%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 AGATGTCGCTGCTAGTCC 185

Db 1 AGATGTCGCTGCTAGTCC 19

RESULT 54

AAQ55856

ID AAQ55856 standard; DNA; 25 BP.

XX AC AAQ55856;

DT 25-MAR-2003 (updated)

DT 25-JUL-1994 (first entry)

XX Fragile X probe.

XX FC; foetal cells; marker; probe; hybridise; denature; dye; label;

CC cells. The method is useful for culturing undifferentiated ES cells to
 CC form differentiated neuronal cells which are useful for treating a
 CC neurological disorder, especially parkinson's disease in a patient. A
 CC gene product such as tyrosine hydroxylase, nerve growth factor (NGF),
 CC brain derived neurotrophic factor (BDNF), bFGF, glial derived growth
 CC factor (GDNF) NT-3, and NT-4/5 can be introduced into a brain of a
 CC subject. The method is useful for culturing dopaminergic, cholinergic and
 CC serotonergic neuronal cells. The differentiated neuronal cells are useful
 CC for treating neurological disorders such as Huntington's disease,
 CC Alzheimer's disease, multiple sclerosis, severe seizure disorders
 CC including epilepsy, familial dysautonomia as well as injury or trauma to
 CC the nervous system such as neurotoxic injury or disorders of mood and
 CC behavior such as addiction and schizophrenia, cerebrovascular disorders
 CC such as stroke and CNS disorders resulting from aging. Assays are useful
 CC for developing drugs capable of regulating the survival, proliferation or
 CC genesis of neuronal cells and to screen for antagonist or agonist of
 CC dopamine or serotonin. Cell cultures comprising 50%-85% neurons which
 CC comprise 20-40% dopaminergic neurons and 1-3% astrocytes are useful for
 CC studying the mechanism of neurotransmitter synthesis and release,
 CC particularly for serotonin and dopamine, neuronal cell survival, and the
 CC electrophysiochemical properties of differentiated neuronal cells.
 CC Sequences AA167692-721 represent gene-specific PCR primers for CNS and
 CC dopaminergic specific regulatory genes, used for examining the
 CC developmental progression of ES cells.

SQ Sequence 24 BP; 11 A; 6 C; 5 G; 2 T; 0 other;

Query Match 1.2%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 342 GGAAGATCTCCAGAACTCCGAGC 365

DB 1 GGAAGATCACAGAACTCCGAC 24

RESULT 50

AAV18410/C

ID AAV18410 standard; cDNA; 19 BP.

XX

AC AAV18410;

XX

DT 14-SEP-1998 (first entry)

XX

DE Human mutated sonic hedgehog (SHH) gene exon 2 PCR primer.

XX

XX Sonic hedgehog; SHH gene; HH gene; tumorigenesis; oncogenesis;

KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;

KW cell proliferation; cell differentiation; diagnosis; therapy;

KW human; PCR; primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9821227-A1.

XX

PD 22-MAY-1998.

XX

PF 12-NOV-1997; 97WO-US20227.

XX

PR 13-NOV-1996; 96US-0748591.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Bonifas J, Epstein E, Hu Z;

XX

XX WPI; 1998-297857/26.

XX

XX New nucleic acid encoding oncogenic human hedgehog protein - useful

PT for, e.g. treatment and diagnosis of cancer and diseases involving

PT cell proliferation or differentiation

XX

XX Example; Page 23; 47pp; English.

PS

XX This human sonic hedgehog (SHH) gene exon 2-specific primer was
 CC used with another exon 2-specific primer (see AAV18410) in a PCR
 CC amplification of genomic DNA from 34 independent basal cell
 CC carcinomas, 14 medulloblastomas and 6 breast carcinomas. PCR
 CC primers (see AAV18407-08 and AAV18411-12) specific for SHH exons 1 and
 CC 3 were also used. PCR products were subjected to single strand
 CC conformation polymorphism analysis. 2 Mutations (see AAV18403 and
 CC AAV18404) were identified in the SHH gene from 4 human cancers. The
 CC mutated SHH genes and the encoded polypeptides (see AAV48735 and
 CC AAV48736) can be used in methods for the treatment and diagnosis of
 CC cancer and other diseases involving cell proliferation or
 CC differentiation.

SQ Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 other;

Query Match 1.2%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 99;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 594 CCAGTCTCGTGAAGCA 712

DB 19 CCAGTCTCGTGAAGCA 1

RESULT 51

AAV18416/C

ID AAV18416 standard; cDNA; 19 BP.

XX

AC AAV18416;

XX

DT 14-SEP-1998 (first entry)

XX

DE Human mutated sonic hedgehog (SHH) gene PCR primer.

XX

XX Sonic hedgehog; SHH gene; HH gene; tumorigenesis; oncogenesis;

KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;

KW cell proliferation; cell differentiation; diagnosis; therapy;

KW human; PCR; primer; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9821227-A1.

XX

PD 22-MAY-1998.

XX

PF 12-NOV-1997; 97WO-US20227.

XX

PR 13-NOV-1996; 96US-0748591.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Bonifas J, Epstein E, Hu Z;

XX

XX WPI; 1998-297857/26.

XX

XX New nucleic acid encoding oncogenic human hedgehog protein - useful

PT for, e.g. treatment and diagnosis of cancer and diseases involving

PT cell proliferation or differentiation

XX

PS Example; Page 25; 47pp; English.

XX

XX cDNA derived from human epidermal keratinocytes was amplified by

CC 3-stage nesting using sonic hedgehog (SHH) gene stage 1 primers

CC (see AAV18413 and AAV18414), stage 2 primers (see AAV18415 and AAV18416)

CC and stage 3 primers (see AAV18417 and AAV18415). The PCR product

CC was identified as authentic SHH. A single somatic mutation

CC (see AAV18403) of the SHH gene was found in cancers arising from

CC 3 different tissues in independent patients. Another mutation (see

CC AAV18404) was identified in another cancer. The mutated SHH genes

CC and the encoded polypeptides (see AAV48735 and AAV48736) can be used in

CC methods for the treatment and diagnosis of cancer and other

XX Example 1; Page 45; 107pp; English.

PS The present sequence is a PCR primer for the sonic hedgehog gene (SHH).

CC It was used in reverse transcription PCR to determine expression patterns

CC of the SHH gene in cultured cells. These cells had been grown in low

CC oxygen conditions, and had differentiated to form various types of

CC neuronal cell. The different expression patterns can be used to determine

CC which set of conditions promotes the differentiation of each type of

CC neurone. The different cell types can be used for tissue transplantation,

CC to treat disorders such as stroke, brain and spinal cord injury,

CC Alzheimer's disease, Huntington's disease, other neurodegenerative

CC disorders, epilepsy, Parkinson's disease, neurological disorders and

CC psychiatric disorders.

XX

SQ Sequence 24 BP; 11 A; 6 C; 5 G; 2 T; 0 other;

Query Match 1.2%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 342 GGAAGATCTCCAGAACTCCGAGC 365

Db 1 GGAAGATCTCCAGAACTCCGAGC 24

RESULT 48

AA13720/C

ID AA13720 standard; DNA; 24 BP.

XX

AC AA13720;

DT 08-MAY-2002 (first entry)

XX

DE Simple sequence repeat, SSR, #17.

XX

KW Simple sequence repeat; plant; ds; SSR; ryegrass; fescue; tandem repeat;

KW cereal profiling; grass profiling; seed batch purity testing.

XX

OS Poaeae.

OS

PN NZ509193-A.

XX

PD 25-MAY-2001.

XX

PF 03-JAN-2001; 2001NZ-0509193.

XX

PR 24-DEC-1999; 99AU-0004906.

PR

PR 04-MAY-2000; 2000AU-0007310.

XX

XX (SAUS-) STATE SOUTH AUSTRALIA SOUTH AUSTRALIAN R.

PA (UYSC-) UNIV SOUTHERN CROSS.

PA (VICT-) STATE VICTORIA DEPT. NATURAL RES & ENVIRO.

PA (UYAD-) UNIV ADELAIDE.

PA (ITMA-) INT MAIZE & WHEAT IMPROVEMENT CENT.

XX

PI Forster JW, Jones ES;

XX

DR WPI; 2001-512563/56.

XX

XX New simple sequence repeats having 2 or more tandemly repeated

PT nucleotide core elements isolated from ryegrass and fescue, useful for

PT selecting of genes in grass or cereal breeding or profiling grass or

PT cereal species varieties -

XX

PS Claim 6; Page 51; 72pp; English.

XX

CC The invention relates to a substantially purified or isolated nucleic

CC acid (1) from ryegrass or fescue species including a simple sequence

CC repeat (SSR), having 2 or more tandemly repeated nucleotide core elements

CC 2-6 nucleotides in length. Also included are a nucleic acid primer

CC suitable for amplifying an SSR, identifying (M1) an SSR by preparing a

CC library of ryegrass or fescue genomic DNA enriched for SSRs and

CC identifying clones in the library containing SSRs, a library of ryegrass

CC or fescue genomic DNA enriched for SSRs prepared by the M1, selecting for

CC a gene in grass or cereal breeding by identifying an SSR that is closely

CC associated with the gene such that the SSR and the gene are

CC preferentially co-inherited, and selecting for the SSR in the

CC breeding, a method for DNA profiling grass or cereal species varieties by

CC assessing variation between SSR varieties and testing the purity of grass

CC or cereal seed batches by assessing variation within seed batch of an

CC SSR. The SSRs may be used in the selection of genes in grass or cereal

CC breeding, for profiling grass or cereal species varieties, for testing

CC the purity of grass or cereal seed batches, and for DNA profiling to

CC establish the distinct identity, uniformity and/or stability of a

CC cultivar. The present sequence is a ryegrass or fescue SSR.

XX

SQ Sequence 24 BP; 0 A; 12 C; 6 G; 6 T; 0 other;

Query Match 1.2%; Score 19.2; DB 1; Length 24;

Best Local Similarity 87.5%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GCGAGCGAGAGCGAGCGGCGCA 36

Db 24 GCGAGCGAGCGAGCGGCGCA 1

RESULT 49

AA167720

ID AA167720 standard; DNA; 24 BP.

XX

AC AA167720;

DT 27-FEB-2002 (first entry)

XX

DE Receptor Shh cDNA amplifying forward primer.

XX

KW Cell culturing; embryonic stem; ES; central nervous system; Shh;

KW dopaminergic; cholinergic; serotonergic; antiparkinsonian; neurotropic;

KW neuroprotective; anticonvulsant; tranquilizer; vulnerary; neuroleptic;

KW cerebroprotective; cell therapy; gene therapy; CNS; PCR primer; ss.

XX

OS Homo sapiens.

OS

PN WO200183715-A2.

XX

PD 08-NOV-2001.

XX

PF 01-MAY-2001; 2001WO-US14051.

XX

PR 01-MAY-2000; 2000US-201005P.

XX

XX (USGO) US GOVERNMENT.

PA (LEES) LEE S.

PA (LUME) LUMELSKY N.

PA (STUD) STUDER L.

PA (MCKA) MCKAY R D G.

XX

PI Lee S, Lumelsky N, Studer L, McKay RDG;

XX

DR WPI; 2002-049345/06.

XX

XX Culturing cells such as neuronal cells for use in treating neurological

PT disorders, comprises generating embryoid bodies from undifferentiated

PT embryonic stem cells, selecting precursor cells, expanding and

PT differentiating them -

XX

PS Example 10; Page 41; 66pp; English.

XX

CC The invention provides a method of culturing cells. The method involves

CC expanding a culture of undifferentiated embryonic stem (ES) cells,

CC generating embryoid bodies (EB), culturing the bodies to select for

CC central nervous system (CNS) precursor cells (PC), culturing PC in an

CC expansion medium comprising a neurologic factor, and differentiating and

CC culturing the expanded PC to form a culture of differentiated neuronal

```

XX 12-JAN-2001; 2001WO-AU00030.
XX 14-JAN-2000; 2000AU-0005098.
XX 20-APR-2000; 2000AU-0007045.
XX 27-APR-2000; 2000AU-0007143.
XX (BRES-) BRESAGEN LTD.
XX Rathjen PD, Rathjen J;
XX WPI; 2001-432908/46.
XX Producing neuroectoderm cells for treatment of Parkinson's and
XX Alzheimer's and for transplantation comprises culturing early primitive
XX ectoderm-like cells in conditioned medium -
XX
XX Example 3; Page 41; 91pp; English.
XX This sequence represents a PCR primer for the Shh gene, used
XX within the scope of the invention. The invention relates to a method for
XX producing neuroectoderm cells (I) comprises: (a) providing a source of
XX early primitive ectoderm-like (EPL) cells and a neural-inducing
XX conditioned medium (CM) or extract of it; and (b) contacting the EPL
XX cells with the CM or extract for a time sufficient to generate controlled
XX differentiation to (i). The cells or partially differentiated progeny are
XX useful in human, or animal cell therapy, transgenic animal production,
XX human or animal gene therapy, the screening of pharmaceutical that induce
XX a biological response in neuroectoderm cells or their partially
XX differentiated progeny and evaluation of biological molecules that
XX direct differentiation of neural cells. The method is useful for
XX producing neuroectoderm cells. It is also useful for producing
XX differentiated or partially differentiated cells from neural ectoderm
XX cells. The method can be also useful for maintaining neuroectoderm cells
XX in vitro in homogeneous cell populations. It can also be used for
XX producing genetically modified neuroectoderm cells. The cells can be used
XX in the treatment of neuronal diseases, including Parkinson's disease,
XX Huntington's disease, lysosomal storage diseases, multiple sclerosis,
XX memory and behavioural disorders, and Alzheimer's disease. The method can
XX also be used for preparation of tissue or organs for transplant. Neural
XX crest cells produced by the method are useful for the treatment of spinal
XX cord disorders and Schwann cells produced by the method are used for the
XX treatment of multiple sclerosis.
XX
XX Sequence 20 BP; 7 A; 8 C; 2 G; 3 T; 0 other;
Query Match 1.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 373 GGAAGTCAACCCCAATTACA 392
DB 1 GGAAGTCAACCCCAATTACA 20
RESULT 46
AAA27226
ID AAA27226 standard; DNA; 24 BP.
XX AAA27226;
XX 20-SEP-2000 (first entry)
XX Forward PCR primer for SHH.
XX Parkinson's disease; neurodegenerative disorder; PCR primer;
XX SHH; sonic hedgehog; ss.
XX Rattus sp.
XX WO200029550-A2.
XX 25-MAY-2000.
XX
XX 18-JAN-1999; 99WO-US27613.
XX 18-NOV-1998; 98US-0195569.
XX 22-OCT-1999; 99US-0425462.
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX Ceste M, Doyle J, Wold BJ, McKay R, Studer L;
XX WPI; 2000-387772/33.
XX Low oxygen culturing of central nervous system progenitor cells useful
XX in treatment of neurodegenerative disorders -
XX Example 1; Page 36; 80pp; English.
XX A method for increasing the differentiation of undifferentiated central
XX nervous system (CNS) cells in culture. This novel method involves
XX culturing the cells in low ambient oxygen conditions. Differentiated CNS
XX cells can be used to treat neurodegenerative diseases such as Parkinson's
XX disease. In order to determine the differentiated phenotype messenger
XX RNA levels can be measured using reverse transcription PCR. This
XX involves using PCR primers specific to certain genes. The present
XX sequence is the forward PCR primer used to monitor the message level of
XX SHH.
XX
XX Sequence 24 BP; 11 A; 6 C; 5 G; 2 T; 0 other;
Query Match 1.2%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 342 GGAAGATCTCCAGAACTCCGAGC 365
DB 1 GGAAGATCTCCAGAACTCCGAGC 24
RESULT 47
AAA30347
ID AAA30347 standard; DNA; 24 BP.
XX AAA30347;
XX 14-SEP-2000 (first entry)
XX Sonic hedgehog mRNA PCR primer #1.
XX Rat; cell differentiation; neurodegenerative disorder; stroke;
XX brain injury; spinal cord injury; Alzheimer's disease; epilepsy;
XX Huntington's disease; Parkinson's disease; neurological disorder;
XX cell transplantation; SHH; sonic hedgehog; PCR primer; ss.
XX Rattus sp.
XX WO200029549-A2.
XX 25-MAY-2000.
XX 18-NOV-1999; 99WO-US27532.
XX 18-NOV-1998; 98US-0195569.
XX 22-OCT-1999; 99US-0425462.
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX Ceste M, Doyle J, Wold BJ, Morrison SJ, Anderson D;
XX WPI; 2000-387771/33.
XX Culturing of neural crest stem cells useful for treatment of
XX neurodegenerative disorders comprises culturing in low ambient oxygen
XX conditions -

```


XX PR 26-JUN-2001; 2001JP-0193503.
XX PA (TAKE) TAKEDA CHEM IND LTD.
XX PI Hikichi Y, Inazuka M;
XX DR WPI; 2003-201422/19.
XX PT Culture method for cartilage differentiation from cells under hypoxic
PT conditions into cartilage cells applicable in cartilage
PT transplantation, and studying genes or proteins relating to joint
PT diseases -
XX PS Example 3; Page 29; 37pp; Japanese.
XX CC The present invention describes a method for cartilage differentiation
CC by culturing cells capable of differentiating into cartilage under
CC hypoxic conditions. Also described: (1) a method for producing cartilage
CC cells or cartilage by culturing the required cells under hypoxic
CC conditions; (2) drugs containing the produced cartilage cells or
CC cartilage; (3) a method for preventing or treating joint diseases by
CC transplanting an effective amount of the cartilage cells or cartilage;
CC (4) the use of the cartilage cells or cartilage for producing preventives
CC or remedies for joint diseases; (5) a method for screening genes relating
CC to cartilage differentiation or joint diseases by using any of the
CC culture methods; (6) a method for screening promoters or inhibitors of
CC cartilage differentiation by using any of the culture methods; (7) a
CC method for screening preventives or remedies for joint diseases by using
CC the culture methods; (8) drugs containing the screened promoters or
CC inhibitors of cartilage differentiation, or preventives or remedies for
CC joint diseases; (9) a method for preventing or treating joint diseases by
CC administering an effective dose of the promoters or inhibitors, or
CC preventives or remedies to mammals; and (10) the use of the promoters or
CC inhibitors, or preventives or remedies for producing drugs for joint
CC diseases. The produced cultured cartilage cells or cartilage can be used
CC in cartilage transplantation, studying genes or proteins relating to
CC joint diseases and screening drugs for their treatment, including
CC diseases of bone fracture, myeloma, osteoporosis and rheumatoid
CC arthritis. The present sequence represents a PCR primer for Indian
CC hedgehog, which is used in an example from the present invention.
XX SQ Sequence 24 BP; 3 A; 4 C; 10 G; 7 T; 0 other;
Query Match 1.4%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 56;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 650 GAGCGCGCTTCGACTGGGTGA 672
DB 1 GAGCGCGCTTCGACTGGGTGA 23
RESULT 44
ABSS5999/c
ID ABSS5999 standard; DNA; 26 BP.
XX AC ABSS5999;
XX DT 23-JAN-2003 (first entry)
XX DE Mouse RT-PCR primer Shh rp #2.
XX KW Mouse; primer: ss; Hedgehog signalling pathway; T-cell mediated disease;
KW T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate;
KW ovary; T-cell activation; T-cell proliferation; lymphoma; carcinoma;
KW autoimmune disease; inflammatory disease; proliferative disorder;
KW viral infection; genetic immunodeficiency; neurodegenerative disease;
KW myelodysplastic syndrome; ischaemic injury; toxin-induced disease;
KW wasting disease; RT-PCR; reverse transcriptase; Shh; sonic hedgehog.
XX OS Mus musculus.
XX PD

PN WO200280952-A2.
XX PD 17-OCT-2002.
XX PF 09-APR-2002; 2002WO-GB01666.
XX PR 09-APR-2001; 2001GB-0008972.
XX PR 09-APR-2001; 2001GB-0008973.
XX PA (LORA-) LORANTIS LTD.
XX PI Lamb JR, Hoyne GF, Dallman MJ, Champion BR;
XX DR WPI; 2003-058470/05.
XX PT Use of a modulator of Hedgehog signalling pathways for treating T-cell
PT mediated disease or infection and diseases associated with increased or
PT decreased T-cell apoptosis and T-cell proliferation -
XX PS Example 11; Page 110; 154pp; English.
XX CC The invention relates to use of a modulator of a Hedgehog signalling
CC pathway or a modulator of a target of the pathway in the preparation of a
CC medicament for treating T-cell mediated disease or infection or a disease
CC or disorder associated with increased or decreased T-cell apoptosis and
CC for modification of (peripheral) T-cell activation or proliferation or
CC T-cell apoptosis, and for modulation of the Notch signalling pathway in
CC immune cells. The modulator is useful for treating cancer of the breast,
CC prostate or ovary, lymphomas and carcinomas, autoimmune diseases such as
CC systemic lupus erythematosus, multiple sclerosis and diabetes,
CC inflammatory diseases such as osteoarthritis and Crohn's disease,
CC proliferative disorders such as atherosclerosis and psoriasis, viral
CC infections such as AIDS and herpesviruses, genetic immunodeficiencies,
CC neurodegenerative diseases such as Alzheimer's disease and Parkinson's
CC disease, myelodysplastic syndromes such as aplastic anaemia, ischaemic
CC injuries such as myocardial infarction, toxin-induced diseases such as
CC cirrhosis and wasting diseases such as cachexia. This sequence represents
CC a reverse transcriptase PCR (RT-PCR) primer used in the scope of the
CC invention.
XX SQ Sequence 26 BP; 3 A; 7 C; 13 G; 13 T; 0 other;
Query Match 1.3%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 87;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 332 AGGTATGAGGGGAGATCTCCAGAA 356
DB 25 AGATATGAGGGGAGATCTCCAGAA 1
RESULT 45
AAF87045
ID AAF87045 standard; DNA; 20 BP.
XX AC AAF87045;
XX DT 18-SEP-2001 (first entry)
XX DE PCR primer for Shh gene.
XX KW PCR primer; neuroectoderm cell; cell production; Parkinson's disease;
KW early primitive ectoderm-like cell; EPL cell; cell therapy;
KW transgenic animal; gene therapy; neuronal disease; Huntington's disease;
KW lysosomal storage disease; multiple sclerosis; memory disorder;
KW behavioural disorder; Alzheimer's disease; organ transplant;
XX KW spinal cord disorder; Shh; ss.
XX OS Unidentified.
XX PN WO200151611-A1.
XX PD 19-JUL-2001.

```

XX OS Synthetic.
XX PN US2002064771-A1.
XX PD 30-MAY-2002.
XX PF 06-APR-2001; 2001US-0828034.
XX PR 07-APR-2000; 2000US-195852P.
XX PA (ZHON/) ZHONG W.
XX PA (HONG/) HONG Z.
XX PA (FERR/) FERRARI E.
XX PI Zhong W, Hong Z, Ferrari E;
XX WPI; 2002-582330/62.
XX PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a
XX 3 nucleotide-long template to which a 2 nucleotide-long primer is
XX annealed, and template and primer which do not form a stable duplex in
XX the absence of HCV NS5B
XX Example; Page 6; 17pp; English.
XX CC The invention relates to a replicase complex comprising a hepatitis C
XX virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
XX complementary nucleic acid primer which is annealed to the 3' terminus of
XX the template, where the template is at least three nucleotides and the
XX primer is two or three nucleotides, and the template and primer do not
XX form a stable duplex in solution in the absence of the HCV NS5B protein.
XX The complex is useful for detecting HCV replicase activity and permits
XX establishment of sensitive RNA-dependent RNA polymerase assays to screen
XX and evaluate antiviral inhibitors and to improve the specificity and
XX efficacy of the inhibitors. The complex is also useful in the development
XX of a reliable system for determining kinetic and thermodynamic constants
XX of HCV NS5B-catalysed nucleotide incorporation and investigation of
XX mechanistic inhibitors for mis-incorporation or chain termination.
XX Specifically, the short RNA template and primer pairs are useful in
XX screening assays which are used for determining kinetic, thermodynamic
XX and mechanistic properties of NS5B replication and ultimately in the
XX development of inhibitors of NS5B. Newly identified inhibitors of
XX replicase activity may be used for developing anti-HCV pharmaceuticals.
XX Sequences ABK9271-ABK9296 represent HCV NS5B replicase RNA synthesis
XX templates.
XX Sequence 30 BP; 0 A; 25 C; 5 G; 0 U; 0 other;
XX Query Match 1.4%; Score 22; DB 1; Length 30;
XX Best Local Similarity 83.3%; Pred. No. 55;
XX Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX QY 1546 GGGGGCGGGGGAGGGGCGGGGGGGGGG 1575
XX DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 30 GGGGGCGGGGGCGGGGCGGGGGGGGGGGG 1
XX RESULT 42
XX AAD34564
XX ID AAD34564 standard; DNA; 24 BP.
XX AC AAD34564;
XX XX Shh specific forward RT-PCR primer.
XX DT 16-JUL-2002 (first entry)
XX DE
XX KW Serum response factor; SRF modulator; signal transduction; disturbance;
XX tumour invasion; tumour metastasis; auto-immune disease; wound healing;
XX lymphocyte homing; immune defense mechanism; chronic renal failure;
XX cellular malfunction; metastatic cancer; illness; hypoglycaemia; RT-PCR;
XX Shh; reverse transcription PCR; primer; ss.

```

```

XX OS Unidentified.
XX PN EP1186319-A1.
XX PD 13-MAR-2002.
XX PF 08-SEP-2000; 2000EP-0119741.
XX PR 08-SEP-2000; 2000EP-0119741.
XX PA (NORD/) NORDHEIM A.
XX PI Nordheim A;
XX WPI; 2002-271068/32.
XX PT Use of active agent stimulating expression of serum response factor,
XX its variants or components of signal transduction pathway of factor in
XX eukaryotic cells, for treating disturbances or illness e.g. cancer
XX Disclosure; Page 7; 58pp; English.
XX CC The invention relates to the use of an active agent stimulating
XX the expression and/or function of the SRF signal transduction pathway in
XX variants and/or members of the SRF signal transduction pathway in
XX eukaryotic cells for the preparation of a therapeutic drug or a
XX pharmaceutical composition for the treatment of disturbances or
XX illness such as tumour invasion, tumour metastasis, auto-immune
XX diseases, disturbances of wound healing, lymphocyte homing and
XX related cellular malfunctions. Pharmaceutical compositions of the
XX invention are used in treating diseases associated with expression
XX or misexpression of SRF target gene, which include formation of
XX diseases like metastatic cancer which is influenced by the gene
XX uPA-R, diseases like chronic renal failure, cancer and various
XX hypoglycaemias. The present sequence is Shh specific reverse
XX transcription PCR (RT-PCR) primer used in the invention.
XX Sequence 24 BP; 7 A; 8 C; 3 G; 6 T; 0 other;
XX Query Match 1.4%; Score 21.4; DB 1; Length 24;
XX Best Local Similarity 95.7%; Pred. No. 56;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 278 GCCTACAGCAGGTTTATCCCAA 300
XX DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 1 GCCTACAGCAGGTTTATCCCAA 23
XX RESULT 43
XX ABZ79785
XX ID ABZ79785 standard; DNA; 24 BP.
XX AC ABZ79785;
XX XX Indian hedgehog PCR primer SEQ ID NO:5.
XX DT 12-MAY-2003 (first entry)
XX DE
XX KW Osteopathic; antirheumatic; antiarthritic; cytostatic; cartilage;
XX cartilage differentiation; joint disease; bone fracture; myeloma;
XX osteoporosis; rheumatoid arthritis; human; Indian hedgehog;
XX PCR primer; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2003000870-A1.
XX PD 03-JAN-2003.
XX PF 25-JUN-2002; 2002WO-JP06351.

```

DE Human oligonucleotide #2 for construction of pUB55 plasmid.

KW Human; hedgehog protein; nootropic; neuroprotective; anticonvulsant;
 KW cytoskeletal; therapy; Alzheimer's disease; Parkinson's disease; injury;
 KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
 KW nervous system aging; neurodegenerative disease; immunological disease;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
 KW extracellular signalling protein; ss.

OS Homo sapiens.

XX WO200134654-A1.

XX 17-MAY-2001.

XX 02-NOV-2000; 2000WO-US30405.

XX 05-NOV-1999; 99US-0164025.

XX (BIOJ) BIOGEN INC.

XX Strauch K;

XX WPI; 2001-329075/34.

XX Novel isolated hedgehog fusion polypeptide useful for treating
 XX neurological conditions such as Alzheimer's disease, Parkinson's
 XX disease, Huntington's chorea, amyotrophic lateral sclerosis, and
 XX multiple sclerosis -

XX Example 1; Page 54; 178pp; English.

XX The present invention relates to hedgehog fusion proteins. Hedgehog
 XX proteins are a family of extracellular signalling proteins that regulate
 XX various aspects of embryonic development both in vertebrates and in
 XX invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 XX treatment of any condition or disease state for which a hedgehog or
 XX patched protein constituent is efficacious and in the diagnosis of
 XX constituents or conditions of disease states in biological system or
 XX specimens and for diagnostic purposes in non-physiological systems.
 XX Hedgehog fusion protein is useful for treating neurological conditions
 XX due to injury, aging of nervous system, including Alzheimer's disease,
 XX chronic neurodegenerative diseases of the nervous system, including
 XX Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 XX and chronic immunological diseases of nervous system including multiple
 XX sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 XX tumours and to specifically target medical therapies against cancers and
 XX tumours which express the receptor for the protein. The present sequence
 XX is an oligonucleotide used in the construction of pUB55 expression
 XX plasmid for expressing human sonic hedgehog protein in Pichia pastoris.

XX Sequence 29 BP; 3 A; 14 C; 5 G; 7 T; 0 other;

Query Match 1.4%; Score 22; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TCGGACCGGGCAGGGGTTTCG 242

DB 22 TCGGACCGGGCAGGGGTTTCG 1

RESULT 40

AAK9702/C

ID AAK9702 standard; DNA; 29 BP.

XX AC AAK9702;

XX 08-JUL-2002 (first entry)

XX Human sonic hedgehog oligonucleotide #2 SEQ ID No 37.

DE Cytostatic; ophthalmological; antirheumatic; antiarthritic; osteopathic;
 KW

KW gastrointestinal general; antiinflammatory; antiulcer; antipsoriatic;
 KW vulnerary; vasotropic; antidiabetic; cerebroprotective; immunomodulator;
 KW muscular active general; hypotensive; antilipemic; hedgehog protein;
 KW contraceptive; antiinfertility; placentation; angiogenesis; retinopathy;
 KW malignant tumour; macular degeneration; non-malignant tumour; keloid;
 KW rheumatoid arthritis; osteoarthritis; neovascular glaucoma; psoriasis;
 KW Crohn's disease; ulcerative colitis; tissue repair; diabetic retinopathy;
 KW ischaemia; inflammation; peripheral; central nervous system; cachexia;
 KW vascular disease; high blood pressure; cholesterol; ovulation; cancer;
 KW menstruation; gynaecological; endometrial lining formation;
 KW sonic hedgehog; ds.

XX Homo sapiens.

XX WO200198344-A2.

XX 27-DEC-2001.

XX 18-JUN-2001; 2001WO-US19435.

XX 16-JUN-2000; 2000US-211919P.

XX (BIOJ) BIOGEN INC.

XX Ling LE, Sanicola-nadel M;

XX WPI; 2002-291693/33.

XX Use of hedgehog polypeptide, its agonists or antagonists for modulating
 XX angiogenesis in the treatment of e.g. malignant tumors, retinopathy,
 XX macular degeneration, non-malignant tumors, rheumatoid arthritis and
 XX osteoarthritis -

XX Example 8; Page 130-131; 269pp; English.

XX The invention relates to new methods for modulating (promoting or
 XX inhibiting) angiogenesis in a subject animal using hedgehog polypeptides
 XX or its modulators. The hedgehog polypeptide or its modulators are useful
 XX for modulating angiogenesis in a subject. The antagonists are useful in
 XX the treatment of angiogenesis related disorders such as malignant
 XX tumours, retinopathy, macular degeneration, non-malignant tumours,
 XX rheumatoid arthritis, osteoarthritis, neovascular glaucoma, keloids,
 XX Crohn's disease, ulcerative colitis and psoriasis. The antagonists of the
 XX invention are also useful for the treatment of tissue repair, ischaemia,
 XX diabetic retinopathy, inflammation, peripheral or central nervous system
 XX vascular disease, cachexia and high blood pressure and cholesterol
 XX levels; for the modulation of ovulation, menstruation, placentation and
 XX endometrial lining formation and maintenance; and for the diagnosis of
 XX e.g. cancer. This polynucleotide sequence represents the DNA of a sonic
 XX hedgehog oligonucleotide of the invention.

XX Sequence 29 BP; 3 A; 14 C; 5 G; 7 T; 0 other;

Query Match 1.4%; Score 22; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TCGGACCGGGCAGGGGTTTCG 242

DB 22 TCGGACCGGGCAGGGGTTTCG 1

RESULT 41

ABK99277/C

ID ABK99277 standard; RNA; 30 BP.

XX AC ABK99277;

XX 21-OCT-2002 (first entry)

XX Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #7.

XX Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.

```

CC invention.
XX
SQ Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 other;

Query Match      1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 TGACCCCTTTAGCTACAGCA 288
Db 1 TGACCCCTTTAGCTACAGCA 22

RESULT 37
ABT03767
ID ABT03767 standard; DNA; 24 BP.
XX
AC ABT03767;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human SHH gene PCR primer SEQ ID NO: 288.
XX
KW Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
KW transcription factor; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200240716-A2.
XX
PD 23-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US43461.
XX
PR 16-NOV-2000; 2000US-249508P.
XX
PA (CEMI-) CEMINES LLC.
XX
PI Palm K;
XX
DR WPI; 2002-537346/57.
XX
PT Determining the presence of neoplastic molecular markers, by
PT identifying the presence of markers in host test sample using array of
PT neoplastic molecular marker specific reagents and analyzing the array
PT of the reagents -
XX
PS Example 1; Page 19; 41pp; English.
XX
CC The present invention relates to a method for determining the presence of
CC neoplastic molecular markers in a host, involving the use of neoplastic
CC molecular marker specific reagents to detect such markers and analyzing
CC the array of reagents, allowing the identification of the neoplastic
CC disease present. This can be used to determine the best treatment for
CC cancers, in particular neural cell, lung and prostate tumours. The
CC present sequence is a PCR primer useful for detecting the coding
CC sequences of markers of the invention.
XX
SQ Sequence 24 BP; 4 A; 4 C; 10 G; 6 T; 0 other;

Query Match      1.4%; Score 22; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGGCAGATGT 172
Db 3 GATGCTGCTGCTGGCAGATGT 24

RESULT 38
AAA28861/c
ID AAA28861 standard; DNA; 29 BP.
XX

CC AAA28861;
XX
SQ Sequence 22 BP; 6 A; 8 C; 3 G; 5 T; 0 other;

Query Match      1.4%; Score 22; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TCGGACCGGCGAGGGGTTCG 242
Db 22 TCGGACCGGCGAGGGGTTCG 1

RESULT 39
AAD09042/c
ID AAD09042 standard; DNA; 29 BP.
XX
AC AAD09042;
XX
DT 04-SEP-2001 (first entry)
XX

```

```

AC AAA28861;
XX
DT 29-AUG-2000 (first entry)
XX
DE Oligo linker for cloning sonic hedgehog fusion protein.
XX
KW Shh; hedgehog; sonic; indian; desert; antagonist; receptor; cytostatic;
KW cerebroprotective; neuroactive; hair growth inhibitor; ss.
XX
OS Synthetic.
XX
PN WO200025725-A2.
XX
PD 11-MAY-2000.
XX
PF 02-NOV-1999; 99WO-US25700.
XX
PR 02-NOV-1998; 98US-0106703.
XX
PA (BIOJ ) BIOGEN INC.
XX
PI Williams K, Rayhorn P, Garber EA, Pepinsky BR;
XX
DR WPI; 2000-365345/31.
XX
PT Polypeptide antagonists of Sonic, Indian and Desert Hedgehog proteins
PT useful for treating cancers, hair loss, nervous system disorders and as
PT diagnostic reagents
XX
PS Example 3; Page 13; 71pp; English.
XX
CC AAA28860-61 form a XhoI-EarI fragment and create the appropriate coding
CC sequence for placing Sonic hedgehog (Shh) adjacent to the alpha factor
CC leader sequence in-frame. The construct was used to produce Shh(N-10)
CC antagonist. The invention concerns Sonic, Desert and Indian HH
CC antagonists, which can bind a HH receptor but do not induce a
CC HH-dependent signaling response and methods of producing an antagonist.
CC The antagonists are produced by altering an N-terminal Cys-1 residue of
CC a mature HH polypeptide. When bound to the receptor (patched-1), the
CC HH protein when tested in an AP assay. The antagonist may also be unable
CC to induce ptc-1 and gli-1 expression. The antagonists may be used for
CC treating conditions characterized by over expression or activity of HH
CC polypeptides, such as some basal cell carcinomas, and other human
CC tumours (e.g. breast tumours, neuronal tumours and medulloblastomas)
CC which have been found to have an oncogenic mutation in the Shh gene. They
CC may also be administered to treat neoplastic or hyperlastic
CC transformations of cells of the central nervous system. Other uses
CC include control of adult neurons with regard to maintenance, functional
CC performance and aging of normal cells, repair and regeneration in
CC lesioned cells, degeneration and premature death. Additionally, they can
CC be used to inhibit hair growth (e.g. to treat trichosis and hirsutism) or
CC to prevent hair loss in patients having chemo- or radiation-therapy.
XX
SQ Sequence 29 BP; 3 A; 14 C; 5 G; 7 T; 0 other;

Query Match      1.4%; Score 22; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 TCGGACCGGCGAGGGGTTCG 242
Db 22 TCGGACCGGCGAGGGGTTCG 1

RESULT 39
AAD09042/c
ID AAD09042 standard; DNA; 29 BP.
XX
AC AAD09042;
XX
DT 04-SEP-2001 (first entry)
XX

```

ABK10414 standard; DNA; 32 BP.
 ABK10414;
 21-MAY-2002 (first entry)
 Synthetic primer sequence 5'-C30GG-3'.
 ss: 5'-C30GG-3'; double stranded DNA generation; promiscuous base;
 target molecule; primer.
 Synthetic.
 US6326143-B1.
 04-DEC-2001.
 22-MAY-1998; 98US-0083123.
 22-NOV-1996; 96WO-EP05149.
 (HOFF) ROCHE DIAGNOSTICS GMBH.
 Orum H, Seeger C;
 WPI; 2002-214947/27.
 Determining an analyte in a sample, for generating multiple double
 stranded nucleic acids, comprises employing a single primer sequence
 PT with a nucleobase sequence having affinity to the sequence contained in
 PT a target nucleic acid
 PS Example 1; Column 14; 25pp; English.

The invention relates to determining an analyte in a sample comprising
 CC (a) providing a target nucleic acid comprising a region A, a nucleobase
 CC sequence B, and a sequence I linked to the 5' terminus of the
 CC nucleobase sequence B, where the nucleobase sequence B is not specific
 CC for the analyte, and the region A specifically binds to the analyte,
 CC (b) binding the target nucleic acid to the analyte, separating the
 CC analyte bound to the target nucleic acid from the remaining part of the
 CC sample, (d) hybridising a primer to the target nucleic acid, where the
 CC primer comprises a nucleobase sequence B', and the nucleobase sequence
 CC B' hybridises to the nucleobase sequence B, (e) elongating the hybridised
 CC primer to produce an elongation product E using the target nucleic acid
 CC as a template and using nucleotides, where at least 30% of the
 CC nucleotides contain at least one promiscuous base which is capable of
 CC base pairing with each of adenine, guanine, cytosine, and thymine,
 CC (f) separating the target nucleic acid from the elongation product E,
 CC (g) hybridising a further primer which comprises the nucleobase
 CC sequence B' to the elongation product E, where the elongation product E
 CC is capable of acting as a template for the elongation of the further
 CC primer, (h) elongating the hybridised further primer of step (g) to
 CC produce an elongation product E' using the elongation product E as a
 CC template and using nucleotides, where at least 30% of the nucleotides
 CC contain at least one promiscuous base, (i) separating the elongation
 CC product E from the elongation product E', (j) hybridising a further
 CC primer comprising a nucleobase sequence B' to the target nucleic acid or
 CC the elongation product E, (k) elongating the further primer of step (j)
 CC to produce another elongation product E' using the target nucleic acid or
 CC elongation product E as a template and using nucleotides, where at least
 CC 30% of the nucleotides contain at least one promiscuous base, (l)
 CC separating product E of step (k) from the target nucleic acid or
 CC elongation product E, (m) optionally repeating steps (g) - (l) a
 CC sufficient number of times to generate a desired amount of double
 CC stranded nucleic acids and (n) determining the elongation product E
 CC and/or elongation product E' as a measure of the presence or amount of
 CC the analyte, where the lengths of the sequence I and the nucleobase
 CC sequence B are chosen such that, when the further primer hybridises to
 CC the elongation product E in step (g), the further primer spans a sequence
 CC formed by elongation of the hybridised primer of step (e) and overlaps at
 CC least a part of the 3' region of the hybridized primer of step (e) by an
 CC overlap length. The method is useful determining an analyte in a sample.

CC In particular, the method is useful for generating multiple double
 CC stranded nucleic acids. The present sequence is a primer molecule
 CC used to exemplify the method of the invention.
 XX
 SQ Sequence 32 BP; 0 A; 30 C; 2 G; 0 U; 0 other;
 Query Match 1.4%; Score 22.4; DB 1; Length 32;
 Best Local Similarity 81.2%; Pred. No. 51;
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1543 CCGGGGGCCGGGGAGGGCCGGGGAGGGGG 1574
 |||||
 Db 32 CCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1
 RESULT 36
 ABS55998
 ID ABS55998 standard; DNA; 22 BP.
 XX
 AC ABS55998;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Mouse RT-PCR primer Shh fp #2.
 XX
 KW Mouse; primer; ss; Hedgehog signalling pathway; T-cell mediated disease;
 KW T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate;
 KW ovary; T-cell activation; T-cell proliferation; lymphoma; carcinoma;
 KW autoimmune disease; inflammatory disease; proliferative disorder;
 KW viral infection; genetic immunodeficiency; neurodegenerative disease;
 KW myelodysplastic syndrome; ischaemic injury; toxin-induced disease;
 KW wasting disease; RT-PCR; reverse transcriptase; Shh; sonic hedgehog.
 XX
 OS Mus musculus.
 XX
 PN WC200280952-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 09-APR-2002; 2002WC-GB01666.
 XX
 PR 09-APR-2001; 2001GB-0008872.
 PR 09-APR-2001; 2001GB-0008873.
 XX
 PA (LORA-) LORANTIS LTD.
 XX
 PI Lamb JR, Hoyme GF, Dallman MJ, Champion BR;
 XX WPI; 2003-058470/05.
 XX
 PT Use of a modulator of Hedgehog signalling pathways for treating T-cell
 PT mediated disease or infection and diseases associated with increased or
 PT decreased T-cell apoptosis and T-cell proliferation -
 XX
 PS Example 11; Page 110; 154pp; English.
 XX
 CC The invention relates to use of a modulator of a Hedgehog signalling
 CC pathway or a modulator of a target of the pathway in the preparation of a
 CC medicament for treating T-cell mediated disease or infection or a disease
 CC or disorder associated with increased or decreased T-cell apoptosis and
 CC for modification of (peripheral) T-cell activation or proliferation or
 CC T-cell apoptosis, and for modulation of the Notch signalling pathway in
 CC immune cells. The modulator is useful for treating cancer of the breast,
 CC prostate or ovary, lymphomas and carcinomas, autoimmune diseases such as
 CC systemic lupus erythematosus, multiple sclerosis and diabetes,
 CC inflammatory diseases such as osteoarthritis and Crohn's disease,
 CC proliferative disorders such as atherosclerosis and psoriasis, viral
 CC infections such as AIDS and herpesviruses, genetic immunodeficiencies,
 CC neurodegenerative diseases such as Alzheimer's disease and Parkinson's
 CC disease, myelodysplastic syndromes such as aplastic anaemia, ischaemic
 CC injuries such as myocardial infarction, toxin-induced diseases such as
 CC cirrhosis and wasting diseases such as cachexia. This sequence represents
 CC a reverse transcriptase PCR (RT-PCR) primer used in the scope of the

[illegible]

CC neurotropic, neuroprotective, anticonvulsant, antiarrhythmic and cytostatic
 CC activities. (I) induces the expression of the BMP-2 and -4 genes, and of
 CC the Hoxd gene. (I) can be used: (i) to promote differentiation of
 CC neuronal cells and survival of the differentiated cells, specifically
 CC dopaminergic or motor neurons, proliferation of chondrocytes, and
 CC proliferation, differentiation and/or survival of mesodermal or
 CC ectodermal cells, either in cell cultures (particularly for preparation
 CC of transplants) or therapeutically; (ii) for detecting loss of response,
 CC in tissues or, to hh proteins; (iii) in drug screening (to identify
 CC (ant)agonists, useful e.g. for inhibition of spermatogenesis); and (iv)
 CC for isolation of cognate receptors. (I) may be used therapeutically to
 CC treat e.g. injuries/defects in the central or peripheral nervous systems,
 CC including Alzheimer's, Parkinson's and Huntington's diseases, or
 CC arrhythmias caused by nerve degeneration; immunological disorders of the
 CC nervous system, e.g. multiple sclerosis; neoplastic and hyperplastic
 CC alterations in the central nervous system, also to promote attachment of
 CC prostheses. The present sequence represents a PCR primer for human sonic
 CC hedgehog (shh), which is used in the exemplification of the present
 CC invention.

XX SQ Sequence 24 BP; 6 A; 5 C; 11 G; 2 T; 0 other;

Query Match 1.5%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 524 ACCGAGGCTGGACGACGAGATGCC 547
 Db 1 ACCGAGGCTGGACGACGAGATGCC 24

RESULT 31

AAV18406/c
 ID AAV18406 standard; cDNA; 25 BP.

XX AC AAV18406;
 XX 14-SEP-1998 (first entry)
 XX Human mutated sonic hedgehog (SHH) gene exon 2 PCR primer.

XX Sonic hedgehog; SHH gene; HH gene; tumorigenesis; oncogenesis;
 KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;
 KW cell proliferation; cell differentiation; diagnosis; therapy;
 KW human; PCR; primer; ss.

XX Synthetic.
 OS Homo sapiens.
 XX WO9821227-A1.

XX 22-MAY-1998.

XX 12-NOV-1997; 97WO-US20227.

XX 13-NOV-1996; 96US-0748591.

XX (REGC) UNIV CALIFORNIA.

XX Bonifas J, Epstein E, Hu Z;

XX WPI; 1998-297857/26.

XX New nucleic acid encoding oncogenic human hedgehog protein - useful
 PT for, e.g. treatment and diagnosis of cancer and diseases involving
 PT cell proliferation or differentiation

XX Example; Page 23; 47pp; English.

XX This human sonic hedgehog (SHH) gene exon 2-specific primer was
 CC used with another exon 2-specific primer (see AAV18406) in a PCR
 CC using DNA from human bacterial artificial chromosome (BAC) DNA
 CC pools. Only pools comprising a BAC that contains the sequence tag

CC defined by the primer pair will yield an amplification product.
 CC The process was continued until a single positive BAC was
 CC identified. The positive clone, BAC270A17, was digested with
 CC restriction enzymes and ligated into vectorette linkers. Mutations
 CC (see AAV18403 and AAV18404) have been identified in the SHH gene in
 CC human cancers. The mutated SHH genes and the encoded polypeptides
 CC (see AAW48735 and AAW48736) can be used in methods for the treatment
 CC and diagnosis of cancer and other diseases involving cell
 CC proliferation or differentiation.

XX SQ Sequence 25 BP; 4 A; 8 C; 8 G; 5 T; 0 other;

Query Match 1.5%; Score 23.4; DB 1; Length 25;
 Best Local Similarity 96.0%; Pred. No. 31;
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 616 CAGCAAGTACGGCATGCTGGCCGCC 640
 Db 25 CAGCAAGTACGGCATGCTGGCTGCC 1

RESULT 32

AAV62418

ID AAV62418 standard; DNA; 33 BP.

XX AC AAV62418;

XX 02-FEB-1999 (first entry)

XX Human Sonic hedgehog gene sense PCR primer.

XX Sonic hedgehog; Desert hedgehog; human; HuDHH; PCR; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX EP874048-A2.

XX 28-OCT-1998.

XX 24-APR-1998; 98EP-0303187.

XX 14-APR-1998; 98JP-0117873.

XX 25-APR-1997; 97JP-0121578.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Ariyasu T, Nakamura S, Ozita K;

XX WPI; 1998-544642/47.

XX Human Desert hedgehog protein - and corresponding DNA and monoclonal
 PT antibody

XX Example 4-1(a); Page 13; 39pp; English.

XX This sense primer is based on the human Sonic hedgehog gene. It
 CC was used with an antisense primer (see AAV62418) in the PCR
 CC amplification of human A549 (ATCC CRL-185) cDNA. A recombinant
 CC DNA clone (see AAV62400) encoding human Sonic hedgehog protein (see
 CC AAW79600) was obtained. The protein was expressed in E. coli cells
 CC and used to raise monoclonal antibodies that showed specificity for
 CC both Sonic hedgehog and for novel human Desert hedgehog proteins.
 CC DNA sequences (see AAV62393-95) encoding mature and precursor forms
 CC (see AAW79593-95) of human Desert hedgehog are claimed. The Desert
 CC hedgehog DNA, protein and a claimed monoclonal antibody can be
 CC used in to elucidate hereditary morphological abnormalities in
 CC humans to establish their treatments and diagnoses.

XX SQ Sequence 33 BP; 5 A; 8 C; 14 G; 6 T; 0 other;

Query Match 1.5%; Score 23.4; DB 1; Length 33;
 Best Local Similarity 81.8%; Pred. No. 39;

CC determining whether a patient is at the risk of disorder characterised by
 CC unwanted cell proliferation or aberrant control of differentiation. The
 CC hedgehog proteins or mimetics can be used to induce foetal neurons
 CC especially neuronal stem cells in intracerebral grafting. The protein
 CC or its mimetic can be used in the treatment of neurological conditions
 CC e.g. injury to nervous system, ischaemia resulting from stroke,
 CC Alzheimer's disease, Parkinson's disease, Huntington's chorea,
 CC amyotrophic lateral sclerosis (ALS) and multiple sclerosis. The present
 CC DNA sequence is forward PCR primer which is used for amplifying human
 CC Sonic hedgehog (Shh) gene.

XX
 SQ Sequence 24 BP; 6 A; 5 C; 11 G; 2 T; 0 other;
 Query Match 1.5%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 524 ACCGAGGCTGGGACGAAGATGGC 547
 |||||
 Db 1 ACCGAGGCTGGGACGAAGATGGC 24

RESULT 29
 AAC87097
 ID AAC87097 standard; DNA; 24 BP.
 XX AC AAC87097;
 XX AC AAC87097;
 DT 20-APR-2001 (first entry)
 XX PCR primer for cDNA encoding human sonic hedgehog protein (Shh).
 DE Hedgehog related-protein; sonic hedgehog protein; Shh; ischemia; stroke;
 KW desert hedgehog protein; Dhh; Indian hedgehog protein; Ihh; neuron;
 KW neurological condition; nervous system injury; tumour-induced injury;
 KW aging; Alzheimer's disease; chronic neurodegenerative disease;
 KW Parkinson's disease; Huntington's chorea; amyotrophic lateral sclerosis;
 KW spinocerebellar degeneration; nerve degeneration; multiple sclerosis;
 KW multiple sclerosis; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX US6165747-A.
 PN 26-DEC-2000.
 PD 05-JUN-1995; 95US-0460900.
 PF 30-DEC-1993; 93US-0176427.
 PR 14-DEC-1994; 94US-0356060.
 PR 04-MAY-1995; 95US-0435093.
 XX (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX Ingham PW, McMahon AP, Tabin CJ, Marti-gorostiza E, Bumcrot DA;
 PI WPI; 2001-079847/09.
 DR Polynucleotides encoding hedgehog proteins, useful for treating
 PT diseases of nervous system such as Alzheimer's disease, Parkinson's
 PT disease, Huntington's chorea, amyotrophic lateral sclerosis, multiple
 PT sclerosis -
 XX
 XX Example 5; Column 86; 119pp; English.
 PS
 XX PCR primers AAC87097-98 were used to amplify cDNA encoding a hedgehog
 CC related-protein. The specification describes a sonic hedgehog protein
 CC (Shh), a desert hedgehog protein (Dhh), and an Indian hedgehog protein
 CC (Ihh). The hedgehog polynucleotides are useful in diagnostic, in
 CC antisense therapy and in therapeutic assays for detecting and treating
 CC disorders involving, e.g., aberrant expression of vertebrate hedgehog
 CC homologue. Hedgehog polypeptides are useful therapeutically to enhance

CC survival of neurons and other neuron cells and in treating neurological
 CC conditions deriving from acute, subacute, or chronic injury to the
 CC nervous system, including traumatic injury, chemical injury, vascular
 CC injury and deficits (such as the ischemia resulting from stroke),
 CC together with infectious/inflammatory and induced-injury, aging
 CC of the nervous system including Alzheimer's disease, chronic
 CC neurodegenerative diseases of the nervous system, including Parkinson's
 CC disease, Huntington's chorea, amyotrophic lateral sclerosis,
 CC spinocerebellar degenerations, and chronic immunological diseases of
 CC the nervous system or affecting the nervous system, including multiple
 CC sclerosis.

XX
 SQ Sequence 24 BP; 6 A; 5 C; 11 G; 2 T; 0 other;
 Query Match 1.5%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 524 ACCGAGGCTGGGACGAAGATGGC 547
 |||||
 Db 1 ACCGAGGCTGGGACGAAGATGGC 24

RESULT 30
 ABB87569
 ID ABB87569 standard; DNA; 24 BP.
 XX AC ABB87569;
 XX AC ABB87569;
 DT 06-AUG-2002 (first entry)
 XX Human sonic hedgehog (Shh) PCR primer SHHF SEQ ID NO:43.
 DE Sonic hedgehog; Shh; desert hedgehog; Dhh; Indian hedgehog; Ihh;
 KW antiparkinsonian; antiarrhythmic; neuroprotective; anticonvulsant;
 KW cytotactic; nontropic; spermatogenesis; peripheral nervous system;
 KW central nervous system; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; arrhythmia; nerve degeneration; multiple sclerosis;
 KW immunological disorder; neoplastic; hyperplastic; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX US6384192-B1.
 PN 07-MAY-2002.
 PD 20-OCT-1997; 97US-0957874.
 PF 05-JUN-1995; 95US-0462386.
 PR 30-DEC-1993; 93US-0176427.
 PR 14-DEC-1994; 94US-0356060.
 PR 04-MAY-1995; 95US-0435093.
 XX (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX Ingham PW, McMahon AP, Tabin CJ;
 PI WPI; 2002-442817/47.
 DR New vertebrate hedgehog-related proteins, useful e.g. for promoting
 PT differentiation, survival and proliferation of cells, e.g. for treating
 PT neurodegeneration -
 XX
 XX Example 5; Column 88; 116pp; English.
 PS
 XX The present invention describes an isolated and/or recombinant
 CC polypeptide (I) comprising a hedgehog (hh) amino acid (aa) sequence
 CC encoded by a nucleic acid (II) that hybridizes under stringent conditions
 CC to 1 of 6 sequences (see ABB87544, and ABB87546 to ABB87550). (I) binds
 CC to a natural patched receptor. Specifically claimed example of (I) are
 CC given in ABB79132 and ABB79134 to ABB79138. (I) has antiparkinsonian,

XX Example; Page 23; 47pp; English.

PS This human sonic hedgehog (SHH) gene exon 2-specific primer was

CC used with another exon 2-specific primer (see AAV18406) in a PCR

CC using DNA from human bacterial artificial chromosome (BAC) DNA

CC pools. Only pools comprising a BAC that contains the sequence tag

CC defined by the primer pair will yield an amplification product.

CC The process was continued until a single positive BAC was

CC identified. The positive clone, BAC270A17, was digested with

CC restriction enzymes and ligated into vectorette linkers. Mutations

CC (see AAV18403 and AAV18404) have been identified in the SHH gene in

CC human cancers. The mutated SHH genes and the encoded polypeptides

CC (see AAW48735 and AAW48736) can be used in methods for the treatment

CC and diagnosis of cancer and other diseases involving cell

CC proliferation or differentiation.

XX Sequence 24 BP; 6 A; 5 C; 11 G; 2 T; 0 other;

XX Query Match 1.5%; Score 24; DB 1; Length 24;

XX Best Local Similarity 100.0%; Pred. No. 25;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 524 ACCGAGGCTGGGACGAAGATGCC 547

Db 1 ACCGAGGCTGGGACGAAGATGCC 24

RESULT 27

AAH76132

ID AAH76132 standard; DNA; 24 BP.

XX AC AAH76132;

XX 29-OCT-2001 (first entry)

XX Human Shh DNA amplifying primer SHH5'.

XX Hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh; Dhh;

XX desert hedgehog; cell differentiation; human; PCR primer; ss.

XX Homo sapiens.

XX US6271363-B1.

XX 07-AUG-2001.

XX 20-OCT-1997; 97US-0954698.

XX 05-JUN-1995; 95US-0462386.

XX 30-DEC-1993; 93US-0176427.

XX 14-DEC-1994; 94US-0356060.

XX 04-MAY-1995; 94US-0435093.

XX (HARD) HARVARD COLLEGE.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX Ingham PW, McMahon AP, Tabin CJ;

XX WPI; 2001-456723/49.

XX Novel nucleic acid encoding a hedgehog polypeptide, used to produce the

XX polypeptide, which is used to promote proliferation, survival, and/or

XX differentiation of neuronal and mesodermal tissue -

XX Example 5; Column 88; 118pp; English.

XX The invention relates to nucleic acids encoding hedgehog proteins

XX selected from sonic hedgehog (Shh), indian hedgehog (Ihh), desert

XX hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the

XX formation of ordered spatial arrangements of differentiated tissue in

XX vertebrates. The nucleic acid sequences are useful for producing hedgehog

XX proteins, used for promoting differentiation of, or survival of

CC differentiated, neuronal cells, and for promoting proliferation, survival

CC or differentiation of mesenchymal, endodermal or ectodermal tissue,

CC particularly chondrocytes, or testicular germ line cells. Sequences

CC AAH76132-133 represent PCR primers for amplifying a human Shh DNA.

XX Sequence 24 BP; 6 A; 5 C; 11 G; 2 T; 0 other;

XX Query Match 1.5%; Score 24; DB 1; Length 24;

XX Best Local Similarity 100.0%; Pred. No. 25;

XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 524 ACCGAGGCTGGGACGAAGATGCC 547

Db 1 ACCGAGGCTGGGACGAAGATGCC 24

RESULT 28

AAH76132

ID AAD10171 standard; DNA; 24 BP.

XX AC AAD10171;

XX 12-SEP-2001 (first entry)

XX Human Sonic hedgehog (Shh) gene amplifying forward PCR primer SHHF.

XX Human; Sonic hedgehog; Shh; morphogenic signal; neuron;

XX embryonic patterning; cell culture; cell differentiation; ischaemia;

XX cell proliferative disorder; intracerebral grating; Huntington's chorea;

XX neurological disorder; Alzheimer's disease; Parkinson's disease;

XX amyotrophic lateral sclerosis; ALS; multiple sclerosis; PCR primer; ss.

XX Homo sapiens.

XX US6261786-B1.

XX 17-JUL-2001.

XX 02-JUL-1996; 96US-0674509.

XX 30-DEC-1993; 93US-0176427.

XX 14-DEC-1994; 94US-0356060.

XX 04-MAY-1995; 95US-0435093.

XX 05-JUN-1995; 95US-0460900.

XX 05-JUN-1995; 95US-0462386.

XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.

XX (HARD) HARVARD COLLEGE.

XX Marigo V, Tabin CJ, Ingham PW, McMahon AP;

XX WPI; 2001-440859/47.

XX Screening compounds that potentiate or inhibit binding of hedgehog

XX polypeptide to naturally occurring patched receptor, comprises

XX contacting polypeptide with receptor and test compound, and detecting

XX change in binding -

XX Example 5; Column 98; 127pp; English.

XX The present invention relates to assay for screening compounds that

XX potentiate or inhibit binding of hedgehog polypeptide to naturally

XX occurring patched receptor. The hedgehog proteins comprise morphogenic

XX signals produced by embryonic patterning centres, and are involved in the

XX formation and maintenance of ordered spatial arrangements of

XX differentiated tissues in vertebrates, both adult and embryonic. The

XX proteins can be used to generate and/or maintain an array of different

XX vertebrate tissues both in vitro and in vivo. The invention also relates

XX to a method for modulating growth, differentiation or survival of a

XX mammalian cell (e.g. neuron, testicular cell) responsive to hedgehog

XX induction. Hedgehog agonists and antagonists can be used in cell culture

XX techniques to enhance survival and maintenance of neurons and various

XX vertebrate organogenic pathways. The hedgehog gene is useful in

```

PF 15-MAR-1994; 94WO-US02806.
XX
PR 15-MAR-1993; 93US-0031778.
XX
XX (UYVA ) UNIV YALE.
PA
PI Altman S, George ST, Goldberg AR, Guerrier-takada C;
PI Robertson HD, Lundberg PUH;
XX
XX WPI; 1994-316924/39.
XX
PT Diagnosis of inflammatory bowel disease - using bodily tissue as
PT well as biopsied tissues.
XX
PS Claim 1; Page 20; 71pp; English.
XX
CC A series of partial nucleic acid sequences (AAQ73438-42) determined from
CC isolated small RNA molecules specific to inflammatory bowel disease such
CC as Crohn's disease or ulcerative colitis. The sequences of the RNAs
CC were determined by alkaline hydrolysis and gel electrophoresis. The
CC nucleic acids of AAQ73440-1 were found to be homologous to a portion of
CC the human 28S rRNA (AAQ73442) when searches of nucleotide sequence
CC databases were carried out. The nucleic acids shown, or their
CC complements, can be used as probes hybridizing to, or as primers to
CC amplify, regions of the small RNAs, or their complementary nucleic acids
CC sequences, present in the diseased tissues. The sequences, or their
CC complements, were used to derive peptides (AAQ63104-116) which could be
CC utilised to generate antibodies against peptides present in the diseased
CC tissues. With this method, it is possible to perform diagnosis from
CC bodily samples as well as biopsied tissue. This allows rapid diagnosis
CC early in the course of the disease, an improvement over methods relying
CC on histopathological detection available only once the disease has become
CC overtly established.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 33 BP; 0 A; 10 C; 22 G; 0 T; 1 other;
SQ
Query Match 1.6%; Score 25; DB 1; Length 33;
Best Local Similarity 84.8%; Pred. No. 23;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1351 CAGCGCGCGGGACCGCGGGCGGGCGGCGG 1383
Db 1 CCGCGCGCGGGYGGCGGCGGGCGGCGGCGG 33

RESULT 25
AAQ91654
ID AAQ91654 standard; cDNA; 24 BP.
XX
AC AAQ91654;
XX
DT 03-MAY-1996 (first entry)
XX
DE Human sonic hedgehog protein gene primer SHHF5'.
XX
KW Human; sonic hedgehog gene; nested polymerase chain reaction; PCR;
KW fetal lung; probe; primer; diagnostic; nervous system disorder;
KW gene therapy; antibody; ss.
XX
OS Synthetic.
XX
PN WO9518856-A1.
XX
PD 13-JUL-1995.
XX
PF 30-DEC-1994; 94WO-US14992.
XX
PR 14-DEC-1994; 94US-0356060.
PR 30-DEC-1993; 93US-0176427.
XX
XX (HARD ) HARVARD COLLEGE.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

```

```

XX Ingham PW, McMahon AP, Tabin CJ;
XX
XX WPI; 1995-255060/33.
XX
PT Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful
PT to treat degenerative nervous system disorder(s) and in gene
PT therapy.
XX
XX Example 5; Page 100; 210pp; English.
XX
CC The sequences given in AAQ91654-57 are primers which were used to
CC amplify a sequence which encodes a human sonic hedgehog protein,
CC homologous to a Drosophila hedgehog protein (AAR77337). The human
CC sequence was isolated by screening of human genome DNA by nested
CC polymerase chain reaction using these primers, followed by use of a clone
CC to screen a human fetal lung 5'-stretch plus cDNA library in phage
CC lambda-gt10. A clone has been isolated from a phage library by
CC polymerase chain reaction, using primers SHHF (AAQ91654) and SHR
CC (AAQ91655), to give clone SHHP1. A 2.5-kb EcoRI CA repeat fragment is
CC amplified using primers SHHCAF (AAQ91656) and SHHCAR (AAQ91657). Probes
CC and primers derived from the sonic hedgehog sequence may be used as
CC diagnostic agents for neuromuscular, autonomic or central nervous system
CC disorders, and the gene may also be used in gene therapy. Antibodies
CC generated from the encoded protein may be used as therapeutic or research
CC reagents.
XX
XX Sequence 24 BP; 6 A; 5 C; 11 G; 2 T; 0 other;
SQ
Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
Db 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 26
AAV18405
ID AAV18405 standard; cDNA; 24 BP.
XX
AC AAV18405;
XX
DT 14-SEP-1998 (first entry)
XX
DE Human mutated sonic hedgehog (SHH) gene exon 2 PCR primer.
XX
KW Sonic hedgehog; SHH gene; HH gene; tumorigenesis; oncogenesis;
KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;
KW cell proliferation; cell differentiation; diagnosis; therapy;
KW human; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9821227-A1.
XX
PD 22-MAY-1998.
XX
PF 12-NOV-1997; 97WO-US20227.
XX
PR 13-NOV-1996; 96US-0748591.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Bonifas J, Epstein E, Hu Z;
XX
XX WPI; 1998-297857/26.
XX
PT New nucleic acid encoding oncogenic human hedgehog protein - useful
PT for, e.g. treatment and diagnosis of cancer and diseases involving
PT cell proliferation or differentiation

```

KW mutagenic primer; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2000073337-A1.
 PN 07-DEC-2000.
 XX 26-MAY-2000; 2000WO-US14741.
 XX 01-JUN-1999; 99US-0137011.
 PR 13-AUG-1999; 99US-0149016.
 XX (BIOJ) BIOGEN INC.
 PA
 XX Pepinsky RB, Taylor F, Garber E;
 XX WPI; 2001-049927/06.
 XX Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 FT polyalkylene glycol group linked to any residue other than the
 PT N-terminal and lysine residues -
 XX
 XX Example 6; Page 77; 157pp; English.
 PS
 XX The invention relates to novel polymer conjugates of hedgehog proteins
 CC which have increased bioavailability. The hedgehog proteins are
 CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
 CC glycol group, with the proviso that the polymer is not conjugated to the
 CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
 CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
 CC (Shh). Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
 CC a hedgehog fusion protein. The invention also relates to methods of
 CC defining and mapping functionally important regions of a protein by
 CC modifying accessible amino acid side chains, and determining the effect
 CC the position and/or type of modification have on the activity of the
 CC protein. The hedgehog polymer conjugates may be used in the management of
 CC various medical conditions including various neurological disorders,
 CC inflammatory and autoimmune diseases, and cancers. In particular, they
 CC may be used to prevent preventing or ameliorate neurodegenerative
 CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
 CC disease); age-associated neurological disease; neurological injury and
 CC trauma; immunological diseases of the nervous system (e.g., multiple
 CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
 CC neuroectodermal tumours. The modifications made to the hedgehog protein
 CC may result in increased half-life, altered tissue distribution (such as
 CC an improved ability to stay in the vasculature for longer periods of
 CC time), increased stability in solution, protection from proteolytic
 CC degradation, or reduced immunogenicity. In particular, the ability to
 CC remain in the vasculature for prolonged periods may allow a hedgehog
 CC protein of the invention to cross the blood-brain barrier, and an
 CC increased thermal stability would be an advantage when formulating the
 CC hedgehog protein in powder form. The present sequence represents a
 CC human Sonic hedgehog mutagenic primer used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 37 BP; 7 A; 8 C; 13 G; 9 T; 0 other;
 Query Match 2.0%; Score 32.2; DB 1; Length 37;
 Best Local Similarity 91.9%; Pred. No. 2.6;
 Matches 34; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 538 CGAAGATGGCCACCACCTCAGAGGAGTCTCTGCATAC 574
 DB 37 CGAAGATGGCCACCACCTCAGAGGAGTCTCTGCATAC 1
 RESULT 23
 ABT03768/c
 ID ABT03768 standard; DNA; 27 BP.
 XX
 AC ABT03768;
 XX 13-SEP-2002 (first entry)
 XX Human SHH gene PCR primer SEQ ID NO: 289.
 XX Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
 KW transcription factor; PCR; primer; ss.
 XX Homo sapiens.
 OS WO200240716-A2.
 PN 23-MAY-2002.
 XX 13-NOV-2001; 2001WO-US43461.
 PF 16-NOV-2000; 2000US-249508P.
 PR (CEMI-) CEMINES LLC.
 PA Palm K;
 XX WPI; 2002-537346/57.
 DR
 XX Determining the presence of neoplastic molecular markers, by
 PT identifying the presence of markers in host test sample using array of
 FT neoplastic molecular marker specific reagents and analyzing the array
 PT of the reagents -
 XX
 XX Example 1; Page 19; 41pp; English.
 PS
 XX The present invention relates to a method for determining the presence of
 CC neoplastic molecular markers in a host, involving the use of neoplastic
 CC molecular marker specific reagents to detect such markers and analysing
 CC the array of reagents, allowing the identification of the neoplastic
 CC disease present. This can be used to determine the best treatment for
 CC cancers, in particular neural cell, lung and prostate tumours. The
 CC present sequence is a PCR primer useful for detecting the coding
 CC sequences of markers of the invention.
 XX
 SQ Sequence 27 BP; 3 A; 11 C; 9 G; 4 T; 0 other;
 Query Match 1.7%; Score 27; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 755 TCGGCACGGTGCACCTGGAGCAGGC 781
 DB 27 TCGGCACGGTGCACCTGGAGCAGGC 1
 RESULT 24
 AAQ73441
 ID AAQ73441 standard; RNA; 33 BP.
 XX
 XX AAQ73441;
 XX 25-MAR-2003 (updated)
 DT 18-MAY-1995 (first entry)
 XX Crohn's disease/ulcerative colitis 3' RNA homologous to 26S rRNA.
 DE
 XX Inflammatory bowel disease; Crohn's disease; ulcerative colitis;
 KW probe; primer; amplify; small RNA; disease; tissue; antibody; biopsy;
 XX diagnosis; histopathology; detection; human; ss.
 OS Synthetic.
 XX WO9421662-A1.
 PN 29-SEP-1994.
 XX

XX PS Example 6; Page 77; 157pp; English.

XX CC The invention relates to novel polymer conjugates of hedgehog proteins

XX CC which have increased bioavailability. The hedgehog proteins are

XX CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene

XX CC glycol group, with the proviso that the polymer is not conjugated to the

XX CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog

XX CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog

XX CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be

XX CC a hedgehog fusion protein. The invention also relates to methods of

XX CC defining and mapping functionally important regions of a protein by

XX CC modifying accessible amino acid side chains, and determining the effect

XX CC the position and/or type of modification have on the activity of the

XX CC protein. The hedgehog polymer conjugates may be used in the management of

XX CC various medical conditions including various neurological disorders,

XX CC inflammatory and autoimmune diseases, and cancers. In particular, they

XX CC may be used to prevent preventing or ameliorate neurodegenerative

XX CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's

XX CC disease), age-associated neurological diseases of the nervous system (e.g., multiple

XX CC sclerosis); stroke; and malignant gliomas, medulloblastomas and

XX CC neuroectodermal tumours. The modifications made to the hedgehog protein

XX CC may result in increased half-life, altered tissue distribution (such as

XX CC an improved ability to stay in the vasculature for longer periods of

XX CC time), increased stability in solution, protection from proteolytic

XX CC degradation, or reduced immunogenicity. In particular, the ability to

XX CC remain in the vasculature for prolonged periods may allow a hedgehog

XX CC protein of the invention to cross the blood-brain barrier, and an

XX CC increased thermal stability would be an advantage when formulating the

XX CC hedgehog protein in powder form. The present sequence represents a

XX CC human Sonic hedgehog mutagenic primer used in an exemplification of the

XX CC invention.

XX SQ Sequence 37 BP; 6 A; 10 C; 12 G; 9 T; 0 other;

Query Match 2.1%; Score 33.8; DB 1; Length 37;

Best Local Similarity 94.6%; Pred. No. 1.6;

Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 538 CGAAGATGGCCACCTCAGAGGAGTCTCGCACTAC 574

DB 37 CGAAGATGGCCACCTCAGAGGAGTCTCGCACTAC 1

RESULT 21

AAF27041/C

ID AAF27041 standard; DNA; 35 BP.

XX AC AAF27041;

XX DT 30-MAR-2001 (first entry)

XX DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:45.

XX KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;

XX KW bioavailability; formulation; neurological disorder;

XX KW inflammatory disorder; autoimmune disorder; cancer;

XX KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;

XX KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;

XX KW malignant glioma; medulloblastoma; neuroectodermal tumour;

XX KW mutagenic primer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200073337-A1.

XX PD 07-DEC-2000.

XX PF 26-MAY-2000; 2000WO-US14741.

XX PR 01-JUN-1999; 99US-0137011.

PR 13-AUG-1999; 99US-0149016.

PA (BIOJ) BIOGEN INC.

XX PI Pepinsky RB, Taylor P, Garber E;

XX DR WPI; 2001-049927/06.

XX PT Modified hedgehog protein, useful in the treatment of Parkinson's

XX PT disease and Huntington's chorea, comprises a polymer containing a

XX PT polyalkylene glycol group linked to any residue other than the

XX PT N-terminal and lysine residues -

PS Example 6; Page 77; 157pp; English.

XX CC The invention relates to novel polymer conjugates of hedgehog proteins

XX CC which have increased bioavailability. The hedgehog proteins are

XX CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene

XX CC glycol group, with the proviso that the polymer is not conjugated to the

XX CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog

XX CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog

XX CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be

XX CC a hedgehog fusion protein. The invention also relates to methods of

XX CC defining and mapping functionally important regions of a protein by

XX CC modifying accessible amino acid side chains, and determining the effect

XX CC the position and/or type of modification have on the activity of the

XX CC protein. The hedgehog polymer conjugates may be used in the management of

XX CC various medical conditions including various neurological disorders,

XX CC inflammatory and autoimmune diseases, and cancers. In particular, they

XX CC may be used to prevent preventing or ameliorate neurodegenerative

XX CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's

XX CC disease); age-associated neurological diseases of the nervous system (e.g., multiple

XX CC sclerosis); stroke; and malignant gliomas, medulloblastomas and

XX CC neuroectodermal tumours. The modifications made to the hedgehog protein

XX CC may result in increased half-life, altered tissue distribution (such as

XX CC an improved ability to stay in the vasculature for longer periods of

XX CC time), increased stability in solution, protection from proteolytic

XX CC degradation, or reduced immunogenicity. In particular, the ability to

XX CC remain in the vasculature for prolonged periods may allow a hedgehog

XX CC protein of the invention to cross the blood-brain barrier, and an

XX CC increased thermal stability would be an advantage when formulating the

XX CC hedgehog protein in powder form. The present sequence represents a

XX CC human Sonic hedgehog mutagenic primer used in an exemplification of the

XX CC invention.

XX SQ Sequence 35 BP; 8 A; 15 C; 9 G; 3 T; 0 other;

Query Match 2.1%; Score 33.4; DB 1; Length 35;

Best Local Similarity 97.1%; Pred. No. 1.7;

Matches 34; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 639 GCCTGGCGGTGGAGGCCGCTTCGACTGGGTGTAC 673

DB 35 GCCTGGCGGTGGAGGCCGCTTCGACTGGGTGTAC 1

RESULT 22

AAF27040/C

ID AAF27040 standard; DNA; 37 BP.

XX AC AAF27040;

XX DT 30-MAR-2001 (first entry)

XX DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:44.

XX KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;

XX KW bioavailability; formulation; neurological disorder;

XX KW inflammatory disorder; autoimmune disorder; cancer;

XX KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;

XX KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;

XX KW malignant glioma; medulloblastoma; neuroectodermal tumour;

CC an improved ability to stay in the vasculature for longer periods of
 CC time), increased stability in solution, protection from proteolytic
 CC degradation, or reduced immunogenicity. In particular, the ability to
 CC remain in the vasculature for prolonged periods may allow a hedgehog
 CC protein of the invention to cross the blood-brain barrier, and an
 CC increased thermal stability would be an advantage when formulating the
 CC hedgehog protein in powder form. The present sequence represents a
 CC human Sonic hedgehog mutagenic primer used in an exemplification of the
 CC invention.

XX Sequence 39 BP; 7 A; 12 C; 13 G; 7 T; 0 other;

Query Match 2.3%; Score 35.8; DB 1; Length 39;
 Best Local Similarity 94.9%; Pred. No. 0.87; 2; Indels 0; Gaps 0;
 Matches 37; Conservative 0; Mismatches 2

QY 597 CCACGCTCTGACCGGACCGGACGAGTACGCGCATGCTGG 635
 DB 39 CCACGCTCTGACCGGATCGCTGCAAGTACGCGCATGCTGG 1

RESULT 19

AAF27035/c
 ID AAF27035 standard; DNA; 42 BP.

XX AAF27035;

XX 30-MAR-2001 (first entry)

DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:39.

XX Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200073337-A1.

PD 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14741.

XX 01-JUN-1999; 99US-0137011.

XX 13-AUG-1999; 99US-0149016.

XX (BIOJ) BIOGEN INC.

XX Pepinsky RB, Taylor F, Garber E;

XX WPI; 2001-049927/06.

XX Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the
 PT N-terminal and lysine residues -

PS Example 6; Page 77; 157pp; English.

XX The invention relates to novel polymer conjugates of hedgehog proteins
 CC which have increased bioavailability. The hedgehog proteins are
 CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
 CC glycol group, with the proviso that the polymer is not conjugated to the
 CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
 CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
 CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
 CC a hedgehog fusion protein. The invention also relates to methods of
 CC defining and mapping functionally important regions of a protein by

CC modifying accessible amino acid side chains, and determining the effect
 CC the position and/or type of modification have on the activity of the
 CC protein. The hedgehog polymer conjugates may be used in the management of
 CC various medical conditions including various neurological disorders,
 CC inflammatory and autoimmune diseases, and cancers. In particular, they
 CC may be used to prevent preventing or ameliorate neurodegenerative
 CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
 CC disease); age-associated neurological disease; neurological injury and
 CC trauma; immunological diseases of the nervous system (e.g., multiple
 CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
 CC neuroectodermal tumours. The modifications made to the hedgehog protein
 CC may result in increased half-life, altered tissue distribution (such as
 CC an improved ability to stay in the vasculature for longer periods of
 CC time), increased stability in solution, protection from proteolytic
 CC degradation, or reduced immunogenicity. In particular, the ability to
 CC remain in the vasculature for prolonged periods may allow a hedgehog
 CC protein of the invention to cross the blood-brain barrier, and an
 CC increased thermal stability would be an advantage when formulating the
 CC hedgehog protein in powder form. The present sequence represents a
 CC human Sonic hedgehog mutagenic primer used in an exemplification of the
 CC invention.

XX Sequence 42 BP; 11 A; 11 C; 10 G; 10 T; 0 other;

Query Match 2.3%; Score 35.6; DB 1; Length 42;

Best Local Similarity 90.5%; Pred. No. 0.98;

Matches 38; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 445 GACTCAGAGGTGTAAGGACAAAGTTGACCGCTTTGGCCATCTC 486

DB 42 GACTCAGAGGTGTAAGGACTGCTTAAACGCTTTGGCCATCTC 1

RESULT 20

AAF27037/c

ID AAF27037 standard; DNA; 37 BP.

XX AAF27037;

XX 30-MAR-2001 (first entry)

DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:41.

XX Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200073337-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14741.

XX 01-JUN-1999; 99US-0137011.

XX 13-AUG-1999; 99US-0149016.

XX (BIOJ) BIOGEN INC.

XX Pepinsky RB, Taylor F, Garber E;

XX WPI; 2001-049927/06.

XX Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the
 PT N-terminal and lysine residues -

XX AC AAF27025;
 XX DE 30-MAR-2001 (first entry)
 XX DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:29.
 XX DE
 XX KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 XX KW bioavailability; formulation; neurological disorder;
 XX KW inflammatory disorder; autoimmune disorder; cancer;
 XX KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 XX KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 XX KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 XX KW mutagenic primer; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200073337-A1.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US14741.
 XX PR 01-JUN-1999; 99US-0137011.
 XX PR 13-AUG-1999; 99US-0149016.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Pepinsky RB, Taylor F, Garber E;
 XX WPI; 2001-049927/06.
 XX DR
 XX PT Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the
 PT N-terminal and lysine residues -
 XX Example 2; Page 67; 157pp; English.
 XX PS
 CC The invention relates to novel polymer conjugates of hedgehog proteins
 CC which have increased bioavailability. The hedgehog proteins are
 CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
 CC glycol group, with the proviso that the polymer is not conjugated to the
 CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
 CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
 CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
 CC a hedgehog fusion protein. The invention also relates to methods of
 CC defining and mapping functionally important regions of a protein by
 CC modifying accessible amino acid side chains, and determining the effect
 CC the position and/or type of modification have on the activity of the
 CC protein. The hedgehog polymer conjugates may be used in the management of
 CC various medical conditions including various neurological disorders,
 CC inflammatory and autoimmune diseases, and cancers. In particular, they
 CC may be used to prevent preventing or ameliorate neurodegenerative
 CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
 CC disease); age-associated neurological disease; neurological injury and
 CC trauma; immunological diseases of the nervous system (e.g., multiple
 CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
 CC neuroectodermal tumours. The modifications made to the hedgehog protein
 CC may result in increased half-life, altered tissue distribution (such as
 CC time), increased stability in solution, protection from proteolytic
 CC degradation, or reduced immunogenicity. In particular, the ability to
 CC remain in the vasculature for prolonged periods may allow a hedgehog
 CC protein of the invention to cross the blood-brain barrier, and an
 CC increased thermal stability would be an advantage when formulating the
 CC hedgehog protein in powder form. The present sequence represents a
 CC human Sonic hedgehog mutagenic primer used in an exemplification of the
 CC invention.
 XX SQ Sequence 49 BP; 8 A; 18 C; 9 G; 14 T; 0 other;

Query Match 2.3%; Score 36; DB 1; Length 49;
 Best Local Similarity 88.6%; Pred. NO. 0.98;
 Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 703 GGTGAAGCAGAGACTCGTGGCGCCCAATCGGAGGCTCT 746
 Db 49 GGTGAAGCAGAGACTCGTGGCGCCCAATCGGAGGCTCT 6
 RESULT 18
 AAF27038/c
 ID AAF27038 standard; DNA; 39 BP.
 XX AC AAF27038;
 XX DT 30-MAR-2001 (first entry)
 XX DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:42.
 XX KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200073337-A1.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US14741.
 XX PR 01-JUN-1999; 99US-0137011.
 XX PR 13-AUG-1999; 99US-0149016.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Pepinsky RB, Taylor F, Garber E;
 XX WPI; 2001-049927/06.
 XX DR
 XX PT Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the
 PT N-terminal and lysine residues -
 XX Example 6; Page 77; 157pp; English.
 XX PS
 CC The invention relates to novel polymer conjugates of hedgehog proteins
 CC which have increased bioavailability. The hedgehog proteins are
 CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
 CC glycol group, with the proviso that the polymer is not conjugated to the
 CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
 CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
 CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
 CC a hedgehog fusion protein. The invention also relates to methods of
 CC defining and mapping functionally important regions of a protein by
 CC modifying accessible amino acid side chains, and determining the effect
 CC the position and/or type of modification have on the activity of the
 CC protein. The hedgehog polymer conjugates may be used in the management of
 CC various medical conditions including various neurological disorders,
 CC inflammatory and autoimmune diseases, and cancers. In particular, they
 CC may be used to prevent preventing or ameliorate neurodegenerative
 CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
 CC disease); age-associated neurological disease; neurological injury and
 CC trauma; immunological diseases of the nervous system (e.g., multiple
 CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
 CC neuroectodermal tumours. The modifications made to the hedgehog protein
 CC may result in increased half-life, altered tissue distribution (such as

```

PR 01-JUN-1999; 99US-0137011.
PR 13-AUG-1999; 99US-0149016.
XX (BIOJ ) BIOGEN INC.
XX
XX Pepinsky RB, Taylor F, Garber E;
XX MPI; 2001-049927/06.
XX
XX Modified hedgehog protein, useful in the treatment of Parkinson's
XX disease and Huntington's chorea, comprises a polymer containing a
XX polyalkylene glycol group linked to any residue other than the
XX N-terminal and lysine residues -
XX
XX Example 6; Page 77; 157pp; English.
XX
XX The invention relates to novel polymer conjugates of hedgehog proteins
XX which have increased bioavailability. The hedgehog proteins are
XX conjugated to a non-naturally-occurring polymer comprising a polyalkylene
XX glycol group, with the proviso that the polymer is not conjugated to the
XX N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
XX protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
XX (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
XX a hedgehog fusion protein. The invention also relates to methods of
XX defining and mapping functionally important regions of a protein by
XX various medical conditions including various neurological disorders,
XX inflammatory and autoimmune diseases, and cancers. In particular, they
XX may be used to prevent preventing or ameliorate neurodegenerative
XX disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
XX disease); age-associated neurological disease; neurological injury and
XX trauma; immunological diseases of the nervous system (e.g., multiple
XX sclerosis); stroke; and malignant gliomas, medulloblastomas and
XX neuroectodermal tumours. The modifications made to the hedgehog protein
XX may result in increased half-life, altered tissue distribution (such as
XX an improved ability to stay in the vasculature for longer periods of
XX time), increased stability in solution, protection from proteolytic
XX degradation, or reduced immunogenicity. In particular, the ability to
XX remain in the vasculature for prolonged periods may allow a hedgehog
XX protein of the invention to cross the blood-brain barrier, and an
XX increased thermal stability would be an advantage when formulating the
XX hedgehog protein in powder form. The present sequence represents a
XX human Sonic hedgehog mutagenic primer used in an exemplification of the
XX invention.
XX
XX Sequence 42 BP; 11 A; 14 C; 9 G; 8 T; 0 other;
XX
XX Query Match 2.4%; Score 37.2; DB 1; Length 42;
XX Best Local Similarity 92.9%; Pred. No. 0.59;
XX Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 474 CTTTGGCCATCTCGGTGATGAACAGTGGCCAGGAGTGAAC 515
XX 42 CTTTGGCCATCTCGGTGATGTCAGTGGCCAGGAGTGAAC 1
XX
XX RESULT 16
XX AAF27039/C
XX ID AAF27039 standard; DNA; 38 BP.
XX
XX AC AAF27039;
XX
XX XX 30-MAR-2001 (first entry)
XX
XX DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:43.
XX
XX KW Sonic hedgehog; Shh; polymer conjugate; polyalkylene glycol group;
XX bioavailability; formulation; neurological disorder;
XX inflammatory disorder; autoimmune disorder; cancer;
XX neurodegenerative disorder; Parkinson's disease; Huntington's disease;
XX Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
XX
XX KW malignant glioma; medulloblastoma; neuroectodermal tumour;
XX mutagenic primer; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FN WO200073337-A1.
XX
XX PD 07-DEC-2000.
XX
XX XX 26-MAY-2000; 2000WO-US14741.
XX
XX PF 01-JUN-1999; 99US-0137011.
XX PR 13-AUG-1999; 99US-0149016.
XX
XX XX (BIOJ ) BIOGEN INC.
XX
XX PI Pepinsky RB, Taylor F, Garber E;
XX MPI; 2001-049927/06.
XX
XX DR Modified hedgehog protein, useful in the treatment of Parkinson's
XX PT disease and Huntington's chorea, comprises a polymer containing a
XX PT polyalkylene glycol group linked to any residue other than the
XX PT N-terminal and lysine residues -
XX
XX XX Example 6; Page 77; 157pp; English.
XX
XX CC The invention relates to novel polymer conjugates of hedgehog proteins
XX CC which have increased bioavailability. The hedgehog proteins are
XX CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
XX CC glycol group, with the proviso that the polymer is not conjugated to the
XX CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
XX CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
XX CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
XX CC a hedgehog fusion protein. The invention also relates to methods of
XX CC defining and mapping functionally important regions of a protein by
XX CC various medical conditions including various neurological disorders,
XX CC inflammatory and autoimmune diseases, and cancers. In particular, they
XX CC may be used to prevent preventing or ameliorate neurodegenerative
XX CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
XX CC disease); age-associated neurological disease; neurological injury and
XX CC trauma; immunological diseases of the nervous system (e.g., multiple
XX CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
XX CC neuroectodermal tumours. The modifications made to the hedgehog protein
XX CC may result in increased half-life, altered tissue distribution (such as
XX CC an improved ability to stay in the vasculature for longer periods of
XX CC time), increased stability in solution, protection from proteolytic
XX CC degradation, or reduced immunogenicity. In particular, the ability to
XX CC remain in the vasculature for prolonged periods may allow a hedgehog
XX CC protein of the invention to cross the blood-brain barrier, and an
XX CC increased thermal stability would be an advantage when formulating the
XX CC hedgehog protein in powder form. The present sequence represents a
XX CC human Sonic hedgehog mutagenic primer used in an exemplification of the
XX CC invention.
XX
XX SQ Sequence 42 BP; 11 A; 14 C; 9 G; 8 T; 0 other;
XX
XX Query Match 2.4%; Score 37.2; DB 1; Length 42;
XX Best Local Similarity 92.9%; Pred. No. 0.59;
XX Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 474 CTTTGGCCATCTCGGTGATGAACAGTGGCCAGGAGTGAAC 515
XX 42 CTTTGGCCATCTCGGTGATGTCAGTGGCCAGGAGTGAAC 1
XX
XX DB
XX
XX RESULT 16
XX AAF27039/C
XX ID AAF27039 standard; DNA; 38 BP.
XX
XX AC AAF27039;
XX
XX XX 30-MAR-2001 (first entry)
XX
XX DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:43.
XX
XX KW Sonic hedgehog; Shh; polymer conjugate; polyalkylene glycol group;
XX bioavailability; formulation; neurological disorder;
XX inflammatory disorder; autoimmune disorder; cancer;
XX neurodegenerative disorder; Parkinson's disease; Huntington's disease;
XX Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
XX
XX KW malignant glioma; medulloblastoma; neuroectodermal tumour;
XX mutagenic primer; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FN WO200073337-A1.
XX
XX PD 07-DEC-2000.
XX
XX XX 26-MAY-2000; 2000WO-US14741.
XX
XX PF 01-JUN-1999; 99US-0137011.
XX PR 13-AUG-1999; 99US-0149016.
XX
XX XX (BIOJ ) BIOGEN INC.
XX
XX PI Pepinsky RB, Taylor F, Garber E;
XX MPI; 2001-049927/06.
XX
XX DR Modified hedgehog protein, useful in the treatment of Parkinson's
XX PT disease and Huntington's chorea, comprises a polymer containing a
XX PT polyalkylene glycol group linked to any residue other than the
XX PT N-terminal and lysine residues -
XX
XX XX Example 6; Page 77; 157pp; English.
XX
XX CC The invention relates to novel polymer conjugates of hedgehog proteins
XX CC which have increased bioavailability. The hedgehog proteins are
XX CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
XX CC glycol group, with the proviso that the polymer is not conjugated to the
XX CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
XX CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
XX CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
XX CC a hedgehog fusion protein. The invention also relates to methods of
XX CC defining and mapping functionally important regions of a protein by
XX CC various medical conditions including various neurological disorders,
XX CC inflammatory and autoimmune diseases, and cancers. In particular, they
XX CC may be used to prevent preventing or ameliorate neurodegenerative
XX CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
XX CC disease); age-associated neurological disease; neurological injury and
XX CC trauma; immunological diseases of the nervous system (e.g., multiple
XX CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
XX CC neuroectodermal tumours. The modifications made to the hedgehog protein
XX CC may result in increased half-life, altered tissue distribution (such as
XX CC an improved ability to stay in the vasculature for longer periods of
XX CC time), increased stability in solution, protection from proteolytic
XX CC degradation, or reduced immunogenicity. In particular, the ability to
XX CC remain in the vasculature for prolonged periods may allow a hedgehog
XX CC protein of the invention to cross the blood-brain barrier, and an
XX CC increased thermal stability would be an advantage when formulating the
XX CC hedgehog protein in powder form. The present sequence represents a
XX CC human Sonic hedgehog mutagenic primer used in an exemplification of the
XX CC invention.
XX
XX SQ Sequence 38 BP; 8 A; 11 C; 9 G; 10 T; 0 other;
XX
XX Query Match 2.3%; Score 36.4; DB 1; Length 38;
XX Best Local Similarity 97.4%; Pred. No. 0.7;
XX Matches 37; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 662 GACTGGGTGTACTACGAGTCCAGGCACATATCCACTG 699
XX 38 GACTGGGTGTACTACGAGTCCAGGCACATATCCACTG 1
XX
XX DB
XX
XX RESULT 17
XX AAF27025/C
XX ID AAF27025 standard; DNA; 49 BP.

```


PT multiple sclerosis -
 XX
 PS Example 1; Page 62; 178pp; English.
 XX
 CC The present invention relates to hedgehog fusion proteins. Hedgehog
 CC proteins are a family of extracellular signalling proteins that regulate
 CC various aspects of embryonic development both in vertebrates and in
 CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 CC treatment of any condition or disease state for which a hedgehog or
 CC patched protein constituent is efficacious and in the diagnosis of
 CC constituents or conditions of disease states in biological systems or
 CC specimens and for diagnostic purposes in non-physiological systems.
 CC Hedgehog fusion protein is useful for treating neurological conditions
 CC due to injury, aging of nervous system, including Alzheimer's disease,
 CC chronic neurodegenerative diseases of the nervous system, including
 CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 CC and chronic immunological diseases of nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is human oligonucleotide HOG-795 used to construct pMWC25 plasmid which
 CC is used in the invention.
 XX
 SQ Sequence 47 BP; 11 A; 16 C; 17 G; 3 T; 0 other;
 Query Match 2.4%; Score 37.4; DB 1; Length 47;
 Best Local Similarity 87.2%; Pred. No. 0.61;
 Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 225 GACCGGCGAGGGGGTTCGGGAGAGAGGAGCGACCCCAAAAAGTGACC 271
 Db 1 GCCCGGCGAGGGGGTTCGGGCGAGAGCGACCGACCCCAAAAAGTGACC 47
 RESULT 14
 ID AAF27032/c
 XX AAF27032 standard; DNA; 42 BP.
 AC AAF27032;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:36.
 XX
 KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200073337-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14741.
 XX
 PR 01-JUN-1999; 99US-0137011.
 PR 13-AUG-1999; 99US-0149016.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Pepinsky RB, Taylor F, Garber E;
 XX
 DR WPI; 2001-049927/06.
 XX
 XX Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the

PT N-terminal and lysine residues -
 XX
 PS Example 6; Page 77; 157pp; English.
 XX
 CC The invention relates to novel polymer conjugates of hedgehog proteins
 CC which have increased bioavailability. The hedgehog proteins are
 CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
 CC glycol group, with the proviso that the polymer is not conjugated to the
 CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
 CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
 CC (Shh), Indian hedgehog (Ihh) or Desert hedgehog (Dhh) protein, or may be
 CC a hedgehog fusion protein. The invention also relates to methods of
 CC defining and mapping functionally important regions of a protein by
 CC modifying accessible amino acid side chains, and determining the effect
 CC the position and/or type of modification have on the activity of the
 CC protein. The hedgehog polymer conjugates may be used in the management of
 CC various medical conditions including various neurological disorders,
 CC inflammatory and autoimmune diseases, and cancers. In particular, they
 CC may be used to prevent preventing or ameliorate neurodegenerative
 CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
 CC disease), age-associated neurological diseases of the nervous system (e.g., multiple
 CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
 CC neuroectodermal tumours. The modifications made to the hedgehog protein
 CC may result in increased half-life, altered tissue distribution (such as
 CC an improved ability to stay in the vasculature for longer periods of
 CC time), increased stability in solution, protection from proteolytic
 CC degradation, or reduced immunogenicity. In particular, the ability to
 CC remain in the vasculature for prolonged periods may allow a hedgehog
 CC protein of the invention to cross the blood-brain barrier, and an
 CC increased thermal stability would be an advantage when formulating the
 CC hedgehog protein in powder form. The present sequence represents a
 CC human Sonic hedgehog mutagenic primer used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 42 BP; 8 A; 13 C; 9 G; 12 T; 0 other;
 Query Match 2.4%; Score 37.2; DB 1; Length 42;
 Best Local Similarity 92.9%; Pred. No. 0.59;
 Matches 39; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 338 GAAGGGAGAGATCTCCAGAACTCCGAGCGCATTTAAGGAATC 379
 Db 42 GAAGGGAGAGATCTCCAGATCTCCGAGCGCATTTAAGGAATC 1
 RESULT 15
 AAF27036/c
 ID AAF27036 standard; DNA; 42 BP.
 XX
 AC AAF27036;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:40.
 XX
 KW Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200073337-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14741.


```

XX DR WPI; 2001-329075/34.
XX PT Novel isolated hedgehog fusion polypeptide useful for treating
XX PT neurological conditions such as Alzheimer's disease, Parkinson's
XX PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
XX PT multiple sclerosis -
XX PS Example 1; Page 62; 178pp; English.
XX CC The present invention relates to hedgehog fusion proteins. Hedgehog
XX CC proteins are a family of extracellular signalling proteins that regulate
XX CC various aspects of embryonic development both in vertebrates and in
XX CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
XX CC treatment of any condition or disease state for which a hedgehog or
XX CC constituent or conditions of disease states in biological system or
XX CC specimens and for diagnostic purposes in non-physiological conditions
XX CC due to injury, aging of nervous system, including Alzheimer's disease,
XX CC chronic neurodegenerative diseases of the nervous system, including
XX CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
XX CC and chronic immunological diseases of nervous system including multiple
XX CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
XX CC tumours and to specifically target medical therapies against cancers and
XX CC tumours which express the receptor for the protein. The present sequence
XX CC is human oligonucleotide HOG-808 used to construct pMNC22, pMNC25
XX CC and pMNC26 plasmids which are used in the invention.
XX SQ Sequence 43 BP; 8 A; 10 C; 14 G; 11 T; 0 other;
XX
Query Match 2.6%; Score 41.4; DB 1; Length 43;
Best Local Similarity 97.7%; Pred. No. 0.16;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 278 GCTTACAGCAGTTTATCCCAATGTGGCGGAGAGACCCCTAG 320
DB 43 GCTTACAGCAGTTTATCCCAATGTGGCGGAGAGACCCCTAG 1
RESULT 12
AAD09076
ID AAD09076 standard; DNA; 47 BP.
AC AAD09076;
XX 04-SEP-2001 (first entry)
XX Human oligonucleotide HOG-797 used to construct pMNC26.
XX Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;
XX cytosstatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
XX Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
XX nervous system aging; neurodegenerative disease; immunological disease;
XX malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
XX extracellular signalling protein; HOG-797; ss.
XX Homo sapiens.
XX WO200134654-A1.
XX 17-MAY-2001.
XX 02-NOV-2000; 2000WO-US30405.
XX 05-NOV-1999; 99US-0164025.
XX (BIOJ ) BIOGEN INC.
XX Strauch K;
XX WPI; 2001-329075/34.
XX PT Novel isolated hedgehog fusion polypeptide useful for treating
XX PT neurological conditions such as Alzheimer's disease, Parkinson's
XX PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
XX PT multiple sclerosis -

```

```

PT Novel isolated hedgehog fusion polypeptide useful for treating
PT neurological conditions such as Alzheimer's disease, Parkinson's
PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
PT multiple sclerosis -
XX Example 1; Page 62; 178pp; English.
XX CC The present invention relates to hedgehog fusion proteins. Hedgehog
XX CC proteins are a family of extracellular signalling proteins that regulate
XX CC various aspects of embryonic development both in vertebrates and in
XX CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
XX CC treatment of any condition or disease state for which a hedgehog or
XX CC patched protein constituent is efficacious and in the diagnosis of
XX CC constituents or conditions of disease states in biological system or
XX CC specimens and for diagnostic purposes in non-physiological systems.
XX CC Hedgehog fusion protein is useful for treating neurological conditions
XX CC due to injury, aging of nervous system, including Alzheimer's disease,
XX CC chronic neurodegenerative diseases of the nervous system, including
XX CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
XX CC and chronic immunological diseases of nervous system including multiple
XX CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
XX CC tumours and to specifically target medical therapies against cancers and
XX CC tumours which express the receptor for the protein. The present sequence
XX CC is human oligonucleotide HOG-797 used to construct pMNC23 plasmid which
XX CC is used in the invention.
XX SQ Sequence 47 BP; 9 A; 15 C; 20 G; 3 T; 0 other;
XX
Query Match 2.6%; Score 40.6; DB 1; Length 47;
Best Local Similarity 91.5%; Pred. No. 0.22;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 225 GACCGGGCAGGGGGTTCGGGAAGAGAGGAGGACCCCAAAAAGCTGACC 271
DB 1 GCCCGGGCAGGGGGTTCGGGAAGAGAGGAGGACCCCAAAAAGCTGACC 47
RESULT 13
AAD09075
ID AAD09075 standard; DNA; 47 BP.
XX AAD09075;
AC AAD09075;
XX 04-SEP-2001 (first entry)
XX Human oligonucleotide HOG-795 used to construct pMNC25 plasmid.
XX Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;
XX cytosstatic; therapy; Alzheimer's disease; Parkinson's disease; injury;
XX Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
XX nervous system aging; neurodegenerative disease; immunological disease;
XX malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
XX extracellular signalling protein; HOG-795; ss.
XX Homo sapiens.
XX WO200134654-A1.
XX 17-MAY-2001.
XX 02-NOV-2000; 2000WO-US30405.
XX 05-NOV-1999; 99US-0164025.
XX (BIOJ ) BIOGEN INC.
XX Strauch K;
XX WPI; 2001-329075/34.
XX PT Novel isolated hedgehog fusion polypeptide useful for treating
XX PT neurological conditions such as Alzheimer's disease, Parkinson's
XX PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
XX PT multiple sclerosis -

```


CC Hedgehog fusion protein is useful for treating neurological conditions
 CC due to injury, aging of nervous system, including Alzheimer's disease,
 CC chronic neurodegenerative diseases of the nervous system, including
 CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 CC and chronic immunological diseases of nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is human oligonucleotide HOG-799 used to construct pMWC22, pMWC23, pMWC25
 CC and pMWC26 plasmids which are used in the invention.

XX Sequence 45 BP; 12 A; 14 C; 10 G; 9 T; 0 other;

Query Match 2.8%; Score 43.4; DB 1; Length 45;
 Best Local Similarity 97.8%; Pred. No. 0.086; 1; Indels 0; Gaps 0;
 Matches 44; Conservative 0; Mismatches 1;

Qy 272 CCTTTAGCTACAGCAGTTTATCCCAATGTGCGGAGAGACC 316

Db 1 CCTTTAGCTACAGCAGTTTATCCCAAGTGTGCGGAGAGACC 45

RESULT 8

ID AAF27031/c
 ID AAF27031 standard; DNA; 48 BP.

AC AAF27031;

XX 30-MAR-2001 (first entry)

XX Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:35.

XX Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2000073337-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14741.

XX 01-JUN-1999; 99US-0137011.

XX 13-AUG-1999; 99US-0149016.

XX (BIOJ) BIOGEN INC.

XX Pepinsky RB, Taylor F, Garber E;

XX WPI; 2001-049927/06.

XX Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the
 PT N-terminal and lysine residues -

PS Example 6; Page 77; 157pp; English.

XX The invention relates to novel polymer conjugates of hedgehog proteins
 CC which have increased bioavailability. The hedgehog proteins are
 CC conjugated to a non-naturally-occurring polymer comprising a polyalkylene
 CC glycol group, with the proviso that the polymer is not conjugated to the
 CC N-terminus, or to lysine residues of the hedgehog protein. The hedgehog
 CC protein used in the conjugate may be a wild-type or mutant Sonic hedgehog
 CC (Shh), Indian hedgehog (Ihh) or desert hedgehog (Dhh) protein, or may be
 CC a hedgehog fusion protein. The invention also relates to methods of

CC defining and mapping functionally important regions of a protein by
 CC modifying accessible amino acid side chains, and determining the effect
 CC the position and/or type of modification have on the activity of the
 CC protein. The hedgehog polymer conjugates may be used in the management of
 CC various medical conditions including various neurological disorders,
 CC inflammatory and autoimmune diseases, and cancers. In particular, they
 CC may be used to prevent preventing or ameliorate neurodegenerative
 CC disorders (e.g., Parkinson's disease, Huntington's disease, Alzheimer's
 CC disease); age-associated neurological disease; neurological injury and
 CC trauma; immunological diseases of the nervous system (e.g., multiple
 CC sclerosis); stroke; and malignant gliomas, medulloblastomas and
 CC neuroectodermal tumours. The modifications made to the hedgehog protein
 CC may result in increased half-life, altered tissue distribution (such as
 CC an improved ability to stay in the vasculature for longer periods of
 CC time), increased stability in solution, protection from proteolytic
 CC degradation, or reduced immunogenicity. In particular, the ability to
 CC remain in the vasculature for prolonged periods may allow a hedgehog
 CC protein of the invention to cross the blood-brain barrier, and an
 CC increased thermal stability would be an advantage when formulating the
 CC hedgehog protein in powder form. The present sequence represents a
 CC human Sonic hedgehog mutagenic primer used in an exemplification of the
 CC invention.

XX Sequence 48 BP; 10 A; 13 C; 15 G; 10 T; 0 other;

Query Match 2.7%; Score 43.2; DB 1; Length 48;

Best Local Similarity 93.8%; Pred. No. 0.097; 3; Indels 0; Gaps 0;

Matches 45; Conservative 0; Mismatches 3;

Qy 278 GCTTACAGCAGTTTATCCCAATGTGCGGAGAGACCCTAGGCGCC 325

Db 48 GCTTACAGCAGTTTATCCCTGTGTGCTGAGAGACCCTAGGCGCC 1

RESULT 9

AAF27034/c

ID AAF27034 standard; DNA; 48 BP.

XX AAF27034;

XX 30-MAR-2001 (first entry)

XX Human Sonic hedgehog (Shh) mutagenic primer, SEQ ID NO:38.

XX Sonic hedgehog; Shh; polymer conjugate; polyalkene glycol group;
 KW bioavailability; formulation; neurological disorder;
 KW inflammatory disorder; autoimmune disorder; cancer;
 KW neurodegenerative disorder; Parkinson's disease; Huntington's disease;
 KW Alzheimer's disease; neurological injury; stroke; multiple sclerosis;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour;
 KW mutagenic primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2000073337-A1.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14741.

XX 01-JUN-1999; 99US-0137011.

XX 13-AUG-1999; 99US-0149016.

XX (BIOJ) BIOGEN INC.

XX Pepinsky RB, Taylor F, Garber E;

XX WPI; 2001-049927/06.

XX Modified hedgehog protein, useful in the treatment of Parkinson's
 PT disease and Huntington's chorea, comprises a polymer containing a
 PT polyalkylene glycol group linked to any residue other than the

CC various aspects of embryonic development both in vertebrates and in
 CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 CC treatment of any condition or disease state for which a hedgehog or
 CC patched protein constituent is efficacious and in the diagnosis of
 CC constituents or conditions of disease states in biological systems or
 CC specimens and for diagnostic purposes in non-physiological conditions
 CC Hedgehog fusion protein is useful for treating neurological conditions
 CC due to injury, aging of nervous system, including Alzheimer's disease,
 CC chronic neurodegenerative diseases of the nervous system, including
 CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 CC and chronic immunological diseases of nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is human oligonucleotide HOG-789 used to construct pMMC22 plasmid which
 CC is used in the invention.

XX
 SQ Sequence 47 BP; 13 A; 13 C; 18 G; 3 T; 0 other;
 Query Match 2.8%; Score 43.8; DB 1; Length 47;
 Best Local Similarity 95.7%; Pred. No. 0.079; 2; Indels 0; Gaps 0;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 225 GACCGGCGAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACC 271
 Db 1 GCCCGGCGAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACC 47

RESULT 6

AAD09074

ID AAD09074 standard; DNA; 47 BP.

XX

AC AAD09074;

XX

DT 04-SEP-2001 (first entry)

XX

DE Human oligonucleotide HOG-791 used to construct pMMC23.

XX

KW Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;
 KW cytosolic; therapy; Alzheimer's disease; Parkinson's disease; injury;
 KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
 KW nervous system aging; neurodegenerative disease; immunological disease;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
 KW extracellular signalling protein; HOG-791; ss.

OS Homo sapiens.

XX

XX WO200134654-A1.

XX

XX 17-MAY-2001.

XX

XX 02-NOV-2000; 2000WO-US30405.

XX

XX 05-NOV-1999; 99US-0164025.

XX

XX (BIOJ) BIOGEN INC.

XX

XX Strauch K;

XX

XX WPI; 2001-329075/34.

XX

PT Novel isolated hedgehog fusion polypeptide useful for treating
 PT neurological conditions such as Alzheimer's disease, Parkinson's
 PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
 PT multiple sclerosis -

XX

XX Example 1; Page 61-62; 178pp; English.

XX

CC The present invention relates to hedgehog fusion proteins. Hedgehog
 CC proteins are a family of extracellular signalling proteins that regulate
 CC various aspects of embryonic development both in vertebrates and in
 CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 CC treatment of any condition or disease state for which a hedgehog or

CC patched protein constituent is efficacious and in the diagnosis of
 CC constituents or conditions of disease states in biological system or
 CC specimens and for diagnostic purposes in non-physiological systems.
 CC Hedgehog fusion protein is useful for treating neurological conditions
 CC due to injury, aging of nervous system, including Alzheimer's disease,
 CC chronic neurodegenerative diseases of the nervous system, including
 CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 CC and chronic immunological diseases of nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is human oligonucleotide HOG-791 used to construct pMMC23 plasmid which
 CC is used in the invention.

XX
 SQ Sequence 47 BP; 11 A; 13 C; 20 G; 3 T; 0 other;

Query Match 2.8%; Score 43.8; DB 1; Length 47;
 Best Local Similarity 95.7%; Pred. No. 0.079; 2; Indels 0; Gaps 0;
 Matches 45; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 225 GACCGGCGAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACC 271
 Db 1 GCCCGGCGAGGGGTTTCGGGAAGAGGAGGACCCCAAAAAGCTGACC 47

RESULT 7

AAD09077

ID AAD09077 standard; DNA; 45 BP.

XX

AC AAD09077;

XX

DT 04-SEP-2001 (first entry)

XX

DE Human oligonucleotide HOG-799 used to construct pMMC22.

XX

KW Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;
 KW cytosolic; therapy; Alzheimer's disease; Parkinson's disease; injury;
 KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
 KW nervous system aging; neurodegenerative disease; immunological disease;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
 KW extracellular signalling protein; HOG-799; ss.

OS Homo sapiens.

XX

XX WO200134654-A1.

XX

XX 17-MAY-2001.

XX

XX 02-NOV-2000; 2000WO-US30405.

XX

XX 05-NOV-1999; 99US-0164025.

XX

XX (BIOJ) BIOGEN INC.

XX

XX Strauch K;

XX

XX WPI; 2001-329075/34.

XX

PT Novel isolated hedgehog fusion polypeptide useful for treating
 PT neurological conditions such as Alzheimer's disease, Parkinson's
 PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
 PT multiple sclerosis -

XX

XX Example 1; Page 62; 178pp; English.

XX

CC The present invention relates to hedgehog fusion proteins. Hedgehog
 CC proteins are a family of extracellular signalling proteins that regulate
 CC various aspects of embryonic development both in vertebrates and in
 CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 CC treatment of any condition or disease state for which a hedgehog or
 CC patched protein constituent is efficacious and in the diagnosis of
 CC constituents or conditions of disease states in biological system or
 CC specimens and for diagnostic purposes in non-physiological systems.

PT multiple sclerosis -
 XX Example 1; Page 62; 178pp; English.
 XX
 CC The present invention relates to hedgehog fusion proteins. Hedgehog
 CC proteins are a family of extracellular signalling proteins that regulate
 CC various aspects of embryonic development both in vertebrates and in
 CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 CC treatment of any condition or disease state for which a hedgehog or
 CC patched protein constituent is efficacious and in the diagnosis of
 CC constituents or conditions of disease states in biological system or
 CC specimens and for diagnostic purposes in non-physiological systems.
 CC Hedgehog fusion protein is useful for treating neurological conditions
 CC due to injury, aging of nervous system, including Alzheimer's disease,
 CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 CC and chronic immunological diseases of the nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is human oligonucleotide HOG-804 used to construct pMWC33 plasmid which
 CC is used in the invention.
 XX
 SQ Sequence 50 BP; 6 A; 19 C; 13 G; 12 T; 0 other;
 Query Match 3.1%; Score 48.4; DB 1; Length 50;
 Best Local Similarity 98.0%; Pred. No. 0.019;
 Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 228 CGGCAGGGGGTTCCGGAGAGGAGGACCCCAAAAGCTGACCCCTTTA 277
 DB 50 CGGCAGGGGGTTCCGGAGAGGAGGACCCCAAAAGCTGACCCCTTTA 1
 RESULT 4
 AAD09081/c
 ID AAD09081 standard; DNA; 50 BP.
 XX
 AC AAD09081;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human oligonucleotide HOG-807 used to construct pMWC36.
 XX
 KW Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;
 KW cytosolic; therapy; Alzheimer's disease; Parkinson's disease; injury;
 KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
 KW nervous system aging; neurodegenerative disease; immunological disease;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
 KW extracellular signalling protein; HOG-807; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200134654-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 02-NOV-2000; 2000WO-US30405.
 XX
 PR 05-NOV-1999; 99US-0164025.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Strauch K;
 XX
 DR WPI; 2001-329075/34.
 XX
 PT Novel isolated hedgehog fusion polypeptide useful for treating
 PT neurological conditions such as Alzheimer's disease, Parkinson's
 PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
 PT multiple sclerosis -
 XX
 PS Example 1; Page 62; 178pp; English.

XX
 CC The present invention relates to hedgehog fusion proteins. Hedgehog
 CC proteins are a family of extracellular signalling proteins that regulate
 CC various aspects of embryonic development both in vertebrates and in
 CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
 CC treatment of any condition or disease state for which a hedgehog or
 CC patched protein constituent is efficacious and in the diagnosis of
 CC constituents or conditions of disease states in biological system or
 CC specimens and for diagnostic purposes in non-physiological systems.
 CC Hedgehog fusion protein is useful for treating neurological conditions
 CC due to injury, aging of nervous system, including Alzheimer's disease,
 CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis
 CC and chronic immunological diseases of the nervous system including multiple
 CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
 CC tumours and to specifically target medical therapies against cancers and
 CC tumours which express the receptor for the protein. The present sequence
 CC is human oligonucleotide HOG-807 used to construct pMWC26 plasmid which
 CC is used in the invention.
 XX
 SQ Sequence 50 BP; 6 A; 19 C; 15 G; 10 T; 0 other;
 Query Match 2.9%; Score 45.2; DB 1; Length 50;
 Best Local Similarity 94.0%; Pred. No. 0.053;
 Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 228 CGGCAGGGGGTTCCGGAGAGGAGGACCCCAAAAGCTGACCCCTTTA 277
 DB 50 CGGCAGGGGGTTCCGGAGAGGAGGACCCCAAAAGCTGACCCCTTTA 1
 RESULT 5
 AAD09073
 ID AAD09073 standard; DNA; 47 BP.
 XX
 AC AAD09073;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human oligonucleotide HOG-789 used to construct pMWC22.
 XX
 KW Human; hedgehog protein; nontropic; neuroprotective; anticonvulsant;
 KW cytosolic; therapy; Alzheimer's disease; Parkinson's disease; injury;
 KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;
 KW nervous system aging; neurodegenerative disease; immunological disease;
 KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;
 KW extracellular signalling protein; HOG-789; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200134654-A1.
 XX
 PD 17-MAY-2001.
 XX
 PF 02-NOV-2000; 2000WO-US30405.
 XX
 PR 05-NOV-1999; 99US-0164025.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Strauch K;
 XX
 DR WPI; 2001-329075/34.
 XX
 PT Novel isolated hedgehog fusion polypeptide useful for treating
 PT neurological conditions such as Alzheimer's disease, Parkinson's
 PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and
 PT multiple sclerosis -
 XX
 PS Example 1; Page 61; 178pp; English.
 XX
 CC The present invention relates to hedgehog fusion proteins. Hedgehog
 CC proteins are a family of extracellular signalling proteins that regulate

DR WPI; 2001-329075/34.

XX Novel isolated hedgehog fusion polypeptide useful for treating

PT neurological conditions such as Alzheimer's disease, Parkinson's

PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and

PT multiple sclerosis -

XX

PS Example 1; Page 60; 178pp; English.

XX

CC The present invention relates to hedgehog fusion proteins. Hedgehog

CC proteins are a family of extracellular signalling proteins that regulate

CC various aspects of embryonic development both in vertebrates and in

CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or

CC treatment of any condition or disease state for which a hedgehog or

CC patched protein constituent is efficacious and in the diagnosis of

CC constituents or conditions of disease states in biological system or

CC specimens and for diagnostic purposes in non-physiological systems.

CC Hedgehog fusion protein is useful for treating neurological conditions

CC due to injury, aging of nervous system, including Alzheimer's disease,

CC chronic neurodegenerative diseases of the nervous system, including

CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis

CC and chronic immunological diseases of nervous system including multiple

CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal

CC tumours and to specifically target medical therapies against cancers and

CC tumours which express the receptor for the protein. The present sequence

CC is human oligonucleotide HOG-403 used to construct pKS285, pKS288,

CC pKS309, pKS310, pKS287 pKS300 and pKS289 plasmids which are used in the

CC invention.

XX

SQ Sequence 50 BP; 11 A; 11 C; 15 G; 13 T; 0 other;

Query Match 3.2%; Score 50; DB 1; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 CTTTAGCTCAAGCAGTTTATCCCAATGTCGCGAGAGACCCCTAGG 321

DB 50 CTTTAGCTCAAGCAGTTTATCCCAATGTCGCGAGAGACCCCTAGG 1

RESULT 2

AAD09078/c

ID AAD09078 standard; DNA; 50 BP.

XX

AC AAD09078;

XX

DT 04-SEP-2001 (first entry)

XX

DE Human oligonucleotide HOG-803 used to construct pMNC22.

XX

KW Human; hedgehog protein; nototropic; neuroprotective; anticonvulsant;

KW cytosolic; therapy; Alzheimer's disease; Parkinson's disease; injury;

KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;

KW nervous system aging; neurodegenerative disease; immunological disease;

KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;

KW extracellular signalling protein; HOG-803; ss.

XX

OS Homo sapiens.

XX

PN WO200134654-A1.

XX

PD 17-MAY-2001.

XX

PF 02-NOV-2000; 2000WO-US30405.

XX

PR 05-NOV-1999; 99US-0164025.

XX

PA (BIOJ) BIOGEN INC.

XX

PI Strauch K;

XX

DR WPI; 2001-329075/34.

XX

PT Novel isolated hedgehog fusion polypeptide useful for treating

PT neurological conditions such as Alzheimer's disease, Parkinson's

PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and

XX multiple sclerosis -

XX

PS Example 1; Page 62; 178pp; English.

XX

CC The present invention relates to hedgehog fusion proteins. Hedgehog

CC proteins are a family of extracellular signalling proteins that regulate

CC various aspects of embryonic development both in vertebrates and in

CC invertebrates. Hedgehog fusion protein is useful for the prophylaxis or

CC treatment of any condition or disease state for which a hedgehog or

CC patched protein constituent is efficacious and in the diagnosis of

CC constituents or conditions of disease states in biological system or

CC specimens and for diagnostic purposes in non-physiological systems.

CC Hedgehog fusion protein is useful for treating neurological conditions

CC due to injury, aging of nervous system, including Alzheimer's disease,

CC chronic neurodegenerative diseases of the nervous system, including

CC Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis

CC and chronic immunological diseases of nervous system including multiple

CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal

CC tumours and to specifically target medical therapies against cancers and

CC tumours which express the receptor for the protein. The present sequence

CC is human oligonucleotide HOG-803 used to construct pMNC22 plasmid which

CC is used in the invention.

XX

SQ Sequence 50 BP; 6 A; 17 C; 13 G; 14 T; 0 other;

Query Match 3.1%; Score 48.4; DB 1; Length 50;

Best Local Similarity 98.0%; Pred. No. 0.019;

Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 228 CGGCGAGGGGTTTCGGGAGAGAGGACACCCCAAAAGCTGACCCCTTTA 277

DB 50 CGGCGAGGGGTTTCGGGAGAGAGGACACCCCAAAAGCTGACCCCTTTA 1

RESULT 3

AAD09079/c

ID AAD09079 standard; DNA; 50 BP.

XX

AC AAD09079;

XX

DT 04-SEP-2001 (first entry)

XX

DE Human oligonucleotide HOG-804 used to construct pMNC23.

XX

KW Human; hedgehog protein; nototropic; neuroprotective; anticonvulsant;

KW cytosolic; therapy; Alzheimer's disease; Parkinson's disease; injury;

KW Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;

KW nervous system aging; neurodegenerative disease; immunological disease;

KW malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;

KW extracellular signalling protein; HOG-804; ss.

XX

OS Homo sapiens.

XX

PN WO200134654-A1.

XX

PD 17-MAY-2001.

XX

PF 02-NOV-2000; 2000WO-US30405.

XX

PR 05-NOV-1999; 99US-0164025.

XX

PA (BIOJ) BIOGEN INC.

XX

PI Strauch K;

XX

DR WPI; 2001-329075/34.

XX

PT Novel isolated hedgehog fusion polypeptide useful for treating

PT neurological conditions such as Alzheimer's disease, Parkinson's

PT disease, Huntington's chorea, amyotrophic lateral sclerosis, and

PT multiple sclerosis, and

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:34:30 ; Search time 24 Seconds
(without alignments)
2.112 Million cell updates/sec

Title: us-10-001-844-3
Perfect score: 1576
Sequence: 1 gggagccagccgagggga.....9sggggcccggagggggcc 1576

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 844 seqs, 16078 residues

Total number of hits satisfying chosen parameters: 1688

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 70 summaries

Database : rng.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	50	3.2	50	1	AAD09047 Human oligonucleot
C 2	48.4	3.1	50	1	AAD09078 Human oligonucleot
C 3	48.4	3.1	50	1	AAD09079 Human oligonucleot
C 4	45.2	2.9	50	1	AAD09081 Human oligonucleot
C 5	43.8	2.8	47	1	AAD09073 Human oligonucleot
C 6	43.8	2.8	47	1	AAD09074 Human oligonucleot
C 7	43.4	2.8	45	1	AAD09077 Human oligonucleot
C 8	43.2	2.7	48	1	AAD09071 Human Sonic hedgeh
C 9	43.2	2.7	48	1	AAF27034 Human Sonic hedgeh
C 10	42	2.7	50	1	AAD09080 Human oligonucleot
C 11	41.4	2.6	43	1	AAD09082 Human oligonucleot
C 12	40.6	2.6	47	1	AAD09076 Human oligonucleot
C 13	37.4	2.4	47	1	AAD09075 Human oligonucleot
C 14	37.2	2.4	42	1	AAF27032 Human Sonic hedgeh
C 15	37.2	2.4	42	1	AAF27036 Human Sonic hedgeh
C 16	36.4	2.3	38	1	AAF27039 Human Sonic hedgeh
C 17	36	2.3	49	1	AAF27025 Human Sonic hedgeh
C 18	35.8	2.3	39	1	AAF27038 Human Sonic hedgeh
C 19	35.6	2.3	42	1	AAF27035 Human Sonic hedgeh
C 20	33.8	2.1	37	1	AAF27037 Human Sonic hedgeh
C 21	33.4	2.1	35	1	AAF27041 Human Sonic hedgeh
C 22	32.2	2.0	37	1	AAF27040 Human Sonic hedgeh
C 23	27	1.7	27	1	ABT03768 Human SHH gene PCR
C 24	25	1.6	33	1	Crohn's disease/ul
C 25	24	1.5	24	1	AAQ91654 Human sonic hedgeh
C 26	24	1.5	24	1	AAV18405 Human mutated soni
C 27	24	1.5	24	1	AAH76132 Human Shh DNA ampl
C 28	24	1.5	24	1	AAD10171 Human Sonic hedgeh
C 29	24	1.5	24	1	AAAC87097 PCR primer for cDN
C 30	24	1.5	24	1	ABEN87569 Human sonic hedgeh
C 31	23.4	1.5	25	1	AAV18406 Human mutated soni
C 32	23.4	1.5	33	1	AAV62418 Human Sonic hedgeh
C 33	23.2	1.5	28	1	ABSS56000 Mouse Shh probe.

ALIGNMENTS

RESULT 1				
AAD09047/c				
ID	AAD09047	standard; DNA; 50 BP.		
XX				
AC	AAD09047;			
XX				
DT	04-SEP-2001.	(first entry)		
XX				
DE	Human oligonucleotide HOG-403 used to construct pKS285.			
XX				
KW	Human; hedgehog protein; neuroprotective; anticonvulsant;			
KW	cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury;			
KW	Huntington's chorea; amyotrophic lateral sclerosis; multiple sclerosis;			
KW	nervous system aging; neurodegenerative disease; immunological disease;			
KW	malignant glioma; medulloblastoma; neuroectodermal tumour; cancer;			
XX	extracellular signalling protein; HOG-403; ss.			
OS	Homo sapiens.			
XX				
PN	WO200134654-A1.			
XX				
PD	17-MAY-2001.			
XX				
PF	02-NOV-2000; 2000WO-US30405.			
XX				
PR	05-NOV-1999; 99US-0164025.			
XX				
PA	(BIOJ) BIOGEN INC.			
XX				
PI	Strauch K;			
XX				

34	22.6	1.4	30	1	ABX80007
35	22.4	1.4	32	1	ABK10414
C 36	22	1.4	22	1	ABSS5998
37	22	1.4	24	1	ABT03767
C 38	22	1.4	29	1	AAAD2861
C 39	22	1.4	29	1	AAAD03042
C 40	22	1.4	29	1	AAK93702
C 41	22	1.4	30	1	ABK99277
C 42	21.4	1.4	24	1	AAAD34564
C 43	21.4	1.4	24	1	ABZ79785
C 44	20.2	1.3	26	1	ABSS5999
C 45	20	1.3	20	1	AAF87045
C 46	19.2	1.2	24	1	AAAD2726
C 47	18.2	1.2	24	1	AAA30347
C 48	19.2	1.2	24	1	AAAS13720
C 49	19.2	1.2	24	1	AAAI67720
C 50	19	1.2	19	1	AAV18410
C 51	19	1.2	19	1	AAV18416
C 52	19	1.2	19	1	AAH45473
C 53	19	1.2	19	1	AAH45477
C 54	18.6	1.2	25	1	AAQ55856
C 55	18.6	1.2	25	1	AAQ85271
C 56	18.6	1.2	25	1	AAQ05267
C 57	18.4	1.2	20	1	AAV62410
C 58	18.4	1.2	20	1	AAF87046
C 59	18.2	1.2	24	1	AAV15200
C 60	18.2	1.2	25	1	AAV59458
C 61	18	1.1	18	1	AAH45474
C 62	17.8	1.1	21	1	AAAG5383
C 63	17.8	1.1	21	1	AAZ49111
C 64	17.8	1.1	21	1	AAAD52804
C 65	17.6	1.1	25	1	ABT03636
C 66	17.2	1.1	22	1	ABSS5991
C 67	17.2	1.1	24	1	AAV01774
C 68	17.2	1.1	24	1	AAAG4229
C 69	17.2	1.1	24	1	AAF74610
C 70	17.2	1.1	24	1	AAAD42796

EST polymorphic DN
Synthetic primer s
Mouse RT-PCR prime
Human SHH gene PCR
Oligo linker for c
Human oligonucleot
Human sonic hedgeh
Hepatitis C virus
Shh specific forma
Indian hedgehog PC
Mouse RT-PCR prime
PCR primer for Shh
Forward PCR primer
Sonic hedgehog mRN
Simple sequence re
Receptor Shh cDNA
Human mutated soni
PCR primer Shh-U2
PCR primer Shh-U1
Fragile X probe.
Probe for Fragile
Fragile X chromoso
Human Desert hedge
PCR primer for Shh
Central region seq
Hedgehog protein d
PCR primer Shh-D s
Rat Shh coding seq
PCR primer for mou
LipA gene sequen
Human Hox-2 gene P
Mouse RT-PCR prime
Human cystic fibro
RACE PCR primer JA
Cystic fibrosis tr
Adaptor oligonucle

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:35:46 ; Search time 16 Seconds
 (without alignments)
 2.082 Million cell updates/sec

Title: us-10-001-844-3
 Perfect score: 1576
 Sequence: 1 gcagccagccagcagggga.....gagggcgcgaggagggggcc 1576

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5

Searched: 592 seqs, 10570 residues

Total number of hits satisfying chosen parameters: 1184

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing first 605 summaries

Database : rni.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	\$			
C	1	36	2.3	49	1	US-09-325-256-31	Sequence 31, Appl
	2	25	1.6	33	1	US-08-068-747-7	Sequence 7, Appl
	3	24	1.5	24	1	US-08-748-591-11	Sequence 11, Appl
	4	24	1.5	24	1	US-08-356-060A-43	Sequence 43, Appl
	5	24	1.5	24	1	US-08-460-900C-43	Sequence 43, Appl
	6	24	1.5	24	1	US-08-674-509B-43	Sequence 43, Appl
	7	24	1.5	24	1	US-08-954-698-43	Sequence 43, Appl
	8	24	1.5	24	1	US-08-957-874-43	Sequence 43, Appl
	9	24	1.5	24	1	US-09-639-695-43	Sequence 43, Appl
10	23.6	1.5	30	1	US-08-068-747-2	Sequence 2, Appl	
11	23.4	1.5	25	1	US-08-748-591-12	Sequence 12, Appl	
12	22.6	1.4	30	1	US-09-475-947A-332	Sequence 332, App	
13	22.4	1.4	32	1	US-09-083-123-5	Sequence 5, Appl	
14	19	1.2	19	1	US-08-748-591-16	Sequence 16, Appl	
15	19	1.2	19	1	US-08-748-591-21	Sequence 21, Appl	
16	19	1.2	19	1	US-09-102-491-5	Sequence 5, Appl	
17	19	1.2	19	1	US-09-102-491-9	Sequence 9, Appl	
18	18.6	1.2	25	1	US-08-374-144-3	Sequence 3, Appl	
19	18.6	1.2	25	1	US-08-775-164-3	Sequence 3, Appl	
20	18.6	1.2	25	1	US-08-775-609-3	Sequence 3, Appl	
21	18.6	1.2	25	1	US-08-775-607-3	Sequence 3, Appl	
22	18.6	1.2	25	1	PCT-US93-06828-3	Sequence 3, Appl	
23	18.2	1.2	24	1	US-08-384-324-6	Sequence 6, Appl	
24	18.2	1.2	24	1	PCT-US96-01473-6	Sequence 6, Appl	
25	18	1.1	18	1	US-09-102-491-6	Sequence 6, Appl	
26	17.8	1.1	21	1	US-09-277-078-24	Sequence 24, Appl	
27	17.2	1.1	24	1	US-08-742-755A-31	Sequence 31, Appl	
28	17.2	1.1	24	1	US-09-226-683-31	Sequence 31, Appl	
29	17.2	1.1	24	1	US-09-387-699-12	Sequence 12, Appl	
30	17.2	1.1	24	1	US-09-035-183-31	Sequence 31, Appl	
31	17.2	1.1	24	1	US-09-641-259B-12	Sequence 12, Appl	
32	16.6	1.1	24	1	US-08-384-324-6	Sequence 6, Appl	
33	16.6	1.1	24	1	PCT-US96-01473-6	Sequence 6, Appl	

C 34	16.4	1.0	18	1	US-09-377-155-23	Sequence 23, Appl
C 35	16.4	1.0	18	1	US-09-669-974-23	Sequence 23, Appl
C 36	16.4	1.0	20	1	US-03-358-382-10	Sequence 10, Appl
C 37	16.2	1.0	21	1	US-08-863-639A-52	Sequence 52, Appl
C 38	16.2	1.0	21	1	US-08-863-639A-55	Sequence 55, Appl
C 39	16.2	1.0	21	1	US-08-863-639A-56	Sequence 56, Appl
C 40	16.2	1.0	21	1	US-08-863-639A-67	Sequence 67, Appl
C 41	16.2	1.0	21	1	US-08-863-639A-68	Sequence 68, Appl
C 42	16.2	1.0	21	1	US-08-863-639A-71	Sequence 71, Appl
C 43	16.2	1.0	21	1	US-08-416-214A-11	Sequence 11, Appl
C 44	16.2	1.0	21	1	US-08-956-254-1	Sequence 1, Appl
C 45	16.2	1.0	22	1	US-08-742-755A-32	Sequence 32, Appl
C 46	16.2	1.0	22	1	US-08-742-755A-35	Sequence 35, Appl
C 47	16.2	1.0	22	1	US-09-226-683-32	Sequence 32, Appl
C 48	16.2	1.0	22	1	US-09-226-683-35	Sequence 35, Appl
C 49	16.2	1.0	22	1	US-09-035-183-32	Sequence 32, Appl
C 50	16.2	1.0	22	1	US-09-035-183-35	Sequence 35, Appl
C 51	16	1.0	16	1	US-08-748-591-13	Sequence 13, Appl
C 52	16	1.0	16	1	US-08-748-591-18	Sequence 18, Appl
C 53	16	1.0	16	1	US-08-748-591-19	Sequence 19, Appl
C 54	16	1.0	16	1	US-08-748-591-20	Sequence 20, Appl
C 55	15.8	1.0	20	1	US-08-914-961-2	Sequence 2, Appl
C 56	15.8	1.0	20	1	US-08-777-286A-26	Sequence 26, Appl
C 57	15.8	1.0	20	1	US-09-030-701-65	Sequence 65, Appl
C 58	15.8	1.0	20	1	US-09-326-186B-26	Sequence 26, Appl
C 59	15.8	1.0	20	1	US-09-082-649B-57	Sequence 57, Appl
C 60	15.8	1.0	20	1	US-09-702-327-46	Sequence 46, Appl
C 61	15.8	1.0	20	1	US-09-898-361-147	Sequence 147, Appl
C 62	15.8	1.0	21	1	US-09-339-944-11	Sequence 11, Appl
C 63	15.6	1.0	22	1	US-08-833-728D-47	Sequence 47, Appl
C 64	15.6	1.0	22	1	US-08-835-728D-151	Sequence 151, Appl
C 65	15.6	1.0	22	1	US-09-490-558-47	Sequence 47, Appl
C 66	15.6	1.0	22	1	US-09-490-558-151	Sequence 151, Appl
C 67	15.4	1.0	17	1	US-09-371-772B-4186	Sequence 4186, App
C 68	15.4	1.0	18	1	US-08-857-946-14	Sequence 14, Appl
C 69	15.4	1.0	18	1	US-08-970-740-14	Sequence 14, Appl
C 70	15.4	1.0	20	1	US-09-198-452A-5935	Sequence 5935, App
C 71	15.4	1.0	22	1	US-09-197-063-4	Sequence 4, Appl
C 72	15.2	1.0	20	1	US-09-101-886B-15	Sequence 15, Appl
C 73	15.2	1.0	20	1	US-09-150-999-6	Sequence 6, Appl
C 74	15.2	1.0	20	1	US-09-487-253A-7	Sequence 7, Appl
C 75	15.2	1.0	20	1	US-09-295-593-8	Sequence 8, Appl
C 76	15.2	1.0	20	1	US-09-982-465-6	Sequence 6, Appl
C 77	15.2	1.0	21	1	US-08-662-963-9	Sequence 9, Appl
C 78	14.8	0.9	18	1	US-08-748-591-22	Sequence 22, Appl
C 79	14.8	0.9	18	1	US-09-205-860-10	Sequence 10, Appl
C 80	14.8	0.9	18	1	US-09-205-860-13	Sequence 13, Appl
C 81	14.8	0.9	18	1	US-08-857-946-8	Sequence 8, Appl
C 82	14.8	0.9	18	1	US-08-970-740-8	Sequence 8, Appl
C 83	14.8	0.9	18	1	US-09-593-323-34	Sequence 34, Appl
C 84	14.8	0.9	18	1	US-09-594-108-34	Sequence 34, Appl
C 85	14.8	0.9	18	1	US-09-344-300-34	Sequence 34, Appl
C 86	14.8	0.9	19	1	US-08-589-939-37	Sequence 37, Appl
C 87	14.8	0.9	19	1	US-09-009-483A-19	Sequence 19, Appl
C 88	14.8	0.9	20	1	US-07-940-242A-19	Sequence 19, Appl
C 89	14.8	0.9	20	1	US-08-465-485A-28	Sequence 28, Appl
C 90	14.8	0.9	20	1	US-09-366-257-11	Sequence 11, Appl
C 91	14.8	0.9	20	1	US-09-080-285-28	Sequence 28, Appl
C 92	14.8	0.9	20	1	US-09-416-758A-4	Sequence 4, Appl
C 93	14.8	0.9	20	1	US-09-488-671-156	Sequence 156, App
C 94	14.8	0.9	20	1	US-09-724-426-28	Sequence 28, Appl
C 95	14.8	0.9	21	1	US-08-410-654B-41	Sequence 41, Appl
C 96	14.8	0.9	21	1	US-08-474-851-41	Sequence 41, Appl
C 97	14.8	0.9	21	1	US-08-481-560-41	Sequence 41, Appl
C 98	14.8	0.9	21	1	US-08-621-841-15	Sequence 15, Appl
C 99	14.8	0.9	21	1	US-08-853-980-20	Sequence 20, Appl
C 100	14.4	0.9	17	1	US-08-281-940-45	Sequence 45, Appl
C 101	14.4	0.9	17	1	US-08-710-134-45	Sequence 45, Appl
C 102	14.4	0.9	17	1	US-08-485-885-45	Sequence 45, Appl
C 103	14.4	0.9	18	1	US-09-496-694B-99	Sequence 99, Appl
C 104	14.4	0.9	18	1	US-08-679-645-1165	Sequence 1165, App
C 105	14.4	0.9	19	1	US-09-422-978-7120	Sequence 7120, App
C 106	14.4	0.9	20	1	US-09-513-729B-15	Sequence 15, Appl

107 14.4 0.9 20 1 US-09-593-711A-37 Sequence 37, Appl
C 108 14.4 0.9 20 1 US-09-593-711A-127 Sequence 127, Appl
C 109 14.4 0.9 20 1 US-09-593-711A-128 Sequence 128, Appl
C 110 14.4 0.9 20 1 US-09-702-246-11 Sequence 12, Appl
C 111 14.2 0.9 19 1 US-08-860-638A-12 Sequence 106, Appl
C 112 14.2 0.9 19 1 US-08-348-548-106 Sequence 12, Appl
C 113 14.2 0.9 19 1 US-09-381-476-12 Sequence 106, Appl
C 114 14.2 0.9 19 1 PCT-US95-15716-106 Sequence 10, Appl
C 115 14.2 0.9 20 1 US-07-626-618A-10 Sequence 62, Appl
C 116 14.2 0.9 20 1 US-08-136-811-23 Sequence 23, Appl
C 117 14.2 0.9 20 1 US-08-219-842-62 Sequence 62, Appl
C 118 14.2 0.9 20 1 US-08-333-977-10 Sequence 95, Appl
C 119 14.2 0.9 20 1 US-08-507-431-35 Sequence 35, Appl
C 120 14.2 0.9 20 1 US-08-451-096-62 Sequence 62, Appl
C 121 14.2 0.9 20 1 US-08-451-096-95 Sequence 95, Appl
C 122 14.2 0.9 20 1 US-08-835-770-23 Sequence 23, Appl
C 123 14.2 0.9 20 1 US-08-628-731-23 Sequence 23, Appl
C 124 14.2 0.9 20 1 US-08-609-443B-45 Sequence 45, Appl
C 125 14.2 0.9 20 1 US-08-888-940-12 Sequence 12, Appl
C 126 14.2 0.9 20 1 US-08-423-355-23 Sequence 23, Appl
C 127 14.2 0.9 20 1 US-08-470-426B-30 Sequence 30, Appl
C 128 14.2 0.9 20 1 US-08-887-365-17 Sequence 17, Appl
C 129 14.2 0.9 20 1 US-08-889-296A-20 Sequence 20, Appl
C 130 14.2 0.9 20 1 US-08-802-655A-35 Sequence 35, Appl
C 131 14.2 0.9 20 1 US-08-848-840A-20 Sequence 20, Appl
C 132 14.2 0.9 20 1 US-08-874-186-48 Sequence 48, Appl
C 133 14.2 0.9 20 1 US-09-366-257-27 Sequence 27, Appl
C 134 14.2 0.9 20 1 US-09-166-622-35 Sequence 35, Appl
C 135 14.2 0.9 20 1 US-08-961-469A-28 Sequence 28, Appl
C 136 14.2 0.9 20 1 US-09-128-49A-20 Sequence 20, Appl
C 137 14.2 0.9 20 1 US-09-435-296-56 Sequence 56, Appl
C 138 14.2 0.9 20 1 US-09-280-805-42 Sequence 42, Appl
C 139 14.2 0.9 20 1 US-09-517-584B-19 Sequence 19, Appl
C 140 14.2 0.9 20 1 US-09-219-277-35 Sequence 35, Appl
C 141 14.2 0.9 20 1 US-08-983-466-29 Sequence 29, Appl
C 142 14.2 0.9 20 1 US-09-599-661-35 Sequence 35, Appl
C 143 14.2 0.9 20 1 US-09-467-082-13 Sequence 13, Appl
C 144 14.2 0.9 20 1 US-09-467-082-22 Sequence 22, Appl
C 145 14.2 0.9 20 1 US-09-326-186B-154 Sequence 154, Appl
C 146 14.2 0.9 20 1 US-08-951-996-45 Sequence 45, Appl
C 147 14.2 0.9 20 1 US-09-448-386-20 Sequence 20, Appl
C 148 14.2 0.9 20 1 US-09-561-497-34 Sequence 34, Appl
C 149 14.2 0.9 20 1 US-09-742-703-32 Sequence 32, Appl
C 150 14.2 0.9 20 1 US-09-920-663-12 Sequence 12, Appl
C 151 14.2 0.9 20 1 US-09-907-843-23 Sequence 23, Appl
C 152 14.2 0.9 20 1 US-09-485-077A-2 Sequence 2, Appl
C 153 14.2 0.9 20 1 US-09-457-346A-11 Sequence 11, Appl
C 154 14.2 0.9 20 1 US-09-322-146-25 Sequence 25, Appl
C 155 14.2 0.9 20 1 US-08-585-684B-50 Sequence 50, Appl
C 156 14.2 0.9 15 1 US-09-377-310-17 Sequence 37, Appl
C 157 14.2 0.9 15 1 US-09-377-310-37 Sequence 37, Appl
C 158 14.2 0.9 15 1 US-09-038-073-50 Sequence 50, Appl
C 159 14.2 0.9 18 1 US-08-627-254C-12 Sequence 12, Appl
C 160 14.2 0.9 18 1 US-08-912-129A-77 Sequence 77, Appl
C 161 14.2 0.9 19 1 US-08-981-321-6 Sequence 6, Appl
C 162 14.2 0.9 19 1 US-09-578-634A-1 Sequence 1, Appl
C 163 14.2 0.9 20 1 US-08-637-201C-5 Sequence 5, Appl
C 164 14.2 0.9 20 1 US-09-428-696-57 Sequence 57, Appl
C 165 14.2 0.9 20 1 US-09-484-617-41 Sequence 41, Appl
C 166 14.2 0.9 20 1 US-09-364-416-5 Sequence 5, Appl
C 167 14.2 0.9 20 1 US-09-422-978-8409 Sequence 457, Appl
C 168 14.2 0.9 17 1 US-08-379-078-457 Sequence 457, Appl
C 169 13.8 0.9 17 1 US-07-974-409C-70 Sequence 70, Appl
C 170 13.8 0.9 17 1 US-07-974-409C-71 Sequence 71, Appl
C 171 13.8 0.9 17 1 US-08-584-040-5562 Sequence 5562, Appl
C 172 13.8 0.9 17 1 US-09-673-809-86 Sequence 86, Appl
C 173 13.8 0.9 17 1 US-09-435-327A-16 Sequence 16, Appl
C 174 13.8 0.9 17 1 US-09-371-772B-2452 Sequence 2452, Appl
C 175 13.8 0.9 17 1 PCT-US93-00977-70 Sequence 70, Appl
C 176 13.8 0.9 17 1 PCT-US93-00977-71 Sequence 71, Appl
C 177 13.8 0.9 17 1 US-08-348-848-56 Sequence 56, Appl
C 178 13.8 0.9 18 1 US-08-348-848-56 Sequence 56, Appl

180 13.8 0.9 18 1 US-08-248-848-57 Sequence 57, Appl
C 181 13.8 0.9 18 1 US-08-111-077-56 Sequence 56, Appl
C 182 13.8 0.9 18 1 US-08-111-077-57 Sequence 57, Appl
C 183 13.8 0.9 18 1 US-08-363-240A-1117 Sequence 1117, Appl
C 184 13.8 0.9 18 1 US-08-363-240A-1203 Sequence 1203, Appl
C 185 13.8 0.9 18 1 US-08-311-486C-1129 Sequence 1129, Appl
C 186 13.8 0.9 18 1 US-09-205-922-48 Sequence 48, Appl
C 187 13.8 0.9 18 1 US-09-176-862-32 Sequence 32, Appl
C 188 13.8 0.9 18 1 US-09-143-212-45 Sequence 45, Appl
C 189 13.8 0.9 18 1 US-09-322-478-2 Sequence 2, Appl
C 190 13.8 0.9 18 1 US-08-584-040-3041 Sequence 3041, Appl
C 191 13.8 0.9 18 1 US-08-679-645-1167 Sequence 1167, Appl
C 192 13.8 0.9 18 1 US-09-025-343-14 Sequence 14, Appl
C 193 13.8 0.9 18 1 US-09-673-809-44 Sequence 44, Appl
C 194 13.8 0.9 18 1 US-09-371-772B-1469 Sequence 1469, Appl
C 195 13.8 0.9 19 1 US-08-486-408-12 Sequence 12, Appl
C 196 13.8 0.9 19 1 US-08-640-672-6 Sequence 6, Appl
C 197 13.8 0.9 19 1 US-08-684-498A-6 Sequence 6, Appl
C 198 13.8 0.9 19 1 US-08-577-858A-6 Sequence 6, Appl
C 199 13.8 0.9 19 1 US-08-611-280-10 Sequence 10, Appl
C 200 13.8 0.9 19 1 US-08-975-570-12 Sequence 12, Appl
C 201 13.8 0.9 19 1 US-08-796-362C-5 Sequence 5, Appl
C 202 13.8 0.9 19 1 US-09-195-940-10 Sequence 10, Appl
C 203 13.8 0.9 19 1 US-09-562-466-10 Sequence 10, Appl
C 204 13.8 0.9 33 1 US-08-068-747-7 Sequence 7, Appl
C 205 13.6 0.9 20 1 US-08-983-466-29 Sequence 29, Appl
C 206 13.4 0.9 15 1 US-08-585-684B-49 Sequence 49, Appl
C 207 13.4 0.9 15 1 US-08-585-684B-51 Sequence 51, Appl
C 208 13.4 0.9 15 1 US-08-863-639A-21 Sequence 21, Appl
C 209 13.4 0.9 15 1 US-08-590-897A-32 Sequence 32, Appl
C 210 13.4 0.9 15 1 US-09-038-073-49 Sequence 49, Appl
C 211 13.4 0.9 15 1 US-09-038-073-51 Sequence 51, Appl
C 212 13.4 0.9 15 1 US-08-730-635-13 Sequence 13, Appl
C 213 13.4 0.9 16 1 US-08-153-051B-58 Sequence 58, Appl
C 214 13.4 0.9 16 1 US-08-060-352C-57 Sequence 57, Appl
C 215 13.4 0.9 16 1 US-08-151-477A-58 Sequence 58, Appl
C 216 13.4 0.9 16 1 US-08-819-867-80 Sequence 80, Appl
C 217 13.4 0.9 16 1 US-08-464-011B-57 Sequence 57, Appl
C 218 13.4 0.9 16 1 US-09-378-535-80 Sequence 80, Appl
C 219 13.4 0.9 17 1 US-08-288-405A-12 Sequence 12, Appl
C 220 13.4 0.9 17 1 US-08-933-749-10 Sequence 10, Appl
C 221 13.4 0.9 17 1 US-08-909-742-3 Sequence 3, Appl
C 222 13.4 0.9 17 1 US-08-909-742-4 Sequence 4, Appl
C 223 13.4 0.9 17 1 US-09-235-583-10 Sequence 10, Appl
C 224 13.4 0.9 17 1 US-09-275-680-9 Sequence 9, Appl
C 225 13.4 0.9 17 1 US-09-599-164-10 Sequence 10, Appl
C 226 13.4 0.9 17 1 US-09-412-289-3 Sequence 3, Appl
C 227 13.4 0.9 17 1 US-09-412-289-4 Sequence 4, Appl
C 228 13.4 0.9 17 1 US-09-412-289-5 Sequence 5, Appl
C 229 13.4 0.9 17 1 US-09-412-289-6 Sequence 6, Appl
C 230 13.4 0.9 17 1 US-09-412-289-7 Sequence 7, Appl
C 231 13.4 0.9 17 1 US-09-412-289-8 Sequence 8, Appl
C 232 13.4 0.9 17 1 US-09-412-289-9 Sequence 9, Appl
C 233 13.4 0.9 17 1 US-09-412-289-10 Sequence 10, Appl
C 234 13.2 0.8 18 1 US-08-128-369-6 Sequence 6, Appl
C 235 13.2 0.8 18 1 US-08-072-063-10 Sequence 10, Appl
C 236 13.2 0.8 18 1 US-08-050-332-11 Sequence 11, Appl
C 237 13.2 0.8 18 1 US-08-145-704-42 Sequence 42, Appl
C 238 13.2 0.8 18 1 US-08-145-704-43 Sequence 43, Appl
C 239 13.2 0.8 18 1 US-08-161-673A-5 Sequence 5, Appl
C 240 13.2 0.8 18 1 US-08-435-350-38 Sequence 38, Appl
C 241 13.2 0.8 18 1 US-08-064-693-10 Sequence 10, Appl
C 242 13.2 0.8 18 1 US-08-483-122-7 Sequence 7, Appl
C 243 13.2 0.8 18 1 US-08-483-122-8 Sequence 8, Appl
C 244 13.2 0.8 18 1 US-08-661-767-11 Sequence 11, Appl
C 245 13.2 0.8 18 1 US-08-117-952-745 Sequence 745, Appl
C 246 13.2 0.8 18 1 US-08-486-648-7 Sequence 7, Appl
C 247 13.2 0.8 18 1 US-08-486-648-8 Sequence 8, Appl
C 248 13.2 0.8 18 1 US-08-875-445-1 Sequence 1, Appl
C 249 13.2 0.8 18 1 US-08-875-445-11 Sequence 11, Appl
C 250 13.2 0.8 18 1 US-08-358-556A-24 Sequence 24, Appl
C 251 13.2 0.8 15 1 US-08-611-280-15 Sequence 15, Appl
C 252 13.2 0.8 18 1 US-08-734-973-30 Sequence 30, Appl

253	13.2	0.8	18	1	US-08-481-876-5	Sequence 5, Appli	326	12.8	0.8	17	1	US-08-584-040-3971	Sequence 3971, Ap
c 254	13.2	0.8	18	1	US-08-885-126-12	Sequence 12, Appli	c 327	12.8	0.8	17	1	US-08-584-040-7869	Sequence 7869, Ap
c 255	13.2	0.8	18	1	US-08-486-307-7	Sequence 7, Appli	c 328	12.8	0.8	17	1	US-09-220-510B-1	Sequence 1, Appli
256	13.2	0.8	18	1	US-08-486-307-8	Sequence 8, Appli	c 329	12.8	0.8	17	1	US-09-343-698-2	Sequence 2, Appli
257	13.2	0.8	18	1	US-09-205-860-14	Sequence 14, Appli	c 330	12.8	0.8	17	1	US-09-474-432B-592	Sequence 592, App
c 258	13.2	0.8	18	1	US-09-205-921-34	Sequence 34, Appli	c 331	12.8	0.8	17	1	US-09-474-432B-815	Sequence 815, App
c 259	13.2	0.8	18	1	US-09-289-376-9	Sequence 9, Appli	c 332	12.8	0.8	17	1	US-09-371-772B-7	Sequence 7, Appli
c 260	13.2	0.8	18	1	US-09-289-376-30	Sequence 30, Appli	c 333	12.8	0.8	17	1	US-09-371-772B-674	Sequence 674, App
c 261	13.2	0.8	18	1	US-09-185-437-5	Sequence 5, Appli	c 334	12.8	0.8	17	1	US-09-371-772B-1738	Sequence 1738, Ap
c 262	13.2	0.8	18	1	US-08-479-795-7	Sequence 7, Appli	c 335	12.8	0.8	17	1	US-09-371-772B-3652	Sequence 3652, Ap
263	13.2	0.8	18	1	US-08-479-795-8	Sequence 8, Appli	c 336	12.8	0.8	17	1	US-09-371-772B-4170	Sequence 4170, Ap
264	13.2	0.8	18	1	US-09-143-212-44	Sequence 44, Appli	c 337	12.8	0.8	17	1	US-09-371-772B-5005	Sequence 5005, Ap
c 265	13.2	0.8	18	1	US-08-987-574-42	Sequence 42, Appli	c 338	12.8	0.8	17	1	US-09-371-772B-5006	Sequence 5006, Ap
c 266	13.2	0.8	18	1	US-08-987-574-43	Sequence 43, Appli	c 339	12.8	0.8	17	1	US-09-371-772B-5007	Sequence 5007, Ap
c 267	13.2	0.8	18	1	US-08-652-425-3	Sequence 3, Appli	c 340	12.8	0.8	17	1	US-09-371-772B-5384	Sequence 5384, Ap
c 268	13.2	0.8	18	1	US-08-538-168-42	Sequence 42, Appli	c 341	12.8	0.8	17	1	US-09-371-772B-674	Sequence 674, App
c 269	13.2	0.8	18	1	US-08-538-168-43	Sequence 43, Appli	c 342	12.8	0.8	17	1	US-09-371-772B-1738	Sequence 1738, Ap
c 270	13.2	0.8	18	1	US-08-849-488-11	Sequence 11, Appli	c 343	12.8	0.8	17	1	US-09-371-772B-3652	Sequence 3652, Ap
271	13.2	0.8	18	1	US-09-195-940-15	Sequence 15, Appli	c 344	12.8	0.8	17	1	US-09-371-772B-5005	Sequence 5005, Ap
c 272	13.2	0.8	18	1	US-09-437-076-3	Sequence 3, Appli	c 345	12.8	0.8	17	1	US-09-371-772B-5006	Sequence 5006, Ap
c 273	13.2	0.8	18	1	US-09-437-076-4	Sequence 4, Appli	c 346	12.8	0.8	17	1	US-09-371-772B-5007	Sequence 5007, Ap
c 274	13.2	0.8	18	1	US-08-885-366-10	Sequence 10, Appli	c 347	12.8	0.8	17	1	US-09-371-772B-5384	Sequence 5384, Ap
c 275	13.2	0.8	18	1	US-09-011-974-42	Sequence 42, Appli	c 348	12.8	0.8	17	1	US-08-448-561-23	Sequence 23, Appli
c 276	13.2	0.8	18	1	US-09-011-974-43	Sequence 43, Appli	c 349	12.8	0.8	17	1	US-08-531-864-9	Sequence 9, Appli
c 277	13.2	0.8	18	1	US-08-484-406-7	Sequence 7, Appli	c 350	12.8	0.8	17	1	US-08-531-864-11	Sequence 11, Appli
c 278	13.2	0.8	18	1	US-08-484-406-8	Sequence 8, Appli	c 351	12.8	0.8	17	1	US-08-373-636C-9	Sequence 9, Appli
c 279	13.2	0.8	18	1	US-08-700-530-4	Sequence 4, Appli	c 352	12.8	0.8	17	1	US-08-373-636C-11	Sequence 11, Appli
c 280	13.2	0.8	18	1	US-08-682-255A-42	Sequence 42, Appli	c 353	12.8	0.8	17	1	US-09-205-921-13	Sequence 13, Appli
c 281	13.2	0.8	18	1	US-08-682-255A-43	Sequence 43, Appli	c 354	12.8	0.8	17	1	US-09-344-520-18	Sequence 18, Appli
c 282	13.2	0.8	18	1	US-09-423-130-42	Sequence 42, Appli	c 355	12.8	0.8	17	1	US-09-029-045-9	Sequence 9, Appli
c 283	13.2	0.8	18	1	US-09-423-130-43	Sequence 43, Appli	c 356	12.8	0.8	17	1	US-08-602-506A-9	Sequence 9, Appli
c 284	13.2	0.8	18	1	US-09-562-466-15	Sequence 15, Appli	c 357	12.8	0.8	17	1	US-08-602-506A-11	Sequence 11, Appli
c 285	13.2	0.8	18	1	US-08-484-203-7	Sequence 7, Appli	c 358	12.8	0.8	17	1	US-09-143-212-46	Sequence 46, Appli
c 286	13.2	0.8	18	1	US-08-484-203-8	Sequence 8, Appli	c 359	12.8	0.8	17	1	US-09-166-186-13	Sequence 13, Appli
c 287	13.2	0.8	18	1	US-08-486-313-7	Sequence 7, Appli	c 360	12.8	0.8	17	1	US-09-197-380-8	Sequence 8, Appli
c 288	13.2	0.8	18	1	US-08-486-313-8	Sequence 8, Appli	c 361	12.8	0.8	17	1	US-08-863-813A-62	Sequence 62, Appli
c 289	13.2	0.8	18	1	US-09-423-978-574	Sequence 574, Ap	c 362	12.8	0.8	17	1	US-08-211-882-15	Sequence 15, Appli
c 290	13.2	0.8	18	1	US-09-423-978-9962	Sequence 9962, Ap	c 363	12.8	0.8	17	1	US-09-487-444-11	Sequence 11, Appli
c 291	13.2	0.8	18	1	US-09-679-298A-25	Sequence 25, Appli	c 364	12.8	0.8	17	1	US-09-266-294-9	Sequence 9, Appli
c 292	13.2	0.8	18	1	PCT-US93-04754-10	Sequence 10, Appli	c 365	12.8	0.8	17	1	US-09-266-294-11	Sequence 11, Appli
c 293	13.2	0.8	18	1	PCT-US96-11786-42	Sequence 42, Appli	c 366	12.8	0.8	17	1	US-09-313-93A-13	Sequence 13, Appli
c 294	13.2	0.8	18	1	PCT-US96-11786-43	Sequence 43, Appli	c 367	12.8	0.8	17	1	US-09-179-281-9	Sequence 9, Appli
c 295	13	0.8	13	1	US-08-623-891-23	Sequence 23, Appli	c 368	12.8	0.8	17	1	US-09-179-281-11	Sequence 11, Appli
c 296	13	0.8	13	1	US-09-340-861-23	Sequence 23, Appli	c 369	12.8	0.8	17	1	US-09-195-940-11	Sequence 11, Appli
c 297	13	0.8	13	1	US-09-634-262-23	Sequence 23, Appli	c 370	12.8	0.8	17	1	US-08-679-645-555	Sequence 555, App
c 298	13	0.8	17	1	US-08-554-612C-35	Sequence 35, Appli	c 371	12.8	0.8	17	1	US-09-562-466-11	Sequence 11, Appli
c 299	13	0.8	18	1	US-09-205-860-11	Sequence 11, Appli	c 372	12.8	0.8	17	1	US-09-633-659-15	Sequence 15, Appli
c 300	13	0.8	18	1	US-09-344-579-42	Sequence 42, Appli	c 373	12.8	0.8	17	1	US-09-015-188-10	Sequence 10, Appli
c 301	13	0.8	18	1	US-09-422-978-5498	Sequence 5498, Ap	c 374	12.8	0.8	17	1	US-09-516-911-4	Sequence 4, Appli
c 302	12.8	0.8	16	1	US-08-181-664-18	Sequence 18, Appli	c 375	12.8	0.8	17	1	US-09-435-321-9	Sequence 9, Appli
c 303	12.8	0.8	16	1	US-09-371-772B-5649	Sequence 5649, Ap	c 376	12.8	0.8	17	1	US-09-362-842-57	Sequence 57, Appli
c 304	12.8	0.8	17	1	US-08-064-400B-14	Sequence 14, Appli	c 377	12.8	0.8	17	1	US-09-422-978-5567	Sequence 5567, Ap
c 305	12.8	0.8	17	1	US-08-281-940-15	Sequence 15, Appli	c 378	12.8	0.8	17	1	US-09-679-298A-30	Sequence 30, Appli
c 306	12.8	0.8	17	1	US-08-281-940-32	Sequence 32, Appli	c 379	12.8	0.8	17	1	US-09-083-123-5	Sequence 5, Appli
c 307	12.8	0.8	17	1	US-08-379-078-459	Sequence 459, App	c 380	12.4	0.8	14	1	US-08-985-162-1770	Sequence 1770, Ap
c 308	12.8	0.8	17	1	US-08-486-408-4	Sequence 4, Appli	c 381	12.4	0.8	15	1	US-07-997-455-4	Sequence 4, Appli
c 309	12.8	0.8	17	1	US-08-758-308-795	Sequence 795, App	c 382	12.4	0.8	15	1	US-08-153-051B-52	Sequence 52, Appli
c 310	12.8	0.8	17	1	US-08-710-134-15	Sequence 15, Appli	c 383	12.4	0.8	15	1	US-08-291-932A-266	Sequence 266, App
c 311	12.8	0.8	17	1	US-08-710-134-32	Sequence 32, Appli	c 384	12.4	0.8	15	1	US-08-060-952C-51	Sequence 51, Appli
c 312	12.8	0.8	17	1	US-08-485-885-15	Sequence 15, Appli	c 385	12.4	0.8	15	1	US-08-363-240A-139	Sequence 139, App
c 313	12.8	0.8	17	1	US-08-485-885-32	Sequence 32, Appli	c 386	12.4	0.8	15	1	US-08-363-240A-140	Sequence 140, App
c 314	12.8	0.8	17	1	US-08-975-570-4	Sequence 4, Appli	c 387	12.4	0.8	15	1	US-08-311-486C-58	Sequence 58, Appli
c 315	12.8	0.8	17	1	US-08-665-259-42	Sequence 42, Appli	c 388	12.4	0.8	15	1	US-08-151-477A-52	Sequence 52, Appli
c 316	12.8	0.8	17	1	US-08-665-259-55	Sequence 55, Appli	c 389	12.4	0.8	15	1	US-08-585-684B-48	Sequence 48, Appli
c 317	12.8	0.8	17	1	US-08-762-500-42	Sequence 42, Appli	c 390	12.4	0.8	15	1	US-08-819-867-79	Sequence 79, Appli
c 318	12.8	0.8	17	1	US-08-762-500-55	Sequence 55, Appli	c 391	12.4	0.8	15	1	US-09-038-073-48	Sequence 48, Appli
c 319	12.8	0.8	17	1	US-08-998-093-32	Sequence 32, Appli	c 392	12.4	0.8	15	1	US-09-081-646-627	Sequence 627, App
c 320	12.8	0.8	17	1	US-08-998-093-49	Sequence 49, Appli	c 393	12.4	0.8	15	1	US-08-464-011B-51	Sequence 51, Appli
c 321	12.8	0.8	17	1	US-09-324-867-54	Sequence 54, Appli	c 394	12.4	0.8	15	1	US-09-378-535-79	Sequence 79, Appli
c 322	12.8	0.8	17	1	US-07-974-409C-72	Sequence 72, Appli	c 395	12.4	0.8	16	1	US-07-991-199B-8	Sequence 8, Appli
c 323	12.8	0.8	17	1	US-09-364-707A-6	Sequence 6, Appli	c 396	12.4	0.8	16	1	US-08-311-760A-349	Sequence 349, App
c 324	12.8	0.8	17	1	US-08-584-040-1462	Sequence 1462, Ap	c 397	12.4	0.8	16	1	US-07-789-738-1	Sequence 1, Appli
c 325	12.8	0.8	17	1	US-08-584-040-2129	Sequence 2129, Ap	c 398	12.4	0.8	16	1	US-08-774-310-349	Sequence 349, App

C 399	12.4	0.8	16	1	PCT-US93-12246-8	Sequence 8, Appli	C 472	12.2	0.8	17	1	US-08-679-645-220	Sequence 220, App	
C 400	12.4	0.8	17	1	US-08-271-3428-77	Sequence 77, Appli	473	12.2	0.8	17	1	US-08-679-645-592	Sequence 652, App	
C 401	12.4	0.8	17	1	US-08-196-218-8	Sequence 8, Appli	C 474	12.2	0.8	17	1	US-09-429-330-79	Sequence 79, Appli	
C 402	12.4	0.8	17	1	US-08-196-218-9	Sequence 9, Appli	C 475	12.2	0.8	17	1	US-09-340-861-30	Sequence 30, Appli	
C 403	12.4	0.8	17	1	US-08-681-953-8	Sequence 8, Appli	C 476	12.2	0.8	17	1	US-09-634-262-30	Sequence 30, Appli	
C 404	12.4	0.8	17	1	US-08-681-953-9	Sequence 9, Appli	477	12.2	0.8	17	1	US-09-343-698-1	Sequence 1, Appli	
C 405	12.4	0.8	17	1	US-08-681-953-11	Sequence 11, Appli	C 478	12.2	0.8	17	1	US-08-912-951-245	Sequence 245, App	
C 406	12.4	0.8	17	1	US-08-748-688-11	Sequence 11, Appli	C 479	12.2	0.8	17	1	US-08-912-951-245	Sequence 245, App	
C 407	12.4	0.8	17	1	US-08-748-688-27	Sequence 27, Appli	480	12.2	0.8	17	1	US-08-912-951-245	Sequence 319, App	
C 408	12.4	0.8	17	1	US-08-476-021A-27	Sequence 27, Appli	481	12.2	0.8	17	1	US-08-474-432B-377	Sequence 377, App	
C 409	12.4	0.8	17	1	US-08-476-021A-27	Sequence 27, Appli	482	12.2	0.8	17	1	US-08-474-432B-377	Sequence 377, App	
C 410	12.4	0.8	17	1	US-08-849-021-16	Sequence 16, Appli	C 483	12.2	0.8	17	1	US-09-474-432B-689	Sequence 689, App	
C 411	12.4	0.8	17	1	US-08-460-890A-8	Sequence 8, Appli	C 484	12.2	0.8	17	1	US-09-371-772B-16	Sequence 16, Appli	
C 412	12.4	0.8	17	1	US-08-167-641C-8	Sequence 8, Appli	485	12.2	0.8	17	1	US-09-371-772B-1739	Sequence 1739, App	
C 413	12.4	0.8	17	1	US-08-985-162-220	Sequence 220, App	C 486	12.2	0.8	17	1	US-09-371-772B-1739	Sequence 1739, App	
C 414	12.4	0.8	17	1	US-08-985-162-221	Sequence 221, App	C 487	12.2	0.8	17	1	US-09-371-772B-1842	Sequence 1842, App	
C 415	12.4	0.8	17	1	US-08-779-916A-77	Sequence 77, Appli	488	12.2	0.8	17	1	US-09-371-772B-1842	Sequence 1842, App	
C 416	12.4	0.8	17	1	US-08-988-099-10	Sequence 10, Appli	C 489	12.2	0.8	17	1	US-09-371-772B-3046	Sequence 3046, App	
C 417	12.4	0.8	17	1	US-08-988-099-47	Sequence 47, Appli	490	12.2	0.8	17	1	US-09-371-772B-4199	Sequence 4199, App	
C 418	12.4	0.8	17	1	US-08-988-099-48	Sequence 48, Appli	C 491	12.2	0.8	17	1	US-09-371-772B-4192	Sequence 4192, App	
C 419	12.4	0.8	17	1	US-08-988-099-75	Sequence 75, Appli	492	12.2	0.8	17	1	US-09-371-772B-4561	Sequence 4561, App	
C 420	12.4	0.8	17	1	US-08-988-099-120	Sequence 120, App	C 493	12.2	0.8	17	1	US-09-371-772B-4608	Sequence 4608, App	
C 421	12.4	0.8	17	1	US-08-460-971A-8	Sequence 8, Appli	C 494	12.2	0.8	20	1	US-08-136-811-23	Sequence 23, Appli	
C 422	12.4	0.8	17	1	US-08-462-040-8	Sequence 8, Appli	C 495	12.2	0.8	20	1	US-08-835-770-23	Sequence 23, Appli	
C 423	12.4	0.8	17	1	US-08-476-023A-27	Sequence 27, Appli	C 496	12.2	0.8	20	1	US-08-634-262-42	Sequence 42, Appli	
C 424	12.4	0.8	17	1	US-08-584-040-5410	Sequence 5410, App	C 504	12	0.8	14	1	US-08-985-162-1759	Sequence 1759, App	
C 425	12.4	0.8	17	1	US-09-474-432B-599	Sequence 599, App	C 505	12	0.8	14	1	US-08-985-162-1760	Sequence 1760, App	
C 426	12.4	0.8	17	1	US-09-474-432B-697	Sequence 697, App	C 506	12	0.8	15	1	US-08-319-492B-57	Sequence 57, Appli	
C 427	12.4	0.8	17	1	US-09-474-432B-758	Sequence 758, App	C 507	12	0.8	15	1	US-08-319-492B-58	Sequence 58, Appli	
C 428	12.4	0.8	17	1	US-09-474-432B-818	Sequence 818, App	508	12	0.8	15	1	US-08-929-856-57	Sequence 57, Appli	
C 429	12.4	0.8	17	1	US-09-371-772B-2309	Sequence 2309, App	C 509	12	0.8	15	1	US-09-275-850-25	Sequence 25, Appli	
C 430	12.4	0.8	17	1	US-09-371-772B-4193	Sequence 4193, App	C 510	12	0.8	15	1	US-08-081-646-571	Sequence 571, App	
C 431	12.4	0.8	17	1	US-09-371-772B-4965	Sequence 4965, App	C 511	12	0.8	15	1	US-09-344-667-9	Sequence 9, Appli	
C 432	12.4	0.8	17	1	US-09-371-772B-4966	Sequence 4966, App	C 512	12	0.8	15	1	US-09-693-352-9	Sequence 9, Appli	
C 433	12.4	0.8	17	1	US-09-371-772B-4967	Sequence 4967, App	C 513	12	0.8	15	1	US-09-565-063-6	Sequence 6, Appli	
C 434	12.4	0.8	17	1	PCT-US95-08604-77	Sequence 77, Appli	C 514	12	0.8	15	1	US-09-693-005A-9	Sequence 9, Appli	
C 435	12.4	0.8	30	1	US-08-068-747-2	Sequence 2, Appli	C 515	12	0.8	15	1	US-09-603-830-9	Sequence 9, Appli	
C 436	12.2	0.8	17	1	US-08-127-954-8	Sequence 8, Appli	C 516	12	0.8	15	1	US-09-976-978A-9	Sequence 9, Appli	
C 437	12.2	0.8	17	1	US-08-136-538-15	Sequence 15, Appli	C 517	12	0.8	15	1	US-09-961-949A-9	Sequence 9, Appli	
C 438	12.2	0.8	17	1	US-08-233-030-48	Sequence 48, Appli	C 518	12	0.8	16	1	PCT-US94-12947A-20	Sequence 20, Appli	
C 439	12.2	0.8	17	1	US-08-373-124A-1477	Sequence 1477, App	519	12	0.8	17	1	US-08-152-313-20	Sequence 20, Appli	
C 440	12.2	0.8	17	1	US-08-530-492-57	Sequence 57, Appli	520	12	0.8	17	1	US-08-579-223-20	Sequence 20, Appli	
C 441	12.2	0.8	17	1	US-08-623-891-30	Sequence 30, Appli	C 522	12	0.8	17	1	US-08-584-040-3970	Sequence 3970, App	
C 442	12.2	0.8	17	1	US-08-758-306-11	Sequence 11, Appli	C 523	12	0.8	17	1	US-08-584-040-7583	Sequence 7583, App	
C 443	12.2	0.8	17	1	US-08-758-306-455	Sequence 455, App	C 524	12	0.8	17	1	US-08-584-040-7584	Sequence 7584, App	
C 444	12.2	0.8	17	1	US-08-758-306-457	Sequence 457, App	C 525	12	0.8	17	1	US-08-679-645-829	Sequence 829, App	
C 445	12.2	0.8	17	1	US-08-758-306-459	Sequence 459, App	C 526	12	0.8	17	1	US-09-474-432B-587	Sequence 587, App	
C 446	12.2	0.8	17	1	US-08-758-306-463	Sequence 463, App	C 527	12	0.8	17	1	US-09-474-432B-878	Sequence 878, App	
C 447	12.2	0.8	17	1	US-08-758-306-811	Sequence 811, App	C 528	12	0.8	17	1	US-09-371-772B-1737	Sequence 1737, App	
C 448	12.2	0.8	17	1	US-08-435-628-1477	Sequence 1477, App	C 529	12	0.8	17	1	US-09-371-772B-3379	Sequence 3379, App	
C 449	12.2	0.8	17	1	US-08-173-489C-96	Sequence 96, Appli	C 530	12	0.8	17	1	US-09-371-772B-3380	Sequence 3380, App	
C 450	12.2	0.8	17	1	US-08-849-021-3	Sequence 3, Appli	531	12	0.8	17	1	US-09-371-772B-6382	Sequence 6382, App	
C 451	12.2	0.8	17	1	US-08-849-021-4	Sequence 4, Appli	C 532	12	0.8	17	1	PCT-US94-12947A-20	Sequence 20, Appli	
C 452	12.2	0.8	17	1	US-08-849-021-5	Sequence 5, Appli	C 533	11.8	0.7	15	1	US-08-182-968A-375	Sequence 375, App	
C 453	12.2	0.8	17	1	US-08-985-162-553	Sequence 5, Appli	C 534	11.8	0.7	15	1	US-08-334-847-117	Sequence 117, App	
C 454	12.2	0.8	17	1	US-08-985-162-554	Sequence 554, App	535	11.8	0.7	15	1	US-08-363-240A-9	Sequence 9, Appli	
C 455	12.2	0.8	17	1	US-08-388-029A-4	Sequence 4, Appli	C 536	11.8	0.7	15	1	US-08-363-240A-199	Sequence 199, App	
C 456	12.2	0.8	17	1	US-08-974-549A-478	Sequence 478, App	537	11.8	0.7	15	1	US-08-363-240A-647	Sequence 647, App	
C 457	12.2	0.8	17	1	US-09-906-517-57	Sequence 57, Appli	C 538	11.8	0.7	15	1	US-08-363-240A-648	Sequence 648, App	
C 458	12.2	0.8	17	1	US-09-040-774-8	Sequence 8, Appli	539	11.8	0.7	15	1	US-08-363-240A-659	Sequence 659, App	
C 459	12.2	0.8	17	1	US-08-324-867-61	Sequence 61, Appli	540	11.8	0.7	15	1	US-08-363-240A-660	Sequence 660, App	
C 460	12.2	0.8	17	1	US-08-861-450A-6	Sequence 6, Appli	C 541	11.8	0.7	15	1	US-08-311-486C-57	Sequence 57, Appli	
C 461	12.2	0.8	17	1	US-09-017-974-79	Sequence 79, Appli	C 542	11.8	0.7	15	1	US-08-311-486C-165	Sequence 165, App	
C 462	12.2	0.8	17	1	US-08-584-040-1471	Sequence 1471, App	C 543	11.8	0.7	15	1	US-08-311-486C-675	Sequence 675, App	
C 463	12.2	0.8	17	1	US-08-584-040-3972	Sequence 3972, App	C 544	11.8	0.7	15	1	US-08-292-630A-200	Sequence 200, App	
C 464	12.2	0.8	17	1	US-08-584-040-3997	Sequence 3997, App								
C 465	12.2	0.8	17	1	US-08-584-040-3997	Sequence 3997, App								
C 466	12.2	0.8	17	1	US-08-584-040-4075	Sequence 4075, App								
C 467	12.2	0.8	17	1	US-08-584-040-7232	Sequence 7232, App								
C 468	12.2	0.8	17	1	US-08-679-645-70	Sequence 70, Appli								
C 469	12.2	0.8	17	1	US-08-679-645-218	Sequence 218, App								
C 470	12.2	0.8	17	1	US-08-679-645-218	Sequence 218, App								
C 471	12.2	0.8	17	1	US-08-679-645-220	Sequence 220, App								

545 11.8 0.7 15 1 US-08-173-489C-329
546 11.8 0.7 15 1 US-08-774-306A-375
547 11.8 0.7 15 1 US-08-232-081B-16
548 11.8 0.7 15 1 US-08-856-141-19
549 11.8 0.7 15 1 US-08-849-021-8
550 11.8 0.7 15 1 US-08-849-021-10
551 11.8 0.7 15 1 US-08-629-039-11
552 11.8 0.7 15 1 US-08-550-120-3
553 11.8 0.7 15 1 US-08-667-939A-11
554 11.8 0.7 15 1 US-08-667-939A-22
555 11.8 0.7 15 1 US-08-994-946A-10
556 11.8 0.7 15 1 US-09-284-782-8
557 11.8 0.7 15 1 US-08-827-036A-14
558 11.8 0.7 15 1 US-09-064-156A-375
559 11.8 0.7 15 1 US-09-071-845-200
560 11.8 0.7 15 1 US-08-787-321-24
561 11.8 0.7 15 1 US-09-043-303-15
562 11.8 0.7 15 1 US-09-081-646-344
563 11.8 0.7 15 1 US-09-081-646-424
564 11.8 0.7 15 1 US-09-081-646-484
565 11.8 0.7 15 1 US-09-081-646-730
566 11.8 0.7 15 1 US-09-495-140-19
567 11.8 0.7 15 1 US-08-433-123-11
568 11.8 0.7 15 1 US-08-433-123-22
569 11.8 0.7 15 1 US-09-586-376-9
570 11.8 0.7 16 1 US-08-086-915-6
571 11.8 0.7 16 1 US-07-977-284A-150
572 11.8 0.7 16 1 US-08-222-177A-439
573 11.8 0.7 16 1 US-08-166-664-10
574 11.8 0.7 16 1 US-08-137-117D-97
575 11.8 0.7 16 1 US-08-367-069-10
576 11.8 0.7 16 1 US-08-436-717-97
577 11.8 0.7 16 1 US-08-574-586-3
578 11.8 0.7 16 1 US-08-574-586-3
579 11.8 0.7 16 1 US-08-256-568B-42
580 11.8 0.7 16 1 US-08-433-871C-52
581 11.8 0.7 16 1 US-08-256-426B-150
582 11.8 0.7 16 1 US-08-883-126-7
583 11.8 0.7 16 1 US-08-883-126-8
584 11.8 0.7 16 1 US-08-883-126-8
585 11.8 0.7 16 1 US-09-113-869-1
586 11.8 0.7 16 1 US-08-941-445A-28
587 11.8 0.7 16 1 US-08-611-587-16
588 11.8 0.7 16 1 US-08-814-412-9
589 11.8 0.7 16 1 US-08-814-412-45
590 11.8 0.7 16 1 US-09-038-369B-42
591 11.8 0.7 16 1 US-09-109-663-69
592 11.8 0.7 16 1 US-09-411-862A-21
593 11.8 0.7 16 1 US-09-411-862A-22
594 11.8 0.7 16 1 US-09-732-990-5
595 11.8 0.7 16 1 US-09-270-956-52
596 11.8 0.7 16 1 US-09-378-900A-42
597 11.8 0.7 16 1 US-09-899-044-42
598 11.8 0.7 16 1 US-09-371-772B-5646
599 11.8 0.7 16 1 US-09-371-772B-5650
600 11.8 0.7 16 1 US-09-371-772B-5656
601 11.8 0.7 16 1 US-09-371-772B-5917
602 11.8 0.7 16 1 US-09-371-772B-6069
603 11.8 0.7 16 1 US-09-371-772B-6070
604 11.8 0.7 16 1 US-09-371-772B-6071
605 11.8 0.7 16 1 US-09-371-772B-6072

ALIGNMENTS

RESULT 1
US-09-325-256-31/c
; Sequence 31, Application US/09325256
; Patent No. 6444793
; GENERAL INFORMATION:
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: BAKER, DARREN P.

; APPLICANT: WEN, DINGYI
; APPLICANT: WILLIAMS, KEVIN P.
; APPLICANT: GARGER, ELLEN A.
; APPLICANT: TAYLOR, FREDERICK R.
; APPLICANT: GALDES, ALPHONSE
; APPLICANT: PORTER, JEFFREY
; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
; FILE REFERENCE: BIV-067 01
; CURRENT APPLICATION NUMBER: US/09/325,256
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 60/099,800
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/078,935
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/089,685
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/067,423
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: PCT/US98/25676
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-325-256-31

Query Match 2.3%; Score 36; DB 1; Length 49;
Best Local Similarity 88.8%; Pred. No. 0.073;
Matches 39; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 703 GGTGAAGCAGAGAACTCGTGGCGCCAAATCGGAGGCTGT 746
Db 49 GGTGAAGCAGAGAACTCGTGGCGCCAAATCGGAGGCTGT 6

RESULT 2
US-08-068-747-7
; Sequence 7, Application US/08068747
; Patent No. 5695933
; GENERAL INFORMATION:
; APPLICANT: Schalling, Martin
; APPLICANT: Hudson, Thomas J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: Direct Determination of Expanded
; TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,747
; FILING DATE: 28-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-6141
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240

```
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic"
US-08-068-747-7

Query Match 1.6%; Score 25; DB 1; Length 33;
Best Local Similarity 84.8%; Pred. No. 4.7;
Matches 28; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1351 CAGCGCGCGCGGACCGCGCGCGCGCGCGG 1383
Db 1 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 33

RESULT 3
US-08-748-591-11
; Sequence 11, Application US/08748591
; Patent No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zhilan
; APPLICANT: Bonifas, Jeanette
; TITLE OF INVENTION: Mucant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson
; STREET: 2200 Sand Hill Road
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,591
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06510/067001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-748-591-11

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCC 547
Db 1 ACCGAGGGCTGGGACGAGATGCC 24

RESULT 4
US-08-356-060A-43
; Sequence 43, Application US/08356060A
; Patent No. 5844079
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,060A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI-006CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-356-060A-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCC 547
Db 1 ACCGAGGGCTGGGACGAGATGCC 24

RESULT 5
US-08-460-900C-43
; Sequence 43, Application US/08460900C
; Patent No. 6165747
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumcrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,900C
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-460-900C-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
DB 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 6
US-08-674-509B-43
; Sequence 43, Application US/08674509B
; Patent No. 6261786
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Marigo, Valeria
; TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,509B
; FILING DATE: 02-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/460,900
; FILING DATE: 05-JUN-1995
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; US-08-674-509B-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGGCTGGGACGAGATGCG 547
DB 1 ACCGAGGGCTGGGACGAGATGCG 24

RESULT 7
US-08-954-698-43
; Sequence 43, Application US/08954698
; Patent No. 6271363
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,698
; FILING DATE: 20-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,386
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 04-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-954-698-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGCTGGGACGAAGATGCC 547
DB 1 ACCGAGGCTGGGACGAAGATGCC 24

RESULT 8

US-08-957-874-43
Sequence 43, Application US/08957874
Patent No. 6384192

GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
McMahon, Andrew P.
Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,874
FILING DATE: 20-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.09
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-08-957-874-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGCTGGGACGAAGATGCC 547
DB 1 ACCGAGGCTGGGACGAAGATGCC 24

RESULT 9

US-09-639-695-43
Sequence 43, Application US/09639695
Patent No. 6576237

GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
McMahon, Andrew P.
Tabin, Clifford J.
Bumcrot, David A.
Marti-Gorostiza, Elisa

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/639,695
FILING DATE: 16-Aug-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995

APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994

APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.05

TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-639-695-43

Query Match 1.5%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 ACCGAGGCTGGGACGAAGATGCC 547
DB 1 ACCGAGGCTGGGACGAAGATGCC 24

RESULT 10

US-08-068-747-2/c
Sequence 2, Application US/08068747
Patent No. 5695933

GENERAL INFORMATION:

APPLICANT: Schalling, Martin

APPLICANT: Hudson, Thomas J.
APPLICANT: Housman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
TITLE OF INVENTION: Nucleotide Repeats in the Human Genome
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-6141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-08-068-747-2

Query Match 1.5%; Score 23.6; DB 1; Length 30;
Best Local Similarity 86.7%; Pred. No. 7;
Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1354 CGCGCGCGGGACCGCGGGCGCGCGCGCGG 1383
DB 30 CGCGCGCGCGCGCGCGCGCGCGCGCGCGG 1

RESULT 11
US-08-748-591-12/C
Sequence 12, Application US/08748591
Patent No. 5759811
GENERAL INFORMATION:
APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-748-591-12

Query Match 1.5%; Score 23.4; DB 1; Length 25;
Best Local Similarity 96.0%; Pred. No. 4.5;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 616 CAGCAAGTACGCGCATGCTGGCCGC 640
DB 25 CAGCAAGTACGCGCATGCTGGCTGC 1

RESULT 12
US-09-475-947A-332
Sequence 332, Application US/09475947A
Patent No. 6472154
GENERAL INFORMATION:
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTS00667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 332
LENGTH: 30
TYPE: DNA
ORGANISM: human
US-09-475-947A-332

Query Match 1.4%; Score 22.6; DB 1; Length 30;
Best Local Similarity 86.2%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1355 GCGCGCGGGACCGCGGGCGCGCGCGG 1383
DB 1 GCGCGCGCGCGCGCGCGCGCGCGCGG 29

RESULT 13
US-09-083-123-5/c
Sequence 5, Application US/09083123
Patent No. 6326143
GENERAL INFORMATION:
APPLICANT: Orum, Hendrik
APPLICANT: Seeger, Corina
TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
FILE REFERENCE: sequence listing
CURRENT APPLICATION NUMBER: US/09/083,123
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: EP 95118600.6
EARLIER FILING DATE: 1995-11-25
EARLIER APPLICATION NUMBER: PCT/EP96/05149
EARLIER FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5


```

/ APPLICANT: Hu, Zhilan
/ APPLICANT: Bonifas, Jeanette
/ TITLE OF INVENTION: Mutant Human Hedgehog Gene
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish and Richardson
/ STREET: 2200 Sand Hill Road
/ CITY: Menlo Park
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/748,591
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sherwood, Pamela J
/ REGISTRATION NUMBER: 36,677
/ REFERENCE/DOCKET NUMBER: 06510/067001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 322-5070
/ TELEFAX: (415) 854-0875
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-748-591-21

Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 784 CACCAAGCTGTTGAAGGAC 802
DB 19 CACCAAGCTGTTGAAGGAC 1

RESULT 16
US-09-102-491-5
/ Sequence 5, Application US/09102491
/ Patent No. 6238876
/ GENERAL INFORMATION:
/ APPLICANT: Altaba, Ariel Ruiz
/ TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND TREATMENT
/ OF SPORADIC BASAL CELL CARCINOMA
/ FILE REFERENCE: 1049-1-008N
/ CURRENT APPLICATION NUMBER: US/09/102,491
/ CURRENT FILING DATE: 1998-06-22
/ EARLIER APPLICATION NUMBER: 60/050,286
/ EARLIER FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-102-491-5

Query Match 1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 GAAGATCTCCAGAACTCC 361

```

```
Db      1 GAAGATCTCCAGAACTCC 19
|||||
RESULT 17
US-09-102-491-9
; Sequence 9, Application US/09102491
; Patent No. 6238876
; GENERAL INFORMATION:
; APPLICANT: Altaba, Ariel Ruizi
; TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND TREATMENT
; FILE OF INVENTION: OF SPORADIC BASAL CELL CARCINOMA
; FILE REFERENCE: 1049-1-008N
; CURRENT APPLICATION NUMBER: US/09/102,491
; CURRENT FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/050,286
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-102-491-9

Query Match      1.2%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      167 AGATGTCGCTGCTAGTCC 185
|||||
Db      1 AGATGTCGCTGCTAGTCC 19
|||||

RESULT 18
US-08-374-144-3
; Sequence 3, Application US/08374144
; Patent No. 5629147
; GENERAL INFORMATION:
; APPLICANT: Arogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; FILE OF INVENTION: Maternal Blood for In Situ Hybridization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman Wilf & Fried
; STREET: 20 West Third Street, P.O. Box 703
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-085
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-374-144-3

Query Match      1.2%; Score 19; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1357 CGCGGGGACCGCGGGGGCGGC 1381
|||||
Db      1 CGCGGGGACCGCGGGGGCGGC 25
|||||

RESULT 19
US-08-775-164-3
; Sequence 3, Application US/08775164
; Patent No. 5766843
; GENERAL INFORMATION:
; APPLICANT: Arogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman & Associates
; STREET: 20 West Third Street, P.O. Box 1969
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-775-164-3

Query Match      1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1357 CGCGGGGACCGCGGGGGCGGC 1381
|||||
Db      1 CGCGGGGACCGCGGGGGCGGC 25
|||||

RESULT 20
US-08-775-609-3
; Sequence 3, Application US/08775609
; Patent No. 5858649
; GENERAL INFORMATION:
; APPLICANT: Arogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
```

```

;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman & Associates
; STREET: 20 West Third Street, P.O. Box 1969
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,609
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-775-609-3

Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGCGGACCGCGGGCGCGCGC 1381
Db 1 CGCGCGGCGCGCGCGCGCGCGC 25

RESULT 21
US-08-775-607-3
; Sequence 3, Application US/08775607
; Patent No. 5861253
; GENERAL INFORMATION:
; APPLICANT: Aptogenex, Inc.
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Elman & Associates
; STREET: 20 West Third Street, P.O. Box 1969
; CITY: Media
; STATE: PA
; COUNTRY: USA
; ZIP: 19063-8969
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 720K diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,607
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerry J. Elman
; REGISTRATION NUMBER: 24,404
; REFERENCE/DOCKET NUMBER: M19-103
; TELECOMMUNICATION INFORMATION:

```

```

;
; TELEPHONE: 610-892-9580
; TELEFAX: 610-892-9577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-775-607-3

Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGCGGACCGCGGGCGCGCGC 1381
Db 1 CGCGCGGCGCGCGCGCGCGCGC 25

RESULT 22
PCT-US93-06828-3
; Sequence 3, Application PC/TUS9306828
; GENERAL INFORMATION:
; APPLICANT: Asgari, Morteza
; APPLICANT: Bresser, Joel
; APPLICANT: Cubbage, Michael L
; APPLICANT: Prashad, Nagindra
; TITLE OF INVENTION: Enriching and Identifying Fetal Cells In Maternal Blood For
; TITLE OF INVENTION: In Situ Hybridization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:
; STREET:
; CITY:
; STATE:
; COUNTRY:
; ZIP:
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Floppy disk - 720 k
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06828
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; PCT-US93-06828-3

Query Match 1.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1357 CGCGCGGACCGCGGGCGCGCGC 1381

```

Db 1 CGCGCGCGCGCGCGCGCGCGCGC 25

RESULT 23
US-08-384-324-6
Sequence 6, Application US/08384324
Patent No. 5844110
GENERAL INFORMATION:
APPLICANT: Gold, Barry I.
TITLE OF INVENTION: Synthetic Triple Helix-Forming Compounds
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,324
FILING DATE: 31-JAN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63076
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: SV40
POSITION IN GENOME:
CHROMOSOME/SEGMENT: CENTRAL REGION
US-08-384-324-6

Query Match 1.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1001 GAGCCCGAGCGGCTCTCGGGCTC 1023
Db 2 GAGCCCGAGCGGCTCTCGGGCTC 24

RESULT 24
PCT-US96-01473-6
Sequence 6, Application PC/TUS9601473
GENERAL INFORMATION:
APPLICANT: University of Nebraska, Board of Regents
TITLE OF INVENTION: Synthetic Triple Helix-Forming Compounds
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

Query Match 1.2%; Score 18.2; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1001 GAGCCCGAGCGGCTCTCGGGCTC 1023
Db 2 GAGCCCGAGCGGCTCTCGGGCTC 24

RESULT 25
US-09-102-491-6/C
Sequence 6, Application US/09102491
Patent No. 6238876
GENERAL INFORMATION:
APPLICANT: Altaba, Ariel Ruiz
TITLE OF INVENTION: METHODS AND MATERIALS FOR THE DIAGNOSIS AND TREATMENT
OF SPORADIC BASAL CELL CARCINOMA
FILE REFERENCE: 1049-1-008N
CURRENT APPLICATION NUMBER: US/09/102,491
CURRENT FILING DATE: 1998-06-22
EARLIER FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-102-491-6

Query Match 1.1%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 559 GGAGTCTCTGCACTACGA 576
Db 18 GGAGTCTCTGCACTACGA 1

```
RESULT 26
US-09-277-078-24/c
; Sequence 24, Application US/09277078
; Patent No. 6312949
; GENERAL INFORMATION:
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Palmer, Theo
; APPLICANT: Gage, Fred H.
; TITLE OF INVENTION: REGULATION OF TYROSINE HYDROXYLASE
; FILE REFERENCE: 07251/031001
; CURRENT APPLICATION NUMBER: US/09/277,078
; PRIORITY FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for PCR
US-09-277-078-24

Query Match      1.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 40;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      604 TGACCGCGACGCGAGCAAGTA 624
Db      21  TGACAGGGGACCGACGAAGTA 1

RESULT 27
US-08-742-755A-31/c
; Sequence 31, Application US/08742755A
; Patent No. 5858671
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA
; FILE REFERENCE: Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,755A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,755
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: UIZ-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-742-755A-31

Query Match      1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1305 CGCTCCTGGCTGCACTGGCGGCC 1327
Db      24  CACTCCTGGCTGCACTGGCGGCCAC 2

RESULT 28
US-09-226-683-31/c
; Sequence 31, Application US/09226683
; Patent No. 6190889
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA
; FILE REFERENCE: Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,683
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,755
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: UIZ-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-226-683-31

Query Match      1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1305 CGCTCCTGGCTGCACTGGCGGCC 1327
Db      24  CACTCCTGGCTGCACTGGCGGCCAC 2

RESULT 29
US-09-387-699-12
; Sequence 12, Application US/09387699
; Patent No. 6221660
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
```

```

; APPLICANT: Adham, Nika
; APPLICANT: Boyle, No. 62216601
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
; FILE REFERENCE: 56095-A
; CURRENT APPLICATION NUMBER: US/09/387,699
; CURRENT FILING DATE: 1999-08-13
; EARLIER APPLICATION NUMBER: 09/255,376
; EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 12
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-387-699-12

Query Match      1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1247 GTCATCGAGGAGCAGACGCTGGG 1268
DB      3 GACAAAGAGGAGCAGACGCTGGG 24

RESULT 30
US-09-035-183-31/c
; Sequence 31, Application US/09035183
; Patent No. 6258533
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,183
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/742,755
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: UI2-022CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-035-183-31

Query Match      1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1305 CGCTCCTGGCTGCACTGGGGCCC 1327
DB      24 CNCTCCTGGCTGGACTGGGGCAC 2

RESULT 31
US-09-641-259B-12
; Sequence 12, Application US/09641259B
; Patent No. 6468756
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A
; APPLICANT: Borowsky, Beth E
; APPLICANT: Adham, Nika
; APPLICANT: Boyle, No. 64687561
; APPLICANT: Thompson, Thelma O.
; TITLE OF INVENTION: DNA Encoding SNORF25 Receptor
; FILE REFERENCE: 1795/56095-B/JPW/ADM
; CURRENT APPLICATION NUMBER: US/09/641,259B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/US00/04413
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 09/387,699
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: US 09/255,376
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer/ Probe
US-09-641-259B-12

Query Match      1.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1247 GTCATCGAGGAGCAGACGCTGGG 1268
DB      3 GACAAAGAGGAGCAGACGCTGGG 24

RESULT 32
US-08-384-324-6/c
; Sequence 6, Application US/08384324
; Patent No. 5844110
; GENERAL INFORMATION:
; APPLICANT: Gold, Barry I.
; TITLE OF INVENTION: Synthetic Triple Helix-Forming Compounds
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pann, Dorfman, Herrell and Skillman
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,324
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: 63076

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
TOPOLOGY: not relevant
STRANDEDNESS: double
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: SV40
POSITION IN GENOME:
CHROMOSOME/SEGMENT: CENTRAL REGION
US-08-384-324-6

Query Match 1.1%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1e+02; 4; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1001 GAGCCCGAGCGCTCTCGGCTC 1023
Db 24 GAGCCCGAGCGCTCTCGGCTC 2

RESULT 33
PCT-US96-01473-6/c
Sequence 6, Application PC/TUS9601473
GENERAL INFORMATION:
APPLICANT: University of Nebraska, Board of Regents
APPLICANT: Gold, Barry I.
TITLE OF INVENTION: Synthetic Triple Helix-Forming Compounds
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01473
FILING DATE: 29-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/384,324
FILING DATE: 01-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: SV40
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Central Region

PCT-US96-01473-6

Query Match 1.1%; Score 16.6; DB 1; Length 24;
Best Local Similarity 82.6%; Pred. No. 1e+02; 4; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1001 GAGCCCGAGCGCTCTCGGCTC 1023
Db 24 GAGCCCGAGCGCTCTCGGCTC 2

RESULT 34
US-09-377-155-23/c
Sequence 23, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for PCR
US-09-377-155-23

Query Match 1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 329 GGAAGGTATGAAGGGAAG 346
Db 18 GGAAGGTTTGAAGGGAAG 1

RESULT 35
US-09-669-974-23/c
Sequence 23, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: Oligonucleotide primer for PCR
US-09-669-974-23

Query Match 1.0%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 329 GGAGGTATGAAGGAAG 346
|||||
Db 18 GGAGGTATGAAGGAAG 1

RESULT 36
US-09-358-382-10
Sequence 10, Application US/09358382
Patent No. 6010906
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF JUN N-TERMINAL KINASE KINASE-1 EXPRESSION
FILE REFERENCE: RTS-0071
CURRENT APPLICATION NUMBER: US/09/358,382
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 10
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-358-382-10

Query Match 1.0%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1015 CTCGGGCTCGGAGCCGCC 1032
|||||
Db 2 CTCGGGCTCGGAGCCGCC 19

RESULT 37
US-08-863-639A-52/c
Sequence 52, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-55

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1341 GCGCGGGGACAGCGCGCG 1361
|||||
Db 21 GCGCGGGGACAGCGCGCG 1

RESULT 39

TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-52

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1342 GCGCGGGGACAGCGCGCG 1362
|||||
Db 21 GCGCGGGGACAGCGCGCG 1

RESULT 38
US-08-863-639A-55/c
Sequence 55, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Mueth
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-55

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1341 GCGCGGGGACAGCGCGCG 1361
|||||
Db 21 GCGCGGGGACAGCGCGCG 1

RESULT 39


```
US-08-863-639A-56
; Sequence 56, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-56

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1342 CGCGCGGACACGCGCGCGG 1362
Db 1 CGCGCGCGCGCGCGCGG 21

RESULT 40
US-08-863-639A-67/c
; Sequence 67, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-68

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1364 GACCGCGGCGCGCGCGG 1384
Db 21 GCGCGCGCGCGCGCGG 1

RESULT 41
US-08-863-639A-68
; Sequence 68, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueh
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-68
```

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1341 GCGCGGGGACAGCGGGCGGC 1361
DB 1 GCGCGGGGCGGGCGGGCGGC 21

RESULT 42

US-08-863-639A-71
; Sequence 71, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muehl

; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-71

Query Match 1.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1364 GACCGCGGGCGGGCGGGCGGC 1384
DB 1 GCGCGGGGCGGGCGGGCGGC 21

RESULT 43

US-08-416-214A-11
; Sequence 11, Application US/08416214A
; Patent No. 5998596

; GENERAL INFORMATION:

; APPLICANT: Bergan, Raymond; Neckers, Len

; TITLE OF INVENTION: Inhibition Of Protein

; TITLE OF INVENTION: Kinase Activity By Aptameric Action Of

; TITLE OF INVENTION: Oligonucleotides

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/416,214A
; FILING DATE: 04-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Kathryn M.
; REGISTRATION NUMBER: 34,556
; REFERENCE/DOCKET NUMBER: 2026-4166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 base pairs

; TYPE: Nucleic acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; MOLECULE TYPE: Other nucleic acid

; HYPOTHETICAL: Yes

; ANTI-SENSE: No

US-08-416-214A-11

Query Match 1.0%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 86;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1364 GACCGCGGGCGGGCGGGCGGC 1384

DB 1 GCGCGGGGCGGGCGGGCGGC 21

RESULT 44

US-08-956-254-1

; Sequence 1, Application US/08956254A

; Patent No. 6013265

; GENERAL INFORMATION:

; APPLICANT: AURELIAN, LAURE

; TITLE OF INVENTION: Vaccine Composition for Herpes Simplex Virus and

; TITLE OF INVENTION: Methods of Using

; FILE REFERENCE: 1421LA

; CURRENT APPLICATION NUMBER: US/08/956,254A

; CURRENT FILING DATE: 1997-10-22

; EARLIER APPLICATION NUMBER: US 60/029,093

; EARLIER FILING DATE: 1996-10-22

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 21

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:HYBRIDIZATION

; OTHER INFORMATION: PROBE CORRESPONDING TO ICPIOR CODING REGION OF

; OTHER INFORMATION: HSV-2

US-08-956-254-1

Query Match 1.0%; Score 16.2; DB 1; Length 21;

Best Local Similarity 85.7%; Pred. No. 86;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 394 CCGGACATCATATTTAAGGA 414

DB 1 CCCCTTCATCATGTTTAAAGGA 21

```

RESULT 45
US-08-742-755A-32
; Sequence 32, Application US/08742755A
; Patent No. 5858671
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA
; TITLE OF INVENTION: Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,755A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanley, Elizabeth A.
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: UIZ-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-742-755A-32

Query Match 1.0%; Score 16.2; DB 1; Length
Best Local Similarity 85.7%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 3; Indels 0

QY 1307 CTCCTGGCTGCACTGGCGCC 1327
DB 1 CTCCTGCTGGACTGGCGCAC 21

RESULT 46
US-08-742-755A-35/c
; Sequence 35, Application US/08742755A
; Patent No. 5858671
; GENERAL INFORMATION:
; APPLICANT: Jones, Douglas H.
; TITLE OF INVENTION: An Iterative and Regenerative DNA
; TITLE OF INVENTION: Sequencing Method
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-09-226-683-32

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1307 CTCCTGCTGCACTGGCGCC 1327
Db |||||
1 CTCCTGCTGCACTGGCGCAC 21

RESULT 48

US-09-226-683-35/c
; Sequence 35, Application US/09226683
; Patent No. 6190889

GENERAL INFORMATION:

;; APPLICANT: Jones, Douglas H.
;; TITLE OF INVENTION: An Iterative and Regenerative DNA
;; TITLE OF INVENTION: Sequencing Method

;; NUMBER OF SEQUENCES: 41

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LAHIVE & COCKFIELD, LLP

;; STREET: 28 State Street

;; CITY: Boston

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02109-1875

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/226,683

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/742,755

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hanley, Elizabeth A.

;; REGISTRATION NUMBER: 33,505

;; REFERENCE/DOCKET NUMBER: UIZ-022

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617)227-7400

;; TELEFAX: (617)742-4214

;; INFORMATION FOR SEQ ID NO: 35:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 22 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA

US-09-226-683-35

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1307 CTCCTGCTGCACTGGCGCC 1327
Db |||||
22 CTCCTGCTGCACTGGCGCAC 2

RESULT 49

US-09-035-183-32

; Sequence 32, Application US/09035183

; Patent No. 6258533

; GENERAL INFORMATION:

;; APPLICANT: Jones, Douglas H.
;; TITLE OF INVENTION: An Iterative and Regenerative DNA Sequencing Method
;; NUMBER OF SEQUENCES: 41
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LAHIVE & COCKFIELD

;; STREET: 28 State Street

;; CITY: Boston

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02109-1875

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/035,183

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/742,755

;; FILING DATE: 01-NOV-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Hanley, Elizabeth A.

;; REGISTRATION NUMBER: 33,505

;; REFERENCE/DOCKET NUMBER: UIZ-022CP

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617)227-7400

;; TELEFAX: (617)742-4214

;; INFORMATION FOR SEQ ID NO: 32:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 22 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA

US-09-035-183-32

Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1307 CTCCTGCTGCACTGGCGCC 1327
Db |||||
1 CTCCTGCTGCACTGGCGCAC 21

RESULT 50

US-09-035-183-35/c

; Sequence 35, Application US/09035183

; Patent No. 6258533

; GENERAL INFORMATION:

;; APPLICANT: Jones, Douglas H.

;; TITLE OF INVENTION: An Iterative and Regenerative DNA Sequencing Method

;; NUMBER OF SEQUENCES: 41

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LAHIVE & COCKFIELD

;; STREET: 28 State Street

;; CITY: Boston

;; STATE: Massachusetts

;; COUNTRY: USA

;; ZIP: 02109-1875

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/035,183

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/742,755

```
/ FILING DATE: 01-NOV-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanley, Elizabeth A.
/ REGISTRATION NUMBER: 33,505
/ REFERENCE/DOCKET NUMBER: UIZ-022CP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 35:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 22 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-09-035-183-35
Query Match 1.0%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1307 CTCCTGGCTGCATGGGGGCC 1327
Db 22 CTCCTGGCTGCATGGGGCAC 2

RESULT 51
US-08-748-591-13
/ Sequence 13, Application US/08748591
/ Patent No. 5759811
/ GENERAL INFORMATION:
/ APPLICANT: Epstein, Ervin
/ APPLICANT: Hu, Zhilan
/ APPLICANT: Bonifas, Jeanette
/ TITLE OF INVENTION: Mutant Human Hedgehog Gene
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish and Richardson
/ STREET: 2200 Sand Hill Road
/ CITY: Menlo Park
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/748,591
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sherwood, Pamela J
/ REGISTRATION NUMBER: 36,677
/ REFERENCE/DOCKET NUMBER: 06510/067001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 322-5070
/ TELEFAX: (415) 854-0875
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-748-591-18
Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1561 GGCGGGGAGGGGGCC 1576
Db 16 GGCGGGGAGGGGGCC 1

RESULT 53
US-08-748-591-19
/ Sequence 19, Application US/08748591
/ Patent No. 5759811
/ GENERAL INFORMATION:
/ APPLICANT: Epstein, Ervin
/ APPLICANT: Hu, Zhilan
/ APPLICANT: Bonifas, Jeanette
/ TITLE OF INVENTION: Mutant Human Hedgehog Gene
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish and Richardson
/ STREET: 2200 Sand Hill Road
/ CITY: Menlo Park
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94025
/ COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-748-591-19

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 CGCGCGGCGGCACTCG 100
DB 1 CGCGCGGCGGCACTCG 16

RESULT 54
US-08-748-591-20/c
Sequence 20, Application US/08748591
Patent No. 5759811
GENERAL INFORMATION:
APPLICANT: Epstein, Ervin
APPLICANT: Hu, Zhilan
APPLICANT: Bonifas, Jeanette
TITLE OF INVENTION: Mutant Human Hedgehog Gene
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish and Richardson
STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-08-748-591-20

Query Match 1.0%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1561 GGCGCGGAGGGGCC 1576
DB 16 GGCGCGGAGGGGCC 1

RESULT 55
US-08-914-961-2/c
Sequence 2, Application US/08914961
Patent No. 6018042
GENERAL INFORMATION:
APPLICANT: Mett, Helmut
APPLICANT: Haner, Robert
APPLICANT: Dean, Nicholas Mark
TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,961
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,753
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 4-20047/P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8615
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
POSITION IN GENOME:
MAP POSITION: -80
UNITS: bp
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..20
OTHER INFORMATION: /note= "All nucleotides are of the
OTHER INFORMATION: phosphorothioate type"
US-08-914-961-2

Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1341 GGCGCGGGGACAGCGCGG 1359
DB 20 GCAGCGGCGGACAGCGCGG 2

```
RESULT 56
US-08-777-266A-26/c
; Sequence 26, Application US/0877266A
; Patent No. 6077833
; GENERAL INFORMATION:
; APPLICANT: Clarence Frank Bennett
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Oligonucleotide Compositions and
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,266A
; FILING DATE: December 31, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-777-266A-26

Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 898 GAAGGTCTTCTACGTGATC 916
Db 19 GAGGCTCTTCTACGTGAGC 1

RESULT 57
US-09-030-701-65
; Sequence 65, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 65
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; US-09-030-701-65

Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1368 GCGGGGGCGGCGGCGGAG 1386
Db 2 GCGGGCGGCGGCGGCGG 20

RESULT 58
US-09-326-186B-26/c
; Sequence 26, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: 08/777,266
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-326-186B-26

Query Match 1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 898 GAAGGTCTTCTACGTGATC 916
Db 19 GAGGCTCTTCTACGTGAGC 1

RESULT 59
US-09-082-649B-57
; Sequence 57, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-57

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGGCGGGCGGAG 1386
      ||||| ||||| ||||| |||||
DB 2 GCGGGGCGGGCGGGCGGGCGG 20

RESULT 60
US-09-702-327-46/c
; Sequence 46, Application US/09702327
; Patent No. 6426220
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CALRETICULIN EXPRESSION
; FILE REFERENCE: RTS-0097
; CURRENT APPLICATION NUMBER: US/09/702,327
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-327-46

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 525 CCGAGGCTGGGACGAGA 543
      ||||| ||||| ||||| |||||
DB 19 CCGAGGACTGGGATGAAGA 1

RESULT 61
US-09-898-361-147/c
; Sequence 147, Application US/09898361
; Patent No. 6503152
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
; FILE REFERENCE: EXPRESSION
; FILE REFERENCE: RTS-0158
; CURRENT APPLICATION NUMBER: US/09/898,361
; CURRENT FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 147
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-361-147

Query Match      1.0%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 522 TGACCGAGGCTGGGACGA 540
      ||||| ||||| ||||| |||||
DB 19 TGACCGAGTGTGGGACCA 1

RESULT 62
```

```
US-09-339-944-11
; Sequence 11, Application US/09339944
; Patent No. 6114129
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, Babita
; APPLICANT: LONGNECKER, B. Michael
; TITLE OF INVENTION: METHODS OF DETECTING T-CELL ACTIVATION AND TREATING
; FILE REFERENCE: DISORDERS ASSOCIATED WITH T-CELL DYSFUNCTION
; FILE REFERENCE: 042881/0129
; CURRENT APPLICATION NUMBER: US/09/339,944
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,916
; EARLIER FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-339-944-11

Query Match      1.0%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 AAATCGGAGGCTGCTTC 749
      ||||| ||||| ||||| |||||
DB 3 ATATCGAGAGGCTGCTTC 21

RESULT 63
US-08-835-728D-47
; Sequence 47, Application US/08835728D
; Patent No. 6017704
; GENERAL INFORMATION:
; APPLICANT: Herman, James G.
; APPLICANT: Baylin, Stephen B.
; TITLE OF INVENTION: Methylation Specific Detection
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,728D
; FILING DATE: April 11, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/656,716
; FILING DATE: June 03, 1996,
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/125001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```



```
; MOLECULE TYPE: DNA
US-08-835-728D-47

Query Match          1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 375 AACTCACCCTCCCAATTACAAACCC 396
Db 1 AACACACACCACTACAAACCC 22

RESULT 64
US-08-835-728D-151/c
; Sequence 151, Application US/08835728D
; Patent No. 6017704
; GENERAL INFORMATION:
; APPLICANT: Herman, James G.
; APPLICANT: Baylin, Stephen B.
; TITLE OF INVENTION: Methylation Specific Detection
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,558
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,728
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/125001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-490-558-47

Query Match          1.0%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 375 AACTCACCCTCCCAATTACAAACCC 396
Db 1 AACACACACCACTACAAACCC 22

RESULT 66
US-09-490-558-151/c
; Sequence 151, Application US/09490558
; Patent No. 6265171
; GENERAL INFORMATION:
; APPLICANT: Herman, James G.
; APPLICANT: Baylin, Stephen B.
; TITLE OF INVENTION: Methylation Specific Detection
; NUMBER OF SEQUENCES: 216
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,558
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,728
; FILING DATE:

QY 375 AACTCACCCTCCCAATTACAAACCC 396
Db 1 AACACACACCACTACAAACCC 22

RESULT 65
US-09-490-558-47
; Sequence 47, Application US/09490558
; Patent No. 6265171
; GENERAL INFORMATION:
; APPLICANT: Herman, James G.
; APPLICANT: Baylin, Stephen B.
; TITLE OF INVENTION: Methylation Specific Detection
```

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halle, Lisa A.
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/DOCKET NUMBER: 07265/125001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 151:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 22 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-09-490-558-151

Query Match 1.0%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. NO. 1.3e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 375 AACTCACCCTTACACCC 396
 Db 22 AACACACCACTACACCC 1

RESULT 67
 US-09-371-772B-4186
 ; Sequence 4186, Application US/09371772B
 ; Patent No. 6566127
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Pavco, Pam
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Stinchcomb, Dan
 ; APPLICANT: Escobedo, Jaime
 ; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
 ; FILE REFERENCE: MEH00, 876-J (237/198)
 ; CURRENT APPLICATION NUMBER: US/09/371,772B
 ; CURRENT FILING DATE: 1999-08-10
 ; PRIOR APPLICATION NUMBER: US 60/005,974
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: US 08/584,040
 ; PRIOR FILING DATE: 1996-01-08
 ; NUMBER OF SEQ ID NOS: 14225
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4186
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; US-09-371-772B-4186

Query Match 1.0%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 69;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1367 CGCGGGGGCGGGCGG 1383
 Db 1 CGCGGGGGCGGGCGG 17

RESULT 68
 US-08-857-946-14
 ; Sequence 14, Application US/08857946
 ; Patent No. 5994075
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodfellow, P.N.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A
 ; TITLE OF INVENTION: GENE OF INTEREST
 ; NUMBER OF SEQUENCES: 162
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner & Witcoff, Inc.
 ; STREET: 75 State Street

```
;
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3529/59829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-7111
; TELEFAX: 617-227-4399
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-970-740-14
;
Query Match
; Sequence 15, Application US/09198452A
; Best Local Similarity 94.1%; Pred. No. 81; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1368 GCGGGCGGGCGGGCGGC 1384
Db 1 GCGGGCGGGCGGGCGGC 17
;
RESULT 70
US-09-198-452A-5835/c
; Sequence 5835, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5835
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5835
;
Query Match
; Sequence 15, Application US/09197063
; Best Local Similarity 94.1%; Pred. No. 1.1e-02; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 190 CTCCTCGCTGCTGGTAT 206
Db 18 CTCCTCGCTGCTGGCAT 2
;
RESULT 71
US-09-197-063-4
; Sequence 4, Application US/09197063
; Patent No. 6261817
; GENERAL INFORMATION:
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Brown, James R.
; APPLICANT: Biswas, Sanjoy
; APPLICANT: Warren, Richard L.
; APPLICANT: Shilling, Lisa K.
; TITLE OF INVENTION: No. 6261817el Guaa
; FILE REFERENCE: GM10121
; CURRENT APPLICATION NUMBER: US/09/197,063
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/066,350
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
```

```
US-09-197-063-4
;
Query Match
; Sequence 15, Application US/09101886B
; Best Local Similarity 94.1%; Pred. No. 1.4e-02; Length 22;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
QY 1520 ATGGCGGTCAGTCCAG 1536
Db 6 ATGGCGGTCAGTCCAG 22
;
RESULT 72
US-09-101-886B-15
; Sequence 15, Application US/09101886B
; Patent No. 6197507
; GENERAL INFORMATION:
; APPLICANT: BERG, THOMAS
; APPLICANT: TOLLERSUD, OLE K
; APPLICANT: NILSEN, OIVIND
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BARBARA G. ERNST
; STREET: 555 13TH STREET, NW SUITE 701E
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/101,886B
; FILING DATE: 29-JANUARY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/00109
; FILING DATE: 12-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1181-240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-09-101-886B-15
;
Query Match
; Sequence 15, Application US/09150999A
; Best Local Similarity 85.0%; Pred. No. 1.2e-02; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1368 GCGGGCGGGCGGGCGGCAG 1387
Db 1 GTGGCGGGCGGGCGGCTCAGA 20
;
RESULT 73
US-09-150-999-6/c
; Sequence 6, Application US/09150999A
; Patent No. 6306831
; GENERAL INFORMATION:
```

APPLICANT: ROBERTS, Peter C.
APPLICANT: DRIVER, Samuel E.
TITLE OF INVENTION: TRANSPLACENTAL DELIVERY OF OLIGONUCLEOTIDES
FILE REFERENCE: 109-942-114
CURRENT APPLICATION NUMBER: US/09/150,999A
CURRENT FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Combined DNA/RNA Molecule:M13
OTHER INFORMATION: oligonucleotide
OTHER INFORMATION: Description of Artificial Sequence:synthetic
OTHER INFORMATION: oligonucleotide
US-09-150-999-6

Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 CGAGCGGAGCGGAGGAGG 53
DB 20 CGAGCGGAGAGAGGAGG 1

RESULT 74

US-09-487-253A-7/c
Sequence 7, Application US/09487253A
Patent No. 6399763

GENERAL INFORMATION:
APPLICANT: Leon G.J. FRENKEN
APPLICANT: Cornells P.E. VAN DER LOOT
TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODY FRAGMENTS
FILE REFERENCE: 60113/266062 - T3076(C)
CURRENT APPLICATION NUMBER: US/09/487,253A
CURRENT FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: EP 99300351.6
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: MS Word
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PRIMER
US-09-487-253A-7

Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 769 CCTGGAGCGGCGGACCA 788
DB 20 CCTGGAGCGGCGGACCA 1

RESULT 75

US-09-295-593-8
Sequence 8, Application US/09295593
Patent No. 6417169

GENERAL INFORMATION:
APPLICANT: WRIGHT, Jim A.
APPLICANT: YOUNG, Aiping H.
APPLICANT: LEE, Yoon S.
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
FILE REFERENCE: 032396-046
CURRENT APPLICATION NUMBER: US/09/295,593

CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 60/082,791
EARLIER FILING DATE: 1998-04-23
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 8
LENGTH: 20
TYPE: DNA
ORGANISM: Human
US-09-295-593-8

Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1540 AAGCGGGGGCGGGGAG 1559
DB 1 ACGTCGAGGGGGCGGGGAG 20

RESULT 76

US-09-982-465-6/c

Sequence 6, Application US/09982465
Patent No. 6576218
GENERAL INFORMATION:
APPLICANT: Roberts, Peter D.
APPLICANT: Driver, Samuel E.
TITLE OF INVENTION: TRANSPLACENTAL DELIVERY OF OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mintz Levin Cohn Ferris Glosky and
Popeo P.C.
STREET: One Financial Center
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,465
FILING DATE: 18-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/150,999
FILING DATE: 11-Apr-00
APPLICATION NUMBER: 60/058,585
FILING DATE: 12-Sep-97
ATTORNEY/AGENT INFORMATION:
NAME: Elrifi, Ivor R.
REGISTRATION NUMBER: 39,529
REFERENCE/DOCKET NUMBER: QIK-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-6000
TELEFAX: 617-542-2241
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA/RNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-982-465-6

Query Match 1.0%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 34 CGAGCGGAGGAGGAGG 53
Db 20 CGAGCGGAGGAGGAGG 1

RESULT 77
US-08-662-963-9
; Sequence 9, Application US/08662963
; Patent No. 5738993
; GENERAL INFORMATION:
; APPLICANT: Mitsubishi Chemical Corporation
; TITLE OF INVENTION: Oligonucleotide and Method for
; ANALYZING BASE SEQUENCE OF NUCLEIC ACID
; Patent No. 5738993
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., Suite 700
; CITY: Washington, D.C.
; STATE:
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,963

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,147
FILING DATE: February 22, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER: 1416-OP297US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX: (202) 371-8856

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other..synthetic oligonucleotide
US-08-662-963-9

Query Match 1.0%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 AGGAAAGGCGAAGAGAGAG 69
Db 1 AGGAAAGGCGAAGAGAGAG 20

RESULT 78
US-08-748-591-22
; Sequence 22, Application US/08748591
; Patent No. 5759811
; GENERAL INFORMATION:
; APPLICANT: Epstein, Ervin
; APPLICANT: Hu, Zhilan
; APPLICANT: Bonifas, Jeanette
; TITLE OF INVENTION: Mutant Human Hedgehog Gene
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish and Richardson

STREET: 2200 Sand Hill Road
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,591

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06510/067001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-748-591-22

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 221 TCGGACCGGCGGCGG 238
Db 1 TCGGACCGGCGGCGG 18

RESULT 79
US-09-205-860-10/c
; Sequence 10, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-10

Query Match 0.9%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1367 CGCGGGCGGCGGCGG 1384
Db 18 CGAGGCGGCGGCGGCGG 1

RESULT 80
US-09-205-860-13
; Sequence 13, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett

;/ TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION

;/ FILE REFERENCE: RTS-0031

;/ CURRENT APPLICATION NUMBER: US/09/205,860

;/ CURRENT FILING DATE: 1998-12-04

;/ NUMBER OF SEQ ID NOS: 87

;/ SEQ ID NO 13

;/ LENGTH: 18

;/ TYPE: DNA

;/ ORGANISM: Artificial Sequence

;/ FEATURE:

;/ OTHER INFORMATION: Antisense Oligonucleotide

;/ US-09-205-860-13

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 605 GACCGCGGACGCGGAG 622

Db 1 GACCGCGGACGCGGAG 18

RESULT 81

US-08-857-946-8

;/ Sequence 8, Application US/08857946

;/ Patent No. 5994075

;/ GENERAL INFORMATION:

;/ APPLICANT: Goodfellow, P.N.

;/ TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A

;/ NUMBER OF SEQUENCES: 162

;/ CORRESPONDENCE ADDRESS:

;/ ADDRESSER: Banner & Witcoff, Inc.

;/ STREET: 75 State Street

;/ CITY: Boston

;/ STATE: Massachusetts

;/ COUNTRY: USA

;/ ZIP: 02109-1807

;/ COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk

;/ COMPUTER: IBM PC compatible

;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: WordPerfect 6.1

;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/08/857,946

;/ FILING DATE: 16-MAY-1997

;/ CLASSIFICATION: 435

;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: US/60/017,824

;/ FILING DATE: 17-MAY-1996

;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Kathleen M. Williams

;/ REGISTRATION NUMBER: 34,380

;/ REFERENCE/DOCKET NUMBER: 3529/05573

;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: 617-345-9100

;/ TELEFAX: 617-345-9111

;/ INFORMATION FOR SEQ ID NO: 8:

;/ SEQUENCE CHARACTERISTICS:

;/ LENGTH: 18 bases

;/ TYPE: nucleic acid

;/ STRANDEDNESS: single

;/ TOPOLOGY: linear

;/ MOLECULE TYPE: other nucleic acid

;/ US-08-857-946-8

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1341 GCGCGGGGACGCGGCG 1358

Db 1 GCGCGGGGACGCGGCG 18

RESULT 82

US-08-970-740-8

;/ Sequence 8, Application US/08970740

;/ Patent No. 6015670

;/ GENERAL INFORMATION:

;/ APPLICANT: Goodfellow, P.N.

;/ TITLE OF INVENTION: METHODS FOR IDENTIFYING A MUTATION IN A

;/ NUMBER OF SEQUENCES: 162

;/ CORRESPONDENCE ADDRESS:

;/ ADDRESSEE: Banner & Witcoff, Inc.

;/ STREET: 28 State Street, 28th Floor

;/ CITY: Boston

;/ STATE: Massachusetts

;/ COUNTRY: USA

;/ ZIP: 02109

;/ COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk

;/ COMPUTER: IBM PC compatible

;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: WordPerfect 6.1

;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/08/970,740

;/ FILING DATE: 14-NOV-1997

;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: 08/857,946

;/ FILING DATE: 16-MAY-1997

;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: 60/017,824

;/ FILING DATE: 17-MAY-1996

;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Kathleen M. Williams

;/ REGISTRATION NUMBER: 34,380

;/ REFERENCE/DOCKET NUMBER: 3529/59829

;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: 617-227-7111

;/ TELEFAX: 617-227-4399

;/ INFORMATION FOR SEQ ID NO: 8:

;/ SEQUENCE CHARACTERISTICS:

;/ LENGTH: 18 bases

;/ TYPE: nucleic acid

;/ STRANDEDNESS: single

;/ TOPOLOGY: linear

;/ MOLECULE TYPE: other nucleic acid

;/ US-08-970-740-8

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1341 GCGCGGGGACGCGGCG 1358

Db 1 GCGCGGGGACGCGGCG 18

RESULT 83

US-09-593-323-34

;/ Sequence 34, Application US/09593323

;/ Patent No. 6265213

;/ GENERAL INFORMATION:

;/ APPLICANT: Morgan, Antony R.

;/ APPLICANT: Severini, Alberto

;/ TITLE OF INVENTION: Compositions and Methods for Determining the Activity

;/ TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of

;/ TITLE OF INVENTION: Transcription

;/ FILE REFERENCE: DNAB-02921

;/ CURRENT APPLICATION NUMBER: US/09/593,323

;/ CURRENT FILING DATE: 2000-06-13

;/ PRIOR APPLICATION NUMBER: 09/344,300

;/ PRIOR FILING DATE: 1999-06-24

;/ NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 34

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-593-323-34

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GCGGGGACCGCGGGGCG 1376

Db 1 GCGGGGACCGCGGGGCG 18

RESULT 84

US-09-594-108-34

; Sequence 34, Application US/09594108

; Patent No. 6284468

; GENERAL INFORMATION:

; APPLICANT: Morgan, Antony R.

; APPLICANT: Severini, Alberto

; TITLE OF INVENTION: Compositions and Methods for Determining the Activity

; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of

; TITLE OF INVENTION: Transcription

; FILE REFERENCE: DNAB-02921

; CURRENT APPLICATION NUMBER: US/09/594,108

; CURRENT FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: 09/344,300

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 34

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-594-108-34

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GCGGGGACCGCGGGGCG 1376

Db 1 GCGGGGACCGCGGGGCG 18

RESULT 85

US-09-344-300-34

; Sequence 34, Application US/09344300B

; Patent No. 6297013

; GENERAL INFORMATION:

; APPLICANT: Morgan, Antony R.

; APPLICANT: Severini, Alberto

; TITLE OF INVENTION: Compositions and Methods for Determining the Activity

; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of

; TITLE OF INVENTION: Transcription

; FILE REFERENCE: DNAB-02921

; CURRENT APPLICATION NUMBER: US/09/344,300B

; CURRENT FILING DATE: 1999-06-24

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 34

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-344-300-34

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GCGGGGACCGCGGGGCG 1376

Db 1 GCGGGGACCGCGGGGCG 18

RESULT 86

US-08-589-939-37/c

; Sequence 37, Application US/08589939

; Patent No. 6015662

; GENERAL INFORMATION:

; APPLICANT: Hackett, Jr., John R.

; APPLICANT: Hoff, Jane A.

; APPLICANT: Ostrow, David H.

; APPLICANT: Golden, Alan M.

; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND

; TITLE OF INVENTION: CONTROLS

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: US

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/589,939

; FILING DATE:

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Becker, Cheryl L.

; REGISTRATION NUMBER: 35,441

; REFERENCE/DOCKET NUMBER: 5865.US.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847-935-1729

; TELEFAX: 847-938-2623

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-589-939-37

Query Match

Best Local Similarity 0.9%; Score 14.8; DB 1; Length 19;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 526 CGAGGCTGGGACGAAGA 543

Db 19 CGCGGGGTGGGACGAAGA 2

RESULT 87

US-09-009-483A-13

; Sequence 13, Application US/09009483A

; Patent No. 6083699

; GENERAL INFORMATION:

; APPLICANT: Leushner, James

; APPLICANT: Hui, May

; APPLICANT: Dunn, James M.

; APPLICANT: Larson, Marina T.

```

; APPLICANT: Lacroix, Jean-Michel
; APPLICANT: Shipman, Robert
; TITLE OF INVENTION: METHOD FOR BI-DIRECTIONAL SEQUENCING OF
; TITLE OF INVENTION: NUCLEIC ACID POLYMERS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street Suite 309
; CITY: Yorktown
; STATE: NY
; COUNTRY: US
; ZIP: 10598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,483A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: primer for sequencing of exon 3 of HLA-C
; OTHER INFORMATION: gene
US-09-009-483A-13

```

```

Query Match 0.9%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.2e-02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1364 GACCGCGGGGGCGGGCGG 1381
Db 1 GACCGCGGGGGCGGGGCC 18

```

```

RESULT 88
US-07-940-242A-19/c
; Sequence 19, Application US/07940242A
; Patent No. 5427909
; GENERAL INFORMATION:
; APPLICANT: OKAMOTO, Hiroaki
; APPLICANT: NAKAMURA, Tetsuo
; TITLE OF INVENTION: OLIGONUCLEOTIDES AND DETERMINATION
; TITLE OF INVENTION: SYSTEM OF HCV GENOTYPES
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beverage, DeGrandi, Weilacher & Young
; STREET: 1850 M Street, N.W. (Suite 800)
; CITY: Washington
; STATE: D.C.

```

```

; COUNTRY: US
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,242A
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 307296/91
; FILING DATE: 09-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 093960/92
; FILING DATE: 28-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilacher, Robert G.
; REGISTRATION NUMBER: 20,531
; REFERENCE/DOCKET NUMBER: 06/87-48095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2811
; TELEFAX: (202) 659-1462
; TELEX: WUI 64470
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-940-242A-19

```

```

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 119 GACAGCTCGGAGTCATC 136
Db 20 GACCGCTCGGAGTCATC 3

```

```

RESULT 89
US-08-465-485A-28
; Sequence 28, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; CITY: Arlington
; STATE: Virginia
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992

```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 18..19
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
US-08-465-485A-28

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1371 GCGGCGGCGGCGGAG 1388
Db 2 GCGGCGGCGGCGGAG 19

RESULT 90
US-09-366-257-11
Sequence 11, Application US/09366257
Patent No. 6030837
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Madeline M. Butler
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-MITOCHONDRIAL EXPRESSION
FILE REFERENCE: RTG-0073
CURRENT APPLICATION NUMBER: US/09/366,257
CURRENT FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-366-257-11

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 623 TACGGCATGCTGGCCGC 640
Db 3 TACGGCATGATGCCAGC 20

RESULT 91
US-09-080-285-28
Sequence 28, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 18..19
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
US-09-080-285-28

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1371 GCGGCGGCGGCGGAG 1388
Db 2 GCGGCGGCGGCGGAG 19

RESULT 92
US-09-416-756A-4
Sequence 4, Application US/09416756A
Patent No. 6171845
GENERAL INFORMATION:
APPLICANT: Degussa-Huls AG
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF PANTOTHENIC ACID BY
TITLE OF INVENTION: AMPLIFICATION OF NUCLEOTIDE SEQUENCES WHICH CODE FOR
TITLE OF INVENTION: KETOPANTOATE REDUCTASE
FILE REFERENCE: Elischewski
CURRENT APPLICATION NUMBER: US/09/416,756A
CURRENT FILING DATE: 1999-10-12

;; PRIOR APPLICATION NUMBER: DE 19846499.1
;; PRIOR FILING DATE: 1998-10-09
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 20
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-09-416-756A-4

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 561 AGTCTCTGCACTACGAGG 578
Db 3 AGTCTCTTCACTACCAGG 20

RESULT 93
US-09-488-671-156/c
; Sequence 156, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
; FILE REFERENCE: RTS-0123
; CURRENT APPLICATION NUMBER: US/09/488,671A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 156
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-156

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 TCCCAATGTGGCGAGA 311
Db 20 TCACCAACGTGGCGAGA 3

RESULT 94
US-09-724-426-28
; Sequence 28, Application US/09724426
; Patent No. 6414134
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of BCL-2 Gene Expression
; FILE REFERENCE: 10412-024
; CURRENT APPLICATION NUMBER: US/09/724,426
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-426-28

Query Match 0.9%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1371 GCGCGCGCGCGCGAG 1388
Db 2 GCGCGCGCGCGCGAGCG 19

RESULT 95
US-08-410-654B-41/c
; Sequence 41, Application US/08410654B
; Patent No. 5833976
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu
; APPLICANT: Anne O'Garra
; APPLICANT: Hergen Spits
; TITLE OF INVENTION: Use of Interleukin-10 to Treat
; TITLE OF INVENTION: Septic Shock
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,654B
; FILING DATE: 24-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,854
; FILING DATE: 19-APR-1994
; APPLICATION NUMBER: US 07/926,853
; FILING DATE: 06-AUG-1992
; APPLICATION NUMBER: US 07/742,129
; FILING DATE: 06-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: DX0221KQ1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-298-2987
; TELEFAX: 908-298-5388
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-410-654B-41

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GGACAGCTCGGAGTCAT 135
Db 18 GGCCAGCTTGAAGTCAT 1

RESULT 96
US-08-474-851-41/c
; Sequence 41, Application US/08474851
; Patent No. 5837232
; GENERAL INFORMATION:
; APPLICANT: Rene de Waal Malefyt
; APPLICANT: Di-Hwei Hsu

APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of An Interleukin-10 Antagonist to Treat
TITLE OF INVENTION: A B Cell Mediated Autoimmune Disorder
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,851
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQIGD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-5388
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-474-851-41

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GGACAGCTCGGAAGTCAT 135
DB 18 GGCCAGCTTGAAGTCAT 1

RESULT 97
US-08-560-41/c
Sequence 41, Application US/08481560
Patent No. 5837293
GENERAL INFORMATION:
APPLICANT: Rene de Waal Malefyt
APPLICANT: Di-Hwei Hsu
APPLICANT: Anne O'Garra
APPLICANT: Hergen Spits
TITLE OF INVENTION: Use of Interleukin-10 to Modulate
TITLE OF INVENTION: Inflammation or T-Cell Mediated
TITLE OF INVENTION: Immune Function
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey

COUNTRY: USA
ZIP: 07033
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7.5.3
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,560
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,654
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/229,854
FILING DATE: 19-APR-1994
APPLICATION NUMBER: US 07/926,853
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 07/742,129
FILING DATE: 06-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: DX0221KQIGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-5388
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-481-560-41

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GGACAGCTCGGAAGTCAT 135
DB 18 GGCCAGCTTGAAGTCAT 1

RESULT 98
US-08-621-841-15/c
Sequence 15, Application US/08621841
Patent No. 6098869
GENERAL INFORMATION:
APPLICANT: Stanley, Margaret A.
APPLICANT: Scarpini, Cinzia G.
TITLE OF INVENTION: TREATMENT OF PAPILLOMAVIRUS-ASSOCIATED
TITLE OF INVENTION: LESIONS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,841
FILING DATE: 22-MAR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505784.0

```

/ FILING DATE: 22-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dreger, Walter H.
/ REGISTRATION NUMBER: 24,190
/ REFERENCE/DOCKET NUMBER: A-63316
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ US-08-621-841-15

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GCACAGCTCGGAAGTCAT 135
DB 18 GCCCAGCTTGAAGTCAT 1

RESULT 99
US-08-853-980-20
/ Sequence 20, Application US/08853980
/ Patent No. 6225082
/ GENERAL INFORMATION:
/ APPLICANT: Carson, John H.
/ APPLICANT: Kwon, Sunjong
/ APPLICANT: Aigner, Kevin
/ APPLICANT: Avossa, Daniela
/ TITLE OF INVENTION: MYELIN BASIC PROTEIN mRNA TRANSPORT AND TRANSLATION
/ FILE REFERENCE: RCT
/ CURRENT FILING DATE: 1997-05-09
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: mouse PKC alpha
/ US-08-853-980-20

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCACGAGGAGGAGNC 26
DB 1 GCCAGCGAGCCAGAGC 18

RESULT 100
US-08-281-940-45/c
/ Sequence 45, Application US/08281940
/ Patent No. 5589330
/ GENERAL INFORMATION:
/ APPLICANT: SHUBER, ANTHONY P.
/ TITLE OF INVENTION: METHOD FOR MULTIPLE ALLELE-SPECIFIC
/ TITLE OF INVENTION: DISEASE ANALYSIS
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DARBY & DARBY P.C.
/ STREET: 805 THIRD AVENUE
/ CITY: NEW YORK

FILING DATE: 22-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63316
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-621-841-15

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 118 GCACAGCTCGGAAGTCAT 135
DB 18 GCCCAGCTTGAAGTCAT 1

RESULT 99
US-08-853-980-20
/ Sequence 20, Application US/08853980
/ Patent No. 6225082
/ GENERAL INFORMATION:
/ APPLICANT: Carson, John H.
/ APPLICANT: Kwon, Sunjong
/ APPLICANT: Aigner, Kevin
/ APPLICANT: Avossa, Daniela
/ TITLE OF INVENTION: MYELIN BASIC PROTEIN mRNA TRANSPORT AND TRANSLATION
/ FILE REFERENCE: RCT
/ CURRENT FILING DATE: 1997-05-09
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 20
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: mouse PKC alpha
/ US-08-853-980-20

Query Match 0.9%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 GCACGAGGAGGAGNC 26
DB 1 GCCAGCGAGCCAGAGC 18

RESULT 100
US-08-281-940-45/c
/ Sequence 45, Application US/08281940
/ Patent No. 5589330
/ GENERAL INFORMATION:
/ APPLICANT: SHUBER, ANTHONY P.
/ TITLE OF INVENTION: METHOD FOR MULTIPLE ALLELE-SPECIFIC
/ TITLE OF INVENTION: DISEASE ANALYSIS
/ NUMBER OF SEQUENCES: 65
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DARBY & DARBY P.C.
/ STREET: 805 THIRD AVENUE
/ CITY: NEW YORK

```

```
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-710-134-45
    Query Match          0.9%; Score 14.4; DB 1; Length 17;
    Best Local Similarity 93.8%; Pred. No. 1.1e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1514 CTGGCGCATGGCGGTCA 1529
    ||| ||||| ||||| |||||
Db 17 CTGGCGCATGGCGGTCA 2

RESULT 102
US-08-485-885-45/c
; Sequence 45, Application US/08485885
; Patent No. 5849483
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/485,885
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-12.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-485-885-45
    Query Match          0.9%; Score 14.4; DB 1; Length 17;
    Best Local Similarity 93.8%; Pred. No. 1.1e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1514 CTGGCGCATGGCGGTCA 1529
    ||| ||||| ||||| |||||
Db 17 CTGGCGCATGGCGGTCA 2

RESULT 103
US-09-496-694B-99/c
; Sequence 99, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/285,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 99
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-496-694B-99
    Query Match          0.9%; Score 14.4; DB 1; Length 18;
    Best Local Similarity 93.8%; Pred. No. 1.3e+02;
    Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGCGCGCGCGGCA 1385
    ||| ||||| ||||| |||||
Db 18 GGTGGCGCGCGGCA 3

RESULT 104
US-08-679-645-1165/c
; Sequence 1165, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
```

FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-1165

Query Match 0.9%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1368 GCGGGGGGGGGGGG 1383
Db 18 GCGGGGGGGGGGGG 3

RESULT 105

US-09-422-978-7120
; Sequence 7120, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSEI.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7120
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-24232 for SEQ 3186,
US-09-422-978-7120

Query Match 0.9%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 445 GACTCAGAGGTGAAG 460
Db 4 GACGACAGGTGAAG 19

RESULT 106

US-09-513-729B-15
; Sequence 15, Application US/09513729B
; Patent No. 6165791
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2F TRANSCRIPTION FACTOR 3 EXPRESSION
; FILE REFERENCE: RTS-0112

; CURRENT APPLICATION NUMBER: US/09/513,729B
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-513-729B-15

Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1351 CAGCGCGCGGGGAC 1366
Db 4 CAGCGCGCGGGGAC 19

RESULT 107

US-09-593-711A-37
; Sequence 37, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-37

Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1368 GCGGGGGGGGGGCGG 1383
Db 5 GCGGGGGGGGGGCGG 20

RESULT 108

US-09-593-711A-127/c
; Sequence 127, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-127

Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 883 CGACGAGCGGCCCAAG 898
Db 16 CGACTACGGCCCAAG 1

RESULT 109

US-09-593-711A-128/c
; Sequence 128, Application US/09593711A
; Patent No. 6271030

; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia

; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118

; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-05-14

; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 128

; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-128

Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 883 CGACGAGCGGCCCAAG 898
Db 20 CGACTACGGCCCAAG 5

RESULT 110

US-09-702-246-11/c
; Sequence 11, Application US/09702246

; Patent No. 6383809
; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF CYTOKINESIN-1 EXPRESSION
; FILE REFERENCE: RTS-0195

; CURRENT APPLICATION NUMBER: US/09/702,246
; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 11

; LENGTH: 20
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-246-11

Query Match 0.9%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 GCGAGCGCGGCGGAG 47
Db 19 GCGAGCGCGGCGGAG 4

RESULT 111

US-08-860-635A-12/c
; Sequence 12, Application US/08860635A

; Patent No. 6143878
; GENERAL INFORMATION:

; APPLICANT: Koopman, Peter
; APPLICANT: Goodfellow, Peter

; TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
; TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza

; CITY: Garden City
; STATE: NY

; COUNTRY: U.S.A.
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/860,635A
; FILING DATE: 29-MAY-1997

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PM9714
; FILING DATE: 29-NOV-1994

; APPLICATION NUMBER: AU PM9835
; FILING DATE: 05-DEC-1994

; APPLICATION NUMBER: PCT/AU95/00799
; FILING DATE: 29-NOV-1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.

; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10981

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366
; TELEX:

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
US-08-860-635A-12

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GCTCTACGCGACTTCCTC 858
Db 19 GTTCTTACCGACTTCCTC 1

RESULT 112

US-08-348-548-106/c
; Sequence 106, Application US/08348548

; Patent No. 6258529
; GENERAL INFORMATION:

; APPLICANT: Berdoz, Jose
; APPLICANT: Kraehenbuhl, Jean Pierre

; TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
; TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES

; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street, Suite 3100

; CITY: Boston
; STATE: MA

; COUNTRY: USA
; ZIP: 02110-2804

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-348-548-106

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1198 GGCCAGGCGCACCATTCTC 1216
DB 19 GGGCCAGGCGCACCATTCTC 1

RESULT 113
US-09-281-476-12/c
Sequence 12, Application US/09281476
Patent No. 6316597
GENERAL INFORMATION:
APPLICANT: Goodman, Peter
APPLICANT: Goodfellow, Peter
TITLE OF INVENTION: SOX-9 GENE AND PROTEIN AND
TITLE OF INVENTION: USE IN THE REGENERATION OF BONE OR CARTILAGE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/281,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/860,635
FILING DATE:
APPLICATION NUMBER: AU PM9835
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: PCT/AU95/00799
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10981
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-281-476-12

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 850 GCTCTACAGGCGCATTCTC 868
DB 19 GTTCTTCCGCGACTTCTC 1

RESULT 114
PCT-US95-15716-106/c
Sequence 106, Application PC/TUS9515716
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
APPLICANT: Kraehenbuhl, Jean Pierre
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15716
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-15716-106

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1198 GGCCAGGCGCACCATTCTC 1216
DB 19 GGGCCAGGCGCACCATTCTC 1

RESULT 115
US-07-626-618A-10/c
Sequence 10, Application US/07626618A
Patent No. 5422265

Query Match 0.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1198 GGCCAGGCGCACCATTCTC 1216
DB 19 GGGCCAGGCGCACCATTCTC 1

GENERAL INFORMATION:
APPLICANT: Van Tol, Hubert H.M.
APPLICANT: Civelli, Olivier
TITLE OF INVENTION: A No. 5422265el Human Dopamine Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/626,618A
FILING DATE: 7 DEC 1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5422265nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1092
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 810-221-8317
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-626-618A-10

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1355 GCGCGCGGACCGCGGG 1373
DB 20 GCGCGCGGACCGCGGG 2

RESULT 116
US-08-136-811-23
Sequence 23, Application US/08136811
Patent No. 5510239
GENERAL INFORMATION:
APPLICANT: Baracchini, Jr., Edgardo and Bennett,
APPLICANT: Clarence Frank
TITLE OF INVENTION: Oligonucleotide Interference with
TITLE OF INVENTION: Multidrug Resistance
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,811
FILING DATE: Herewith
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 1SPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-136-811-23

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 GCGTGGCGCAGCGCTCTCT 1311
DB 1 GCCAGGCTCAGCGCTGCT 19

RESULT 117
US-08-219-842-62/c
Sequence 62, Application US/08219842
Patent No. 5565323
GENERAL INFORMATION:
APPLICANT: Parker, W. D.
APPLICANT: Herrstadt, Corinna
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: for Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,842
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-219-842-62

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 656 GGCTTCGACTGGGTGACT 674
 Db 19 GGCTTCACCGGAGTACT 1

RESULT 118

US-08-219-842-95
 ; Sequence 95, Application US/08219842
 ; Patent No. 556323
 ; GENERAL INFORMATION:
 ; APPLICANT: Parker, W. D.
 ; APPLICANT: Herinstad, Corinna
 ; TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
 ; TITLE OF INVENTION: for Alzheimer's Disease
 ; NUMBER OF SEQUENCES: 95
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/219,842
 ; FILING DATE: 30-MAR-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-AG 9504
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 95:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-219-842-95

Query Match 0.9%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 656 GGCTTCGACTGGGTGACT 674
 Db 2 GGCTTCACCGGAGTACT 20

RESULT 119

US-08-333-977-10/c
 ; Sequence 10, Application US/08333977
 ; Patent No. 5594108
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Tol, Hubert H.M.
 ; APPLICANT: Civealli, Olivier
 ; TITLE OF INVENTION: A No. 5594108a1 Human Dopamine Receptor and Uses
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Allegretti & Witcoff, Ltd.
 ; STREET: 10 South Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,977
 FILING DATE: 03-NOV-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/626,618
 FILING DATE: 7 DEC 1990
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5594108nan, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 90,1092
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 TELEX: 810-221-8317
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-333-977-10

Query Match 0.9%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 1.9e+02;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1355 GGCGCGGGGACCGCGGG 1373
 Db 20 GGCGCGAGGACCGCGGG 2

RESULT 120

US-08-507-431-35/c
 ; Sequence 35, Application US/08507431
 ; Patent No. 5693518
 ; GENERAL INFORMATION:
 ; APPLICANT: Kofod, Lene V.
 ; APPLICANT: Kauppinen, Markus S.
 ; APPLICANT: Christgau, Stephan
 ; APPLICANT: Heldt-Hansen, Hans P.
 ; APPLICANT: Dalboge, Henrik
 ; APPLICANT: Andersen, Lene N.
 ; APPLICANT: Si, Joan Q.
 ; APPLICANT: Jacobson, Tina
 ; APPLICANT: Munk, Niels
 ; APPLICANT: Mullertz, Anette
 ; TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
 ; TITLE OF INVENTION: ASPERGILLUS ACULEATUS
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 56935180 No. 5693518disk of No. 5693518th America, Inc.
 ; STREET: 405 Lexington Avenue, 64th Floor
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: United States of America
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/507,431
 ; FILING DATE: 15-FEB-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/002,800
 ; FILING DATE: 25-AUG-1996

ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3954.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-507-431-35

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1373 GCGCGCGCGCGCAGTAG 1391
DB 20 GCGCGCGCGCGCAGGAAG 2

RESULT 121
US-08-451-096-62/c
Sequence 62, Application US/08451096
Patent No. 5760205
GENERAL INFORMATION:
APPLICANT: Parker, W. D.
APPLICANT: HerrinStadt, Corinna
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: for Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,096
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-451-096-62

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 656 GCGTCGACTGGGTGACT 674
DB 19 GCGTCACCGGGAGTACT 1

RESULT 122
US-08-451-096-95
Sequence 95, Application US/08451096
Patent No. 5760205
GENERAL INFORMATION:
APPLICANT: Parker, W. D.
APPLICANT: HerrinStadt, Corinna
TITLE OF INVENTION: Diagnostic and Therapeutic Compositions
TITLE OF INVENTION: for Alzheimer's Disease
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,096
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,842
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-AG 9504
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-451-096-95

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 656 GCGTCGACTGGGTGACT 674
DB 2 GCGTCACCGGGAGTACT 20

RESULT 123
US-08-835-770-23
Sequence 23, Application US/08835770
Patent No. 5801154
GENERAL INFORMATION:
APPLICANT: Edgardo Baracchini, Jr., C. Frank Bennett
APPLICANT: and Nicholas M. Dean
TITLE OF INVENTION: Oligonucleotide Modulation of Multidrug
TITLE OF INVENTION: Resistance-Associated Protein
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ

COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFICATION: 514
APPLICATION NUMBER: US/08/835,770
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/136,811
FILING DATE: 10/18/93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/628,731
FILING DATE: 04/16/96
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0208
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-835-770-23

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 GCCTGGCGCACGGCTCCT 1311
Db 1 GCCAGGCTCAGCGCTGCT 19

RESULT 124
US-08-628-731-23
Sequence 23, Application US/08628731
Patent No. 5807838
GENERAL INFORMATION:
APPLICANT: Baracchini, Jr., Edgardo and Bennett,
APPLICANT: Clarence Frank
TITLE OF INVENTION: Oligonucleotide Interference with
TITLE OF INVENTION: Multidrug Resistance
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,731
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/136,811
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata

COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFICATION: 514
APPLICATION NUMBER: US/08/835,770
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/136,811
FILING DATE: 10/18/93
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/628,731
FILING DATE: 04/16/96
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0208
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-835-770-23

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1293 GCCTGGCGCACGGCTCCT 1311
Db 1 GCCAGGCTCAGCGCTGCT 19

RESULT 125
US-08-609-443B-45/c
Sequence 45, Application US/08609443B
Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,259
REFERENCE/DOCKET NUMBER: 1064/41979CP4
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```
;
; MOLECULE TYPE: DNA (genomic)
; US-08-609-443B-45
;
; Query Match 0.9%; Score 14.2; DB 1; Length 20;
; Best Local Similarity 84.2%; Pred. No. 1.9e+02;
; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
QY 1331 CGCAGCGACGGCGGGG 1349
Db 19 CGCAGCTACGTGGCGGGG 1

RESULT 126
US-08-488-940-12/c
; Sequence 12, Application US/08488940
; Patent No. 5854049
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: PLASMIN-RESISTANT STREPTOKINASE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,940
; FILING DATE: 09-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-488-940-12

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 960 ACCTGCTCTTTGTGGCGCC 978
Db 19 ACCTGCTCATGGAGCGCC 1

RESULT 127
US-08-223-355-23/c
; Sequence 23, Application US/08223355
; Patent No. 5854410
; GENERAL INFORMATION:
; APPLICANT: Arnold Jr., Lyle J.
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Schwartz, David A.
; APPLICANT: Daily, William J.
; TITLE OF INVENTION: Oligonucleoside Cleavage Compounds and
; THERAPIES

; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 W. Sixth St.
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,355
; FILING DATE: 31-MAR-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Meier, Paul H.
; REGISTRATION NUMBER: 32,274
; REFERENCE/DOCKET NUMBER: 200/069
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213/489-1600
; TELEFAX: 213/355-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: Yes
; ANTI-SENSE: No
; FEATURE:
; NAME/KEY: R183
; OTHER INFORMATION: target strand
; US-08-223-355-23

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 CAGCGAGGGAGAGCGAG 29
Db 20 CAGAGAGAGAGAGAGAG 2

RESULT 128
US-08-470-426B-30/c
; Sequence 30, Application US/08470426B
; Patent No. 5856458
; GENERAL INFORMATION:
; APPLICANT: Okamoto, Hiroaki
; APPLICANT: Nakamura, Tatsuo
; TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS, AND THEIR
; APPLICATION FOR HIGH-FIDELITY DETECTION OF NON-A, NON-B
; HEPATITIS VIRUS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beveridge, DeGrandi, Weilacher & Young,
; ADDRESS: L.L.P.
; STREET: 1850 M Street, N.W., Suite 800
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weillacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2811
TELEFAX: (202) 659-1462
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-470-426B-30

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 117 GCGACGCTCGGAGTCAT 135
DB 19 GCGACGCTCGGAGTCAT 1

RESULT 129
US-08-887-365-17/c
Sequence 17, Application US/08087365
Patent No. 5858760
GENERAL INFORMATION:
APPLICANT: Dalboege, Henrik
APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Andersen, Lene N.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
TITLE OF INVENTION: AN ENZYME WITH PECTIN LYASE ACTIVITY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 58587600 No. 5858760disk of No. 5858760th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,365
FILING DATE: 02-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/513,928
FILING DATE: 26-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3955.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-887-365-17

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 816 ACCGCGTCTGGCGGCGGA 834
DB 20 ACGACGCTGGCGGCGGA 2

RESULT 130
US-08-889-296A-20/c
Sequence 20, Application US/08889296A
Patent No. 5872242
GENERAL INFORMATION:
APPLICANT: Monia, B.P., Cowser, L.M. and Manoharan, M.
TITLE OF INVENTION: Antisense Oligonucleotide
TITLE OF INVENTION: Inhibition of ras
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,296A
FILING DATE: herewith
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,734
FILING DATE: April 3, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09346
FILING DATE: October 1, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 958,134
FILING DATE: October 5, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/007,996
FILING DATE: January 21, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0213
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-889-296A-20

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGGCGGCGGCGGAG 1386

Db 19 GCCGCGCGCGCGGAGCAG 1

RESULT 131

US-08-902-655A-35/C
; Sequence 35, Application US/08902655A
; Patent No. 5885819
; GENERAL INFORMATION:
; APPLICANT: Kofod, Lene V.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Christgau, Stephan
; APPLICANT: Heldt-Hansen, Hans P.
; APPLICANT: Dalboge, Henrik
; APPLICANT: Andersen, Lene N.
; APPLICANT: Si, Joan Q.
; APPLICANT: Jacobson, Tina
; APPLICANT: Munk, Niels
; APPLICANT: Mullertz, Anette
; TITLE OF INVENTION: ENZYMS WITH XYLANASE ACTIVITY FROM
; TITLE OF INVENTION: ASPERGILLUS ACULEATUS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5885819c No. 5885819disk of No. 5885819th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,655A
; FILING DATE: 30-July-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis, Cheryl T.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3954.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-902-655A-35

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1373 GCCGCGCGCGCGAGTAG 1391

Db 20 GCCGCGCGCGCGAGCAG 2

RESULT 132

US-08-848-840A-20/C
; Sequence 20, Application US/08848840A
; Patent No. 5965722
; GENERAL INFORMATION:
; APPLICANT: Monia, et al.
; TITLE OF INVENTION: ANTISENSE INHIBITION OF ras GENE WITH
; TITLE OF INVENTION: CHIMERIC AND ALTERNATING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5965722 is LLP

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,840A
FILING DATE: 30-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,289
FILING DATE: 03-OCT-1994
APPLICATION NUMBER: 08/794,493
FILING DATE: 04-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/335,046
FILING DATE: 07-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,256
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,866
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,037
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,734
FILING DATE: 03-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/227,180
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-848-840A-20

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCCGCGCGCGCGGAGCAG 1386

Db 19 GCCGCGCGCGCGGAGCAG 1

RESULT 133

US-08-874-186-48
; Sequence 48, Application US/08874186
; Patent No. 5989885
; GENERAL INFORMATION:
; APPLICANT: Teng, David H-F.
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Perry III, William L.
; APPLICANT: Skolnick, Mark H.
; TITLE OF INVENTION: SPECIFIC MUTATIONS OF MAP KINASE KINASE
; TITLE OF INVENTION: 4 (MKK4) IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR

;/ TITLE OF INVENTION: SUPPRESSOR IN VARIOUS TYPES OF CANCER
;/ NUMBER OF SEQUENCES: 96
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
;/ STREET: 1201 New York Avenue, N.W., Suite 1000
;/ CITY: Washington
;/ STATE: DC
;/ COUNTRY: U.S.A.
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/874,186
;/ FILING DATE:
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/782,482
;/ FILING DATE: 10-JAN-1997
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Saxe, Stephen A.
;/ REGISTRATION NUMBER: 38,609
;/ REFERENCE/DOCKET NUMBER: 24884-121392-01
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-962-4848
;/ TELEFAX: 202-962-8300
;/ INFORMATION FOR SEQ ID NO: 48:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: other nucleic acid
;/ DESCRIPTION: /desc = "Primer."
;/ US-08-874-186-48

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 CAGCGAGGAGGAGGAGGAG 29
Db 1 CCGGGAGGAGGAGGAGGAG 19

RESULT 134
US-09-366-257-27
;/ Sequence 27, Application US/09366257
;/ Patent No. 6030837
;/ GENERAL INFORMATION:
;/ APPLICANT: Robert McKay
;/ APPLICANT: Madeline M. Butler
;/ APPLICANT: Lex M. Cowsett
;/ TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-MITOCHONDRIAL EXPRESSION
;/ FILE REFERENCE: RIS-0073
;/ CURRENT APPLICATION NUMBER: US/09/366,257
;/ CURRENT FILING DATE: 1999-08-03
;/ NUMBER OF SEQ ID NOS: 47
;/ SEQ ID NO 27
;/ LENGTH: 20
;/ TYPE: DNA
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Antisense Oligonucleotide
;/ US-09-366-257-27

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 636 CCGCCTGGCGGTGGAGGC 654

Db 2 CCAGCCTGGCAGTGCAGGC 20
RESULT 135
US-09-116-622-35/C
;/ Sequence 35, Application US/09116622
;/ Patent No. 6080567
;/ GENERAL INFORMATION:
;/ APPLICANT: Kofod, Lene V.
;/ APPLICANT: Kauppinen, Markku S.
;/ APPLICANT: Christgau, Stephan
;/ APPLICANT: Heldt-Hansen, Hans P.
;/ APPLICANT: Dalboge, Henrik
;/ APPLICANT: Andersen, Lene N.
;/ APPLICANT: Si, Joan Q.
;/ APPLICANT: Jacobson, Tina
;/ APPLICANT: Munk, Niels
;/ APPLICANT: Mullertz, Anette
;/ TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
;/ TITLE OF INVENTION: ASPERGILLUS ACULEATUS
;/ NUMBER OF SEQUENCES: 42
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: NO. 6080567C NO. 6080567disk of No. 6080567th America, Inc.
;/ STREET: 405 Lexington Avenue, 64th Floor
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: United States of America
;/ ZIP: 10174-6401
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/116,622
;/ FILING DATE: 16-July-1998
;/ CLASSIFICATION:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Agtis, Cheryl H.
;/ REGISTRATION NUMBER: 34,086
;/ REFERENCE/DOCKET NUMBER: 3954.224-US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212-867-0123
;/ TELEFAX: 212-878-9655
;/ INFORMATION FOR SEQ ID NO: 35:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: cDNA
;/ US-09-116-622-35

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1373 GCGCGCGCGCGCAGTAG 1391
Db 20 GCGCGCGCGCGCAGGAAG 2

RESULT 136
US-08-961-469A-28/c
;/ Sequence 28, Application US/08961469A
;/ Patent No. 6083923
;/ GENERAL INFORMATION:
;/ APPLICANT: Greg Hardee, Richard Geary, Arthur Levin,
;/ APPLICANT: Mike Templin, Randy Howard, Rahul Mehta
;/ TITLE OF INVENTION: LIPOSOMAL OLIGONUCLEOTIDE COMPOSITIONS
;/ NUMBER OF SEQUENCES: 61
;/ CORRESPONDENCE ADDRESS:


```

; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.469A
; FILING DATE: October 31, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-779-2400
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-961-469A-28

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGGCGGCAG 1386
DB 19 GCCGGCGGGCGGAGCAG 1

RESULT 137
US-09-128-494-20/c
; Sequence 20, Application US/09128494
; Patent No. 6117848
; GENERAL INFORMATION:
; APPLICANT: Monia, B.P., Cowser, L.M. and Manoharan, M.
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Inhibition of ras
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/128,494
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/889,296
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/411,734

; ADDRESS: Jane Massey Licata, Esq.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.469A
; FILING DATE: October 31, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-09-128-494-20

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGGCGGCAG 1386
DB 19 GCCGGCGGGCGGAGCAG 1

RESULT 138
US-09-435-296-56/c
; Sequence 56, Application US/09435296
; Patent No. 6171860
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF RANK EXPRESSION
; FILE REFERENCE: RTS-0116
; CURRENT APPLICATION NUMBER: US/09/435,296
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-435-296-56

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGGCGGCAG 1386
DB 19 GAGGGCGGGCGGGCGCTG 1

RESULT 139
US-09-280-805-42/c
; Sequence 42, Application US/09280805
; Patent No. 6184212
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
; APPLICANT: Graham, Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDV2
; TITLE OF INVENTION: EXPRESSION

```

NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,805
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/048,810
FILING DATE: March 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-280-805-42

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 144 TGGCGGAGTCCTGCTGCT 162
Db 20 TGACCGAGATCCTGCTGCT 2

RESULT 140
US-09-517-584A-19/c
Sequence 19, Application US/09517584A
Patent No. 6187587
GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Vickie L. Brown-Driver
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF B2F TRANSCRIPTION FACTOR 1 EXPRESSION
FILE REFERENCE: RTS-0121
CURRENT APPLICATION NUMBER: US/09/517,584A
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 19
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-19

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1123 CGCGCGCTCTGTCGCCGCC 1141
Db 20 CGCGCGCTCTGTCGCCGCC 2

RESULT 141
US-09-219-277-35/c
Sequence 35, Application US/09219277
Patent No. 6197564
GENERAL INFORMATION:
APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markku S.
APPLICANT: Christgau, Stephan
APPLICANT: Heldt-Hansen, Hans P.
APPLICANT: Dalboge, Henrik
APPLICANT: Andersen, Lene N.
APPLICANT: Si, Joan Q.
APPLICANT: Jacobson, Tina
APPLICANT: Munk, Niels
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6197564 No. 6197564disk of No. 6197564th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/219,277
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/116,622
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Agrie, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3954.224-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-219-277-35

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1373 GCGCGCGCGCGCAGTAG 1391
Db 20 GCGCGCGCGCGCAGTAG 2

RESULT 142
US-08-983-456-29
Sequence 29, Application US/08983466
Patent No. 6207372
GENERAL INFORMATION:
APPLICANT: SHUBER, ANTHONY P.
TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX
TITLE OF INVENTION: DNA AMPLIFICATION
NUMBER OF SEQUENCES: 95

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: RAE-VENTER LAW GROUP
;; STREET: 260 Sheridan Ave., Ste. 440
;; City: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/983,466
;; FILING DATE: 10-FEB-1998
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/474,450
;; FILING DATE: 07-JUNE-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO96/41012
;; FILING DATE: 06-JUNE-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rae-Venter, Barbara
;; REGISTRATION NUMBER: 32,750
;; REFERENCE/DOCKET NUMBER: GECO.001.01US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 328-4400
;; TELEFAX: (650) 328-4477
;; INFORMATION FOR SEQ ID NO: 29:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "Oligonucleotide primer"
US-08-983-466-29

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1344 GCGGGACAGCGCGCGCG 1362
|||||
Db 2 GCGGGCCCGCGCGCGCG 20

RESULT 143
US-09-599-661-35/c
; Sequence 35, Application US/09599661
; Patent No. 6228630
; GENERAL INFORMATION:
; APPLICANT: Kofod, Lene V.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Christgau, Stephan
; APPLICANT: Heldt-Hansen, Hans P.
; APPLICANT: Dalboge, Henrik
; APPLICANT: Andersen, Lene N.
; APPLICANT: Si, Joan Q.
; APPLICANT: Jacobson, Tina
; APPLICANT: Munk, Niels
; APPLICANT: Mullertz, Anette
; TITLE OF INVENTION: ENZYMES WITH XYLANASE ACTIVITY FROM
; TITLE OF INVENTION: ASPERGILLUS ACULEATUS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6228630 of No. 6228630th America, Inc.
; STREET: 405 Lexington Avenue, 54th Floor
; City: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/599,661
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/116,622
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Agtis, Cheryl H.
;; REGISTRATION NUMBER: 34,086
;; REFERENCE/DOCKET NUMBER: 3954.224-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-867-0123
;; TELEFAX: 212-878-9655
;; INFORMATION FOR SEQ ID NO: 35:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
US-09-599-661-35

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1373 GCGGGCGCGCGCGAGTAG 1391
|||||
Db 20 GCGGGCGCGCGCGAG 2

RESULT 144
US-09-467-082-13
; Sequence 13, Application US/09467082
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0088
; CURRENT APPLICATION NUMBER: US/09/467,082
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-082-13

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1365 ACCGGCGCGCGCGCGCG 1383
|||||
Db 2 ATCGCGCGCGCGCGCG 20

RESULT 145
US-09-467-082-22
; Sequence 22, Application US/09467082
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PKA CATALYTIC SUBUNIT C-ALPHA EXPRESSION
; FILE REFERENCE: RTS-0088

;/ CURRENT APPLICATION NUMBER: US/09/467,082
;/ CURRENT FILING DATE: 1999-12-17
;/ NUMBER OF SEQ ID NOS: 49
;/ SEQ ID NO 22
;/ LENGTH: 20
;/ TYPE: DNA
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-082-22

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1376 GCGCGGGGAGAGTAGCC 1394
Db 1 GCGCGGGGCGGCTTGCC 19

RESULT 146
US-09-326-186B-154/c
;/ Sequence 154, Application US/09326186B
;/ Patent No. 6319906
;/ GENERAL INFORMATION:
;/ APPLICANT: Bennett, Clarence Frank
;/ APPLICANT: Vickers, Timothy A.
;/ TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
;/ FILE OF INVENTION: Modulation of the Expression of B7 Protein
;/ FILE REFERENCE: ISPR-0376
;/ CURRENT APPLICATION NUMBER: US/09/326,186B
;/ CURRENT FILING DATE: 1999-06-04
;/ PRIOR APPLICATION NUMBER: 08/777,266
;/ PRIOR FILING DATE: 1996-12-31
;/ NUMBER OF SEQ ID NOS: 226
;/ SOFTWARE: Patentin Ver. 2.0
;/ SEQ ID NO 154
;/ LENGTH: 20
;/ TYPE: DNA
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Synthetic
US-09-326-186B-154

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 898 GAAGTCTTCTAGTGATC 916
Db 19 GAAGGTGTTCTTGTGAGC 1

RESULT 147
US-08-851-896-45/c
;/ Sequence 45, Application US/08851896
;/ Patent No. 6331301
;/ GENERAL INFORMATION:
;/ APPLICANT: ERIKSSON, Ulf
;/ APPLICANT: OLOFSSON, Birgitta
;/ APPLICANT: ALITALO, Kari
;/ APPLICANT: PATUSOLA, Katri
;/ TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
;/ TITLE OF INVENTION: DNA CODING THEREFOR
;/ NUMBER OF SEQUENCES: 57
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
;/ STREET: 1200 G Street, N.W., Suite 700
;/ CITY: Washington
;/ STATE: DC
;/ COUNTRY: USA
;/ ZIP: 20005
;/ COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patentin Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA: US/08/851,896
;/ APPLICATION NUMBER: US/08/851,896
;/ FILING DATE: 06-MAY-1997
;/ PRIOR APPLICATION NUMBER: US/08/609,443B
;/ FILING DATE: 01-MAR-1996
;/ APPLICATION NUMBER: US 08/397,651
;/ FILING DATE: 01-MAR-1995
;/ PRIOR APPLICATION DATA: US 09/469,427
;/ FILING DATE: 06-JUN-1995
;/ PRIOR APPLICATION NUMBER: US 08/569,063
;/ FILING DATE: 06-DEC-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: EVANS, Joseph D
;/ REGISTRATION NUMBER: 26,269
;/ REFERENCE/DOCKET NUMBER: 1064/41979CP4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (202) 628-8800
;/ TELEFAX: (202) 628-8844
;/ INFORMATION FOR SEQ ID NO: 45:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: DNA (genomic)
US-08-851-896-45

Query Match 0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1331 CGCAGCGACCGCGCGGG 1349
Db 19 CGCAGCTACCTGGCGGGG 1

RESULT 148
US-09-248-386-20/c
;/ Sequence 20, Application US/09248386
;/ Patent No. 6359124
;/ GENERAL INFORMATION:
;/ APPLICANT: Monia, Brett P
;/ APPLICANT: Freier, Susan M
;/ APPLICANT: Sanghvi, Yogesh S
;/ APPLICANT: Cook, Phillip D
;/ APPLICANT: Ecker, David J
;/ TITLE OF INVENTION: Antisense Inhibition of RAS Gene with Chimeric and
;/ TITLE OF INVENTION: Alternating Oligonucleotides
;/ FILE REFERENCE: ISIS3350
;/ CURRENT APPLICATION NUMBER: US/09/248,386
;/ CURRENT FILING DATE: 1999-01-12
;/ EARLIER APPLICATION NUMBER: 08/848,840
;/ EARLIER FILING DATE: 1997-04-30
;/ EARLIER APPLICATION NUMBER: 07/411,734
;/ EARLIER FILING DATE: 1989-09-25
;/ EARLIER APPLICATION NUMBER: PCT/US93/09346
;/ EARLIER FILING DATE: 1993-10-01
;/ EARLIER APPLICATION NUMBER: 07/715,196
;/ EARLIER FILING DATE: 1991-06-14
;/ EARLIER APPLICATION NUMBER: 07/958,134
;/ EARLIER FILING DATE: 1992-10-05
;/ EARLIER APPLICATION NUMBER: 08/007,996
;/ EARLIER FILING DATE: 1993-01-21
;/ EARLIER APPLICATION NUMBER: 07/703,619
;/ EARLIER FILING DATE: 1991-05-21

```

; EARLIER APPLICATION NUMBER: 08/040,903
; EARLIER FILING DATE: 1993-03-31
; EARLIER APPLICATION NUMBER: 07/040,526
; EARLIER FILING DATE: 1987-04-20
; EARLIER APPLICATION NUMBER: 08/174,379
; EARLIER FILING DATE: 1993-12-28
; EARLIER APPLICATION NUMBER: 08/040,933
; EARLIER FILING DATE: 1993-03-31
; EARLIER APPLICATION NUMBER: 08/300,072
; EARLIER FILING DATE: 1994-09-02
; EARLIER APPLICATION NUMBER: 08/039,979
; EARLIER FILING DATE: 1993-03-30
; EARLIER APPLICATION NUMBER: 08/395,168
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: 07/814,961
; EARLIER FILING DATE: 1991-12-24
; EARLIER APPLICATION NUMBER: 08/244,993
; EARLIER FILING DATE: 1994-06-21
; EARLIER APPLICATION NUMBER: 08/468,037
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6359124el Sequence
US-09-248-386-20

```

```

Query Match          0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1368 GCGGGGGCGCGCGCGGCGAG 1386
      |||||
DB 19 GCGGGGGCGCGCGGAGCGAG 1

```

```

RESULT 149
US-09-561-497-34
; Sequence 34, Application US/09561497
; Patent No. 6372433
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION
; FILE REFERENCE: RTS-0149
; CURRENT APPLICATION NUMBER: US/09/561,497
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-561-497-34

```

```

Query Match          0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 958 GCACCTGCTCTTTGGGG 976
      |||||
DB 1 GCACCACTCTCTTGAGCG 19

```

```

RESULT 150
US-09-742-703-32/c
; Sequence 32, Application US/09742703
; Patent No. 6423543

```

```

; GENERAL INFORMATION:
; APPLICANT: Patrick Allen Marcotte
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HEPsin EXPRESSION
; FILE REFERENCE: RTS-0090
; CURRENT APPLICATION NUMBER: US/09/742,703
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-742-703-32

```

```

Query Match          0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 808 CCGCGGGGACCGCTGCTG 826
      |||||
DB 20 CTCGGGGGACTGGTGCTG 2

```

```

RESULT 151
US-09-920-663-12/c
; Sequence 12, Application US/09920663
; Patent No. 6426221
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF RIP2 EXPRESSION
; FILE REFERENCE: RTS-0233
; CURRENT APPLICATION NUMBER: US/09/920,663
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-663-12

```

```

Query Match          0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 800 GACCTGAGCCCGGGGACC 818
      |||||
DB 20 GGCTGAGCGCCCGGACC 2

```

```

RESULT 152
US-09-907-843-23
; Sequence 23, Application US/09907843
; Patent No. 6440739
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-2 EXPRESSION
; FILE REFERENCE: RTS-0279
; CURRENT APPLICATION NUMBER: US/09/907,843
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-907-843-23

```

```
Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 150 AGATGCTGCTGCTGCGGAG 168
    |||||
Db 1 AGTGTGCTGCTGCTGTGAG 19
    |||||

RESULT 153
US-09-485-077A-2
; Sequence 2, Application US/09485077A
; Patent No. 6458590
; GENERAL INFORMATION:
; APPLICANT: Mukherjee, Anil
; APPLICANT: Kundu, Gopal
; APPLICANT: Panda, Dibyendu
; TITLE OF INVENTION: Methods and Compositions for Treatment of Restenosis
; FILE REFERENCE: NIH-05047
; CURRENT APPLICATION NUMBER: US/09/485,077A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCI/US98/16569
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: 60/054,967
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-485-077A-2

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 548 CACCACTCAGAGAGTCTC 566
    |||||
Db 1 CACCACTCAGAGTCTC 19
    |||||

RESULT 154
US-09-657-346A-11/c
; Sequence 11, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
; FILE REFERENCE: RTS-0135
; CURRENT APPLICATION NUMBER: US/09/657,346A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-657-346A-11

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 170 TGTCTGCTGCTAGTCTCG 188
    |||||
Db 20 TGTCTGCTGCTAGTCTCG 2
    |||||
```

```
RESULT 155
US-09-922-146-25/c
; Sequence 25, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-922-146-25

Query Match      0.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1298 GCGCAGCGCTCTCGCTG 1316
    |||||
Db 20 GTGCGCGCTCTCGCTG 2
    |||||

RESULT 156
US-08-585-684B-50
; Sequence 50, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF CRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-664B-50

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 93;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 901 GGTCTTCTACGTGA 914
DB 2 GGUCUUCUACGUGA 15

RESULT 157
US-09-377-310-37
Sequence 37, Application US/09377310B
Patent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-37

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 TCCTCGCTGCTGGT 204
DB 1 TCCTCGCTGCTGGT 14

RESULT 158
US-09-038-073-50
Sequence 50, Application US/09038073
Patent No. 6194150
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 216/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-038-073-50

Query Match 0.9%; Score 14; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 93;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 901 GGTCTTCTACGTGA 914
DB 2 GGUCUUCUACGUGA 15

RESULT 159
US-08-627-254C-12/c
Sequence 12, Application US/08627254C
Patent No. 5859229
GENERAL INFORMATION:
APPLICANT: Kniss, Douglas A.
TITLE OF INVENTION: Eicosanoid Formation
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griwold LLP
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: USA
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,254C
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gollrick, Mary E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 18525/00107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8200
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ANTI-SENSE: YES
US-08-627-254C-12

Query Match 0.9%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

```

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1132 CTTGCCCGCGCGTGG 1145
Db 15 CTTGCCCGCGCGTGG 2

RESULT 160
US-08-912-129A-77/c
; Sequence 77, Application US/08912129A
; Patent No. 5922533
; GENERAL INFORMATION:
; APPLICANT: VALLARI, ANADRUZELA S.
; APPLICANT: HACKETT, JOHN JR.
; APPLICANT: HICKMAN, ROBERT K.
; APPLICANT: VARITEK, VINCENT A. JR.
; APPLICANT: NECKLAWS, ELIZABETH A.
; APPLICANT: GOLDEN, ALAN M.
; APPLICANT: BRENNAN, CATHERINE A.
; APPLICANT: DEVARE, SUSHIL G.
; TITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATION
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS (Windows 95)
; SOFTWARE: Microsoft Word (ASCII format output)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,129A
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dankers, Andreas M.
; REGISTRATION NUMBER: 32,652
; REFERENCE/DOCKET NUMBER: 6109.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-937-9803
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-912-129A-77

Query Match 0.9%; Score 14; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 764 GTGCACCTGGAGCAGG 779
Db 16 GYGCACCTGGAGTAGG 1

RESULT 161
US-08-981-321-6/c
; Sequence 6, Application US/08981321A
; Patent No. 6146871
; GENERAL INFORMATION:
; APPLICANT: GARCIA LOPEZ, et al, Jose Luis
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE ENZYME

```

```

; TITLE OF INVENTION: 7B-(4-CARBOXYBUTANAMIDE) CE PHALOS PORI NACYLAS E AND
; TITLE OF INVENTION: PURIFYING SAID ENZYME IN A SINGLE CHROMATOGRAPHIC STEP
; FILE REFERENCE: U-011559-6
; CURRENT APPLICATION NUMBER: US/08/981,321A
; CURRENT FILING DATE: 1998-08-13
; EARLIER APPLICATION NUMBER: PCT/ES97/00098
; EARLIER FILING DATE: 1997-04-19
; EARLIER APPLICATION NUMBER: P9600890
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide from gla gene modified
; OTHER INFORMATION: to include a Sma. I restriction site
; FEATURE:
; OTHER INFORMATION: Gla gene modified to encode six histidines
US-08-981-321-6

Query Match 0.9%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 748 CCCGGGCTCGGCCA 761
Db 15 CCCGGGCTCGGCCA 2

RESULT 162
US-09-578-634A-1
; Sequence 1, Application US/09578634A
; Patent No. 6515120
; GENERAL INFORMATION:
; APPLICANT: Kwagh, Jae-Gyu
; APPLICANT: Macklin, John J.
; APPLICANT: Mitsis, Paul G.
; APPLICANT: Ulmer, Kevin M.
; TITLE OF INVENTION: METHOD FOR SEQUENCING AND CHARACTERIZING POLYMERIC
; TITLE OF INVENTION: BIONOMOLECULES USING APTAMERS AND A METHOD FOR PRODUCING
; TITLE OF INVENTION: APTAMERS
; FILE REFERENCE: PL/2CIP
; CURRENT APPLICATION NUMBER: US/09/578,634A
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/135,863
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...19
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: sequence
; OTHER INFORMATION: Description of Artificial Sequence: n is any one of
; OTHER INFORMATION: g, a, t or c
US-09-578-634A-1

Query Match 0.9%; Score 14; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 1.8e+02;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1552 CGGGGAGGGCGCGGGAG 1570
Db 1 CGGGGAGGGCGGGAG 19

RESULT 163

```


US-08-837-201C-5/c
; Sequence 5, Application US/08837201C
; Patent No. 5985558
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia, Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201C
; FILING DATE: April 14, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-837-201C-5

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1351 CAGCGCGCGCGGG 1364
Db 16 CAGCGCGCGCGGG 3

RESULT 164
US-09-377-310-17
; Sequence 17, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0389
; CURRENT APPLICATION NUMBER: US/09/377,310B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: antisense sequence
US-09-377-310-17

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;
QY 191 TCCTGCTGCTGGT 204
Db 3 TCCTGCTGCTGGT 16

RESULT 165
US-09-428-696-57/c
; Sequence 57, Application US/09428696
; Patent No. 6165789
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HNRNP A1 EXPRESSION
; FILE REFERENCE: RTS-0111
; CURRENT APPLICATION NUMBER: US/09/428,696
; CURRENT FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 57
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-428-696-57

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 642 TGGCGGTGGAGGCC 655
Db 19 TGGCGGTGGAGGCC 6

RESULT 166
US-09-484-617-41
; Sequence 41, Application US/09484617
; Patent No. 6303374
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTS-0103
; CURRENT APPLICATION NUMBER: US/09/484,617
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-484-617-41

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1442 GGCATCCACTGGTA 1455
Db 7 GGCATCCACTGGTA 20

RESULT 167
US-09-364-416-5/c
; Sequence 5, Application US/09364416

```
; Patent No. 6312900
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; APPLICANT: Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; TITLE OF INVENTION: Compositions and Methods for the Modulation of
; TITLE OF INVENTION: Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,416
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,201
; FILING DATE: April 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-09-364-416-5

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1351 CAGCGGCGCGGG 1364
Db 16 CAGCGGCGCGGG 3

RESULT 168
US-09-422-978-8409/c
; Sequence 8409, Application US/09422978
; Patent No. 8537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8409
; LENGTH: 20
```

```
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-15296 for SEQ 544, in complemer
US-09-422-978-8409

Query Match 0.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 705 TGAAGCAGAGAAC 718
Db 14 TGAAGCAGAGAAC 1

RESULT 169
US-08-379-078-457/c
; Sequence 457, Application US/08379078
; Patent No. 5839812
; GENERAL INFORMATION:
; APPLICANT: Mitsuhashi, Masato
; APPLICANT: Cooper, Allan
; TITLE OF INVENTION: Gene Detection System
; NUMBER OF SEQUENCES: 726
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,078
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/974,406
; FILING DATE: 12-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HITACHI.011CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-379-078-457

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 641 CTGGCGGTGGAGCGG 657
Db 17 CTGGCGGTGGAGCGG 1

RESULT 170
```

US-08-379-078-458/c
 ; Sequence 458, Application US/08379078
 ; Patent No. 5639612
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitsuhashi, Masato
 ; APPLICANT: Cooper, Allan
 ; TITLE OF INVENTION: Gene Detection System
 ; NUMBER OF SEQUENCES: 726
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: KNOBBE, MARTENS, OLSON AND BEAR
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/379,078
 ; FILING DATE: 12-NOV-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION NUMBER: US 07/974,406
 ; FILING DATE: 12-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: HITACHI.011CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; INFORMATION FOR SEQ ID NO: 458:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-379-078-458

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CTGGCGGTGGAGCGCG 657
 Db 17 CTGGCGGTGGAGCGCG 1

RESULT 171
 US-07-974-409C-70/c
 ; Sequence 70, Application US/07974409C
 ; Patent No. 6300058
 ; GENERAL INFORMATION:
 ; APPLICANT: Akitaya, Tatsuo
 ; APPLICANT: Mitsuhashi, Masato
 ; APPLICANT: Cooper, Allan
 ; TITLE OF INVENTION: METHOD AND REAGENT
 ; TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
 ; NUMBER OF SEQUENCES: 457
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: KNOBBE, MARTENS, OLSON, AND BEAR
 ; STREET: 620 Newport Center Dr. Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/974,409C
 ; FILING DATE: 12-NOV-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: HITACHI.006CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; INFORMATION FOR SEQ ID NO: 70:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-07-974-409C-70

Query Match 0.9%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.4e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CTGGCGGTGGAGCGCG 657
 Db 17 CTGGCGGTGGAGCGCG 1

RESULT 172
 US-07-974-409C-71/c
 ; Sequence 71, Application US/07974409C
 ; Patent No. 6300058
 ; GENERAL INFORMATION:
 ; APPLICANT: Akitaya, Tatsuo
 ; APPLICANT: Mitsuhashi, Masato
 ; APPLICANT: Cooper, Allan
 ; TITLE OF INVENTION: METHOD AND REAGENT
 ; TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
 ; NUMBER OF SEQUENCES: 457
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: KNOBBE, MARTENS, OLSON, AND BEAR
 ; STREET: 620 Newport Center Dr. Sixteenth Floor
 ; CITY: Newport Beach
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/974,409C
 ; FILING DATE: 12-NOV-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Altman, Daniel E.
 ; REGISTRATION NUMBER: 34,115
 ; REFERENCE/DOCKET NUMBER: HITACHI.006CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 714-760-0404
 ; TELEFAX: 714-760-9502
 ; INFORMATION FOR SEQ ID NO: 71:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17
 ; TYPE: nucleic acid

```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-974-409C-71

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CTGGCGGTGGAGCCGG 657
DB 17 CTGGCGGTGGAGCCAG 1

RESULT 173
US-08-584-040-5562
; Sequence 5562, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5562:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5562

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1447 CCACTGGTACTGCGCAG 1463

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-07-974-409C-71

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 641 CTGGCGGTGGAGCCGG 657
DB 17 CTGGCGGTGGAGCCAG 1

RESULT 174
US-09-673-809-86
; Sequence 86, Application US/09673809
; Patent No. 6528261
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86 HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 86
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-809-86

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 798 AGGACCTGAGCCCCGGG 814
DB 1 AGGACCTGAGCTCTGG 17

RESULT 175
US-09-435-327A-16/c
; Sequence 16, Application US/09435327A
; Patent No. 6537766
; GENERAL INFORMATION:
; APPLICANT: Uckun, Fatih M.
; APPLICANT: Croffy, Mya L.
; TITLE OF INVENTION: IKAROS ISOFORMS AND MUTANTS
; FILE REFERENCE: 12152.35USUL
; CURRENT APPLICATION NUMBER: US/09/435,327A
; CURRENT FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,229
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-435-327A-16

Query Match
Best Local Similarity 0.9%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1499 GAGGCCCTGCACCCGCT 1515
DB 17 GAGTCCCTGCGCCGCT 1

RESULT 176
US-09-371-772B-2452
; Sequence 2452, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
```

;; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
;; FILE REFERENCE: MHB00.876-J (237/198)
;; CURRENT APPLICATION NUMBER: US/09/371,772B
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: US 60/005,974
;; PRIOR FILING DATE: 1995-10-26
;; PRIOR APPLICATION NUMBER: US 08/584,040
;; PRIOR FILING DATE: 1996-01-08
;; NUMBER OF SEQ ID NOS: 14225
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2452
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Mus sp.
US-09-371-772B-2452

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 1.4e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1447 CCACGTGCTACTGCGCAGC 1463
Db 1 CCAGUGGUACUGGCAGC 17

RESULT 177
PCT-US93-00977-70/c
;; GENERAL INFORMATION:
;; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
;; NUMBER OF SEQUENCES: 711
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Knobbe, Martens, Olson, and Bear
;; STREET: 620 Newport Center Dr. Sixteenth Floor
;; CITY: Newport Beach
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92660
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/00977
;; FILING DATE: 19930129
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Altman, Daniel E.
;; REGISTRATION NUMBER: 34,115
;; REFERENCE/DOCKET NUMBER: HITACHI.006H
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 714-760-0404
;; TELEFAX: 714-760-9502
;; INFORMATION FOR SEQ ID NO: 70:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
PCT-US93-00977-70

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 641 CTGGCGGTGGAGCGCGG 657
Db 17 CTGGCGGTGGAGCGCCAG 1

RESULT 178
PCT-US93-00977-71/c
;; GENERAL INFORMATION:
;; TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
;; NUMBER OF SEQUENCES: 711
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Knobbe, Martens, Olson, and Bear
;; STREET: 620 Newport Center Dr. Sixteenth Floor
;; CITY: Newport Beach
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92660
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/00977
;; FILING DATE: 19930129
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Altman, Daniel E.
;; REGISTRATION NUMBER: 34,115
;; REFERENCE/DOCKET NUMBER: HITACHI.006H
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 714-760-0404
;; TELEFAX: 714-760-9502
;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA to mRNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
PCT-US93-00977-71

Query Match 0.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 641 CTGGCGGTGGAGCGCGG 657
Db 17 CTGGCGGTGGAGCGCCAG 1

RESULT 179
US-08-248-848-56/c
;; GENERAL INFORMATION:
;; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
;; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
;; PATENT NO. 5523217
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski
;; STREET: 1301 McKinney, Suite 5100
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: U.S.A.
;; ZIP: 77010-3095
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,848
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/781,424
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
US-08-248-848-56

```

```

Query Match      0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      111 CGCACGGGACAGCTCG 127
DB      17 CGGACTGGGACAGCTCG 1

```

```

RESULT 180
US-08-248-848-57
; Sequence 57, Application US/08248848
; Patent No. 5523217
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R.
; APPLICANT: Versalovic, James
; APPLICANT: Koeuth, Thearith
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
; Patent No. 5523217
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,848
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/781,424
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325

```

```

; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
US-08-248-848-57

```

```

Query Match      0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      111 CGCACGGGACAGCTCG 127
DB      2 CGGACTGGGACAGCTCG 18

```

```

RESULT 181
US-08-111-077-56/c
; Sequence 56, Application US/08111077
; Patent No. 5691136
; GENERAL INFORMATION:
; APPLICANT: Lupski, James R.
; APPLICANT: Versalovic, James
; APPLICANT: Koeuth, Thearith
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification
; Patent No. 5691136
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,077
; FILING DATE: 19930824
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
US-08-111-077-56

```

```

Query Match      0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      111 CGCACGGGACAGCTCG 127

```

Db 17 CGGACTGGGACAGCTCG 1

RESULT 182

US-08-111-077-57

Sequence 57, Application US/08111077

Patent No. 5691136

GENERAL INFORMATION:

APPLICANT: Lupski, James R.

APPLICANT: Versalovic, James

APPLICANT: Koeuth, Thearith

TITLE OF INVENTION: Fingerprinting Bacterial Strains Using

TITLE OF INVENTION: Repetitive DNA Sequence Amplification

Patent No. 5691136

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski

STREET: 1301 McKinney, Suite 5100

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77010-3095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/111,077

FILING DATE: 19930824

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Paul, Thomas D.

REGISTRATION NUMBER: 32,714

REFERENCE/DOCKET NUMBER: D-5394

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/651-5325

TELEFAX: 713/651-5246

TELEX: 762829

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: YES

US-08-111-077-57

Query Match 0.9%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 1.7e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 111 CGGACGGGACAGCTCG 127

Db 2 CGGACTGGGACAGCTCG 18

RESULT 183

US-08-363-240A-1117/c

Sequence 1117, Application US/08363240A

Patent No. 5705388

GENERAL INFORMATION:

APPLICANT: Couture, Larry

APPLICANT: McSwiggen, James

APPLICANT: Bisgaier, Charles

APPLICANT: Pape, Michael

TITLE OF INVENTION: METHOD AND REAGENT FOR

TITLE OF INVENTION: PREVENTION, INHIBITION OF

TITLE OF INVENTION: PROGRESSION AND REGRESSION

TITLE OF INVENTION: OF VASCULAR DISEASES

NUMBER OF SEQUENCES: 1243

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

ADDRESS: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word

APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1203:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-1203

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 1.7e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1023 CCGGGCGCGCTTCGGG 1039
DB 1 CAGGGCGCCUUCAGG 17

RESULT 185

US-08-311-486C-1129
Sequence 1129, Application US/08311486C
Patent No. 5811300

GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327

two

REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1129:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-1129

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 58.8%; Pred. No. 1.7e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 132 TCATCAGTTCATGGGC 148
DB 2 UCAUCAGUCUUGGCC 18

RESULT 186

US-09-205-922-48
Sequence 48, Application US/09205922
Patent No. 5951455

GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-AFLHA-11 EXPRESSION
FILE REFERENCE: RTS-0030
CURRENT APPLICATION NUMBER: US/09/205,922
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 48
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-922-48

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1450 CTGGTACTCGCAGCTGC 1466
DB 2 CTGGTACTCGCAGCTGC 18

RESULT 187

US-09-176-862-32
Sequence 32, Application US/09176862B
Patent No. 6046319

GENERAL INFORMATION:
APPLICANT: Power, Christopher
APPLICANT: Mayne, Michael B.
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION
FILE REFERENCE: 3045.00002
CURRENT APPLICATION NUMBER: US/09/176,862B
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: 60/062,718
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-176-862-32

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 235 GGGTTTCGGGAAGAGCA 251
|||
Db 1 GGGTTTCGAGAAGATGA 17
|||

RESULT 188

US-09-143-212-45
; Sequence 45, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-45

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGGGCGGC 1384
|||
Db 2 GTGGCGGGCGGGCGGC 18
|||

RESULT 189

US-09-322-478-2/c
; Sequence 2, Application US/09322478
; Patent No. 6331662
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; APPLICANT: Voytas, Daniel F.
; TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
; CURRENT APPLICATION NUMBER: US/09/322,478
; CURRENT FILING DATE: 1999-05-28
; EARLIER APPLICATION NUMBER: 60/087125
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-322-478-2

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 880 CCGGACGACGCGGCA 896
|||
Db 17 CCGGACGACGCGGCA 1
|||

RESULT 190

US-08-584-040-3041
; Sequence 3041, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:

APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3041:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-3041

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 70.6%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 939 GCCTGCTGCTCACCAGC 955
|||
Db 1 GCGGCGGCGGCGGCGC 17
|||

RESULT 191

US-08-679-645-1167/c
; Sequence 1167, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS

```
;
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-679-645-1167

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGGCGCGCGCGC 1384
Db 18 GCTGCGCGCGCGCGC 2

RESULT 192
US-09-025-343-14
; Sequence 14, Application US/09025343
; Patent No. 6380170
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Rolf
; LIU, Ningshu
; SEDLACEK, Joerk
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR THE CELL
CYCLE REGULATED EXPRESSION OF STRUCTURAL GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,343
; FILING DATE: 18-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97 102 547.3
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 026083/0180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-025-343-14

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 327 GCGGAGGTATGAAGG 343
Db 2 GCGGAGGTATGAATGG 18

RESULT 193
US-09-673-809-44
; Sequence 44, Application US/09673809
; Patent No. 6528261
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99.86.HLA
; CURRENT APPLICATION NUMBER: US/09/673,809
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-809-44

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 798 AGGACCTGAGCCCGGG 814
Db 2 AGGACCTGAGCTCTGG 18

RESULT 194
US-09-371-772B-1469
; Sequence 1469, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
```

;; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
;; FILE REFERENCE: MHB00,876-J (237/198)
;; CURRENT APPLICATION NUMBER: US/09/371,772B
;; CURRENT FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: US 60/005,974
;; PRIOR FILING DATE: 1995-10-26
;; PRIOR APPLICATION NUMBER: US 08/584,040
;; PRIOR FILING DATE: 1996-01-08
;; NUMBER OF SEQ ID NOS: 14225
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 1469
;; LENGTH: 18
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-09-371-772B-1469

Query Match 0.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 70.6%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 939 GCGTCTGCTCAGCCGC 955
Db 1 GCGUGUGCGUCCCCGCC 17

RESULT 195
US-08-486-408-12/c
;; Sequence 12, Application US/08486408
;; Patent No. 5716846
;; GENERAL INFORMATION:
;; APPLICANT: Brown, Steven Joel
;; APPLICANT: Dattagupta, Nanibhushan
;; APPLICANT: Naidu, Yathi M.
;; TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
;; TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
;; NUMBER OF SEQUENCES: 19
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Gen-Probe Incorporated
;; STREET: 9880 Campus Point Drive
;; CITY: San Diego
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 92121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq Version 1.5
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,408
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fisher, Carlos A
;; REGISTRATION NUMBER: 36,510
;; REFERENCE/DOCKET NUMBER: CBI009
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-535-2807
;; TELEFAX: 619-546-7929
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-486-408-12

Query Match 0.9%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1303 CGCGCTCTCTGGCTGCAC 1319
Db 17 CGCGCTCTCTGGCTGCC 1

RESULT 196
US-08-640-672-6/c
;; Sequence 6, Application US/08640672
;; Patent No. 5789189
;; GENERAL INFORMATION:
;; APPLICANT: Leustner, James
;; APPLICANT: Hui, May
;; APPLICANT: Dunn, James M.
;; APPLICANT: Stevens, John K.
;; TITLE OF INVENTION: METHOD FOR AMPLIFICATION AND SEQUENCING
;; TITLE OF INVENTION: OF NUCLEIC ACID POLYMERS
;; NUMBER OF SEQUENCES: 20
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppedahl & Larson
;; STREET: 1992 Commerce Street Suite 309
;; CITY: Yorktown
;; STATE: NY
;; COUNTRY: US
;; ZIP: 10598
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: MS DOS
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/640,672
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Larson, Marina T.
;; REGISTRATION NUMBER: 32,038
;; REFERENCE/DOCKET NUMBER: VGEN.P-020-US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (914) 245-3252
;; TELEFAX: (914) 962-4330
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; HYPOTHETICAL: no
;; ANTI-SENSE: no
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; ORGANISM: human
;; FEATURE:
;; OTHER INFORMATION: amplification primer for DR2 alleles of
;; OTHER INFORMATION: HLA Class II genes
US-08-640-672-6

Query Match 0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 579 GCGCGCAGTGGACATC 595
Db 18 GCGCGCGGTGGACACC 2

RESULT 197
 US-08-684-498A-6/c
 ; Sequence 6, Application US/08684498A
 ; Patent No. 5830657
 ; GENERAL INFORMATION:
 ; APPLICANT: Leushner, James
 ; APPLICANT: Hui, May
 ; APPLICANT: Dunn, James M.
 ; APPLICANT: Larson, Marina T.
 ; TITLE OF INVENTION: METHOD FOR SINGLE-TUBE SEQUENCING OF
 ; TITLE OF INVENTION: NUCLEIC ACID POLYMERS
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Opedahl & Larson
 ; STREET: 1992 Commerce Street Suite 309
 ; CITY: Yorktown
 ; STATE: NY
 ; COUNTRY: US
 ; ZIP: 10598
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/684,498A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/640,672
 ; FILING DATE: 1 May 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Larson, Marina T.
 ; REGISTRATION NUMBER: 32,038
 ; REFERENCE/DOCKET NUMBER: VGEN.P-031-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 245-3252
 ; TELEFAX: (914) 962-4330
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: no
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; FEATURE:
 ; OTHER INFORMATION: amplification primer for DR2 alleles of
 ; OTHER INFORMATION: HLA Class II genes
 US-08-684-498A-6

Query Match 0.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 579 GCCGCGCAGTGGACATC 595
 Db 18 GCCGCGCGGTGGACACC 2

RESULT 198
 US-08-577-858A-6/c
 ; Sequence 6, Application US/08577858A
 ; Patent No. 5834189
 ; GENERAL INFORMATION:
 ; APPLICANT: Stevens, John K.
 ; APPLICANT: Dunn, James M.
 ; APPLICANT: Leushner, James

; APPLICANT: Green, Ronald
 ; TITLE OF INVENTION: Method for Evaluation of Polymorphic
 ; TITLE OF INVENTION: Genetics Sequences, and Use Thereof in Identification of HLA
 ; TITLE OF INVENTION: Types
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Opedahl & Larson
 ; STREET: 1992 Commerce Street Suite 309
 ; CITY: Yorktown
 ; STATE: NY
 ; COUNTRY: US
 ; ZIP: 10598
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: MS DOS
 ; SOFTWARE: Word Perfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/577,858A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Larson, Marina T.
 ; REGISTRATION NUMBER: 32,038
 ; REFERENCE/DOCKET NUMBER: VGEN.P-019-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (914) 245-3252
 ; TELEFAX: (914) 962-4330
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: no
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; FEATURE:
 ; OTHER INFORMATION: amplification primer for DR2 alleles of
 ; OTHER INFORMATION: HLA Class II genes
 US-08-577-858A-6

Query Match 0.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 579 GCCGCGCAGTGGACATC 595
 Db 18 GCCGCGCGGTGGACACC 2

RESULT 199
 US-08-611-280-10
 ; Sequence 10, Application US/08611280
 ; Patent No. 5891666
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuyama, Toshifumi
 ; APPLICANT: Grossman, Alex
 ; APPLICANT: Richardson, Christopher D.

; TITLE OF INVENTION: NOVEL GENES ENCODING LSIRP POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Canada Inc.
 ; STREET: 6733 Mississauga Road, Suite 303
 ; CITY: Mississauga
 ; STATE: Ontario

COUNTRY: Canada
ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-611-280-10

Query Match 0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 504 CAGGAGTGAACCTGGG 520
DB 3 CAGAAGTGAACCTGAGG 19

RESULT 200

US-08-975-570-12/c
Sequence 12, Application US/08975570
Patent No. 5945336

GENERAL INFORMATION:
APPLICANT: Brown, Steven Joel
APPLICANT: Dattagupta, Nanihushan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
TITLE OF INVENTION: mRNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,570
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,408
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A.
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-570-12

Query Match 0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1303 CGCGCTCCGCTGCAC 1319
DB 17 CGCGCTGCTGGCTGCC 1

RESULT 201

US-08-796-362C-5/c
Sequence 5, Application US/08796362C
Patent No. 5952200

GENERAL INFORMATION:
APPLICANT: Johnson, Lewis D., Hunt, D. Margaret, and Nachtigal,
APPLICANT: Maurice
TITLE OF INVENTION: Method of Diagnosing Cancer in Human Cells
TITLE OF INVENTION: Using a Reverse Transcriptase-Polymerase Chain Reaction for
TITLE OF INVENTION: the Presence of Stromelysin-3
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Neil C. Jones
ADDRESS: Dority & Manning, P.A.
STREET: 700 E. No. 5952200th Street, Suite 15
CITY: Greenville
STATE: South Carolina
COUNTRY: USA
ZIP: 29601

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible (SAMPO/Alphascan
OPERATING SYSTEM: MS Dos; Windows 95
SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,362C
FILING DATE: 06-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA: No. 5952200 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Neil C. Jones
REGISTRATION NUMBER: 35,561
REFERENCE/DOCKET NUMBER: USC-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (864) 271-1592
TELEFAX: (864) 233-7342

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: Nucleic acid

STRANDEDNESS: Single

TOPOLOGY: Linear

MOLECULE TYPE: Other Nucleic Acid

DESCRIPTION: -actin primer

HYPOTHETICAL: No

ANTI-SENSE: complementary to file sequence

ORIGINAL SOURCE: Genbank X00351 (originally designed from 04

IMMEDIATE SOURCE: synthesized at the University of South Carolina

POSITION IN GENOME:

UNITS: NT 1382-1364 (position in 25 May 1997 file version)

FEATURE: primer designed from sequence as listed in

OTHER INFORMATION: 04 August 1986 Genbank file.

PUBLICATION INFORMATION:

AUTHORS: Johnson, Lewis D., Hunt, D. Margaret, Kim, Keanhoi, and

TITLE: Amplification of Stromelysin-3 Transcripts from Carcinomas of

JOURNAL: Human Pathology

August 198

Nacht

```
/
/ VOLUME: 27
/ ISSUE: 9
/ PAGES: 964-968
/ DATE: SEPT-1996
/ RELEVANT RESIDUES IN SEQ ID NO: 5: NT 1382-1364 (position according
US-08-796-362C-5

Query Match          0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 294 TCCCAATGTGGCCGAG 310
Db 17 TTCACATGTGGCCGAG 1

RESULT 202
US-09-195-940-10
Sequence 10, Application US/09195940
Patent No. 6258935
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6J8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,466
FILING DATE: 01-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/195,940
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-562-466-10

Query Match          0.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 504 CAGAGTGAAGTGGCGG 520
Db 3 CAGAAGTGAAGTGGCGG 19

RESULT 204
US-08-068-747-7/C
Sequence 7, Application US/08068747
Patent No. 5695933
GENERAL INFORMATION:
APPLICANT: Schalling, Martin
APPLICANT: Hudson, Thomas J.
APPLICANT: Houseman, David E.
TITLE OF INVENTION: Direct Determination of Expanded
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,747
FILING DATE: 28-MAY-1993
CLASSIFICATION: 435
```

```

;
; DESCRIPTION: /desc = "Oligonucleotide primer"
US-08-983-466-29

```

```

; APPLICANT: Jarvis, Thale
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-585-684B-51

```

```

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 902 GTCTTCTAGTGATC 916
Db 1 GUCUUCACGUGAGC 15

```

```

RESULT 208
US-08-863-639A-21
; Sequence 21, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Matson, Robert S.
; APPLICANT: Coassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95

```

```

; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Muech
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; US-08-863-639A-21

```

```

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1370 GGGGGCGCGCGGC 1384
Db 1 GCGCGCGCGCGGC 15

```

```

RESULT 209
US-08-590-897A-32/c
; Sequence 32, Application US/08590897A
; Patent No. 6031071
; GENERAL INFORMATION:
; APPLICANT: Mandeville, Rosemonde
; APPLICANT: Popkov, Mikhail
; TITLE OF INVENTION: METHODS OF GENERATING NOVEL PEPTIDES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
; STREET: 100 Tharlet Circle, Suite 306
; CITY: Princeton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08540-3662
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,897A
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernstein, Scott N.
; REGISTRATION NUMBER: 38,827
; REFERENCE/DOCKET NUMBER: 3987-102US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-924-8555
; TELEFAX: 609-924-3036
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-590-897A-32

```

```

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;

```


Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1046 CTGGGGCTCGGGG 1060
Db 15 CTGGGGCTCGGGC 1

RESULT 210
US-09-038-073-49
; Sequence 49, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-49

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 899 AGGCTCTCTACGTG 913
Db 1 AGGGUCUUCUACGUG 15

RESULT 211
US-09-038-073-51
; Sequence 51, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE

; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-038-073-51

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 902 GTCTTCTACGTGATC 916
Db 1 GUCUUCUACGUGAC 15

RESULT 212
US-08-730-635-13
; Sequence 13, Application US/08730635
; Patent No. 6514693
; GENERAL INFORMATION:
; APPLICANT: Lansdorp, Peter
; TITLE OF INVENTION: Method for Detecting Multiple Copies of
; TITLE OF INVENTION: a Repeat Sequence in a Nucleic Acid Molecule
; Patent No. 6514693
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWSON & HOWSON
; STREET: 321 No. 6514693ristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19477

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,635
; FILING DATE: 11-OCT-1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: B&PTUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818
TELEX: N/A
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-730-635-13

Query Match 0.9%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 1.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGCGGCGGCGGCGC 1384
DB 1 GGCGGCGGCGGCGC 15

RESULT 213

US-08-153-051B-58/c
Sequence 58, Application US/08153051B
Patent No. 5645986

GENERAL INFORMATION:

APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,051B
FILING DATE: No. 5645986member 12, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/195
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-153-051B-58

Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACCC 86
DB 16 CACACGCACACCC 2

RESULT 214

US-08-060-952C-57/c
Sequence 57, Application US/08060952C
Patent No. 5695932

GENERAL INFORMATION:

APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/060,952C
FILING DATE: May 13, 1993

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-060-952C-57

Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACCCC 86
 Db 16 CACACACACACCCC 2

RESULT 215

US-08-151-477A-58/c
 ; Sequence 58, Application US/08151477A
 ; Patent No. 5830644

GENERAL INFORMATION:
 ; APPLICANT: Michael D. West
 ; APPLICANT: Jerry W. Shay
 ; APPLICANT: Woodring E. Wright
 ; APPLICANT: Elizabeth Blackburn
 ; APPLICANT: Nam Woo Kim
 ; APPLICANT: Calvin B. Harley
 ; APPLICANT: Scott L. Weinrich
 ; APPLICANT: Catherine Strahl
 ; APPLICANT: Michael J. McEachern
 ; APPLICANT: Homayoun Vaziri
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CONDITIONS RELATED TO
 ; TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/151,477A
 ; FILING DATE: No. 5830644ember 12, 1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/038,766
 ; FILING DATE: March 24, 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 202/189
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

US-08-151-477A-58

Query Match 0.9%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACCCC 86
 Db 16 CACACACACACCCC 2

RESULT 216

US-08-819-867-80/c
 ; Sequence 80, Application US/08819867

Patent No. 6007989
 GENERAL INFORMATION:
 ; APPLICANT: Michael D. West
 ; APPLICANT: Calvin B. Harley
 ; APPLICANT: Scott L. Weinrich
 ; APPLICANT: Catherine M. Strahl
 ; APPLICANT: Michael J. McEachern
 ; APPLICANT: Jerry Shay
 ; APPLICANT: Woodring E. Wright
 ; APPLICANT: Elizabeth H. Blackburn
 ; APPLICANT: Nam Woo Kim
 ; APPLICANT: Homayoun Vaziri
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
 ; TITLE OF INVENTION: CONDITIONS RELATED TO
 ; TITLE OF INVENTION: TELOMERASE LENGTH AND/OR
 ; TITLE OF INVENTION: TELOMERASE ACTIVITY
 ; NUMBER OF SEQUENCES: 80
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSEQ for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/819,867
 ; FILING DATE: March 14, 1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/153,051
 ; FILING DATE: No. 6007989ember 12, 1993
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Chambers, Daniel M.
 ; REGISTRATION NUMBER: 34,561
 ; REFERENCE/DOCKET NUMBER: 224/232
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 80:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-819-867-80

Query Match 0.9%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACCCC 86
 Db 16 CACACACACACCCC 2

RESULT 217

US-08-464-011B-57/c
 ; Sequence 57, Application US/08464011B
 ; Patent No. 6368789
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael D. West
 ; APPLICANT: Jerry W. Shay
 ; APPLICANT: Woodring E. Wright

;; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
;; RELATED TO TELOMERE LENGTH AND/OR
;; TELOMERASE ACTIVITY

;; NUMBER OF SEQUENCES: 61

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; Suite 4700

;; CITY: Los Angeles

;; STATE: California

;; COUNTRY: U.S.A.

;; ZIP: 90071-2066

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; storage

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: IBM P.C. DOS 5.0

;; SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/464,011B

;; FILING DATE: 05-Jun-1995

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 07/882,438

;; FILING DATE: May 13, 1992

;; APPLICATION NUMBER: 08/038,766

;; FILING DATE: March 24, 1993

;; APPLICATION NUMBER: 08/060,952

;; FILING DATE: May 13, 1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Warburg, Richard J.

;; REGISTRATION NUMBER: 32,327

;; REFERENCE/DOCKET NUMBER: 202/045

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (213) 489-1600

;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510

;; INFORMATION FOR SEQ ID NO: 57:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 16 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 57:

US-08-464-011B-57

Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACACCC 86

Db 16 CACACACACACACCC 2

RESULT 218

US-09-378-535-80/c

; Sequence 80, Application US/09378535

; Patent No. 6551774

; GENERAL INFORMATION:

; APPLICANT: Michael B. West

; Calvin D. Harley

; Scott L. Weinrich

; Catherine M. Strahl

; Michael J. McEachern

; Jerry Shay

; Woodring B. Wright

; Elizabeth H. Blackburn

; Nam Woo Kim

; Homayoun Vaziri

;; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF

;; CONDITIONS RELATED TO

;; TELOMERE LENGTH AND/OR

;; TELOMERASE ACTIVITY

;; NUMBER OF SEQUENCES: 80

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Lyon & Lyon
;; STREET: 633 West Fifth Street
;; Suite 4700

;; CITY: Los Angeles

;; STATE: California

;; COUNTRY: U.S.A.

;; ZIP: 90071-2066

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;; storage

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: IBM P.C. DOS 5.0

;; SOFTWARE: FastSeq for Windows 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/378,535

;; FILING DATE: 20-Aug-1999

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/819,867

;; FILING DATE: <Unknown>

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Chambers, Daniel M.

;; REGISTRATION NUMBER: 34,561

;; REFERENCE/DOCKET NUMBER: 224/232

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (213) 489-1600

;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510

;; INFORMATION FOR SEQ ID NO: 80:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 16 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; SEQUENCE DESCRIPTION: SEQ ID NO: 80:

US-09-378-535-80

Query Match 0.9%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACACCC 86

Db 16 CACACACACACCC 2

RESULT 219

US-08-288-405A-12

; Sequence 12, Application US/08288405A

; Patent No. 5559009

; GENERAL INFORMATION:

; APPLICANT: Chardy, Kanianthara G.

; Applicant: Kalman, Katelin

; APPLICANT: Chardy, Grischa

; APPLICANT: Gutman, George A.

; TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel

; TITLE OF INVENTION: Gene

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,

; ADDRESSEE: Attn: Walter H. Dregler

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: United States

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.125
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/288,405A
;; FILING DATE: 10-AUG-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/207,431
;; FILING DATE: 04-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dreger, Walter H.
;; REGISTRATION NUMBER: 24,190
;; REFERENCE/DOCKET NUMBER: A-59844-1/WHI
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 17 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: both
US-08-288-405A-12

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGCGCGCGCGG 1383
Db 2 GCTGGGGCGCGCGG 17

RESULT 220
US-08-933-749-10/c
; Sequence 10, Application US/08933749
; Patent No. 5935791
; GENERAL INFORMATION:
; APPLICANT: Nadeau, James G.
; APPLICANT: Hsieh, Helen V.
; APPLICANT: Pitner, James B.
; APPLICANT: Linn, Carl P.
; TITLE OF INVENTION: Detection of Nucleic Acids by
; TITLE OF INVENTION: Fluorescence Quenching
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,749
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3749
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-933-749-10

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GAGCGAGCGCGGAG 37
Db 16 GAGCGAGCGCGGAG 2

RESULT 221
US-08-909-742-3/c
; Sequence 3, Application US/08909742
; Patent No. 6007991
; GENERAL INFORMATION:
; APPLICANT: Vimala S. Sivaraman
; APPLICANT: Hsien-Yu Wang
; APPLICANT: Craig C. Malbon
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
; TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
; TITLE OF INVENTION: BREAST CANCER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,742
; FILING DATE: August 12, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/831,994
; FILING DATE: April 1, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,520
; FILING DATE: March 28, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Adams, Lindsay S.
; REGISTRATION NUMBER: 36,425
; REFERENCE/DOCKET NUMBER: 178-225 CIP II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-909-742-3

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GCGGGCGCGCGGCG 1384
Db 15 GCGGGCGCGCGGCG 1

RESULT 222
US-08-909-742-4/c
; Sequence 4, Application US/08909742

Patent No. 6007991
 GENERAL INFORMATION:
 APPLICANT: Vimale S. Sivaraman
 APPLICANT: Hsien-Yu Wang
 APPLICANT: Craig C. Malbon
 TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-
 TITLE OF INVENTION: ACTIVATED PROTEIN KINASES AS THERAPY FOR
 TITLE OF INVENTION: BREAST CANCER
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann & Baron, LLP
 STREET: 350 Jericho Turnpike
 City: Jericho
 STATE: New York
 COUNTRY: USA
 ZIP: 11753
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for windows
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/909,742
 FILING DATE: August 12, 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/831,994
 FILING DATE: April 1, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/827,520
 FILING DATE: March 28, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Adams, Lindsey S.
 REGISTRATION NUMBER: 36,425
 REFERENCE/DOCKET NUMBER: 178-225 CIP II
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 822-3550
 TELEFAX: (516) 822-3582
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 US-08-909-742-4

Query Match 0.9%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGCGGGCGGC 1384
 Db 15 GCGGCGGGCGGGC 1

RESULT 223
 US-09-235-583-10/c
 Sequence 10, Application US/09235583
 Patent No. 6130047
 GENERAL INFORMATION:
 APPLICANT: Nadeau, James G.
 APPLICANT: Heieh, Helen V.
 APPLICANT: Pitner, James B.
 APPLICANT: Linn, Carl P.
 TITLE OF INVENTION: Detection of Nucleic Acids by
 TITLE OF INVENTION: Fluorescence Quenching
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company
 STREET: 1 Becton Drive

CITY: Franklin Lakes
 STATE: NJ
 COUNTRY: US
 ZIP: 07417
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/235,583
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Fugit, Donna R.
 REGISTRATION NUMBER: 32,135
 REFERENCE/DOCKET NUMBER: P-3749
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-235-583-10

Query Match 0.9%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GAGCGAGCGGGCGAG 37
 Db 16 GAGCGAGCGGGAG 2

RESULT 224

US-09-275-680-9
 Sequence 9, Application US/09275680
 Patent No. 6221630
 GENERAL INFORMATION:
 APPLICANT: Hopper, James E.
 TITLE OF INVENTION: A High Copy Number Recombinant Expression Construct for
 TITLE OF INVENTION: Regulated High-level Production of Polypeptides in
 TITLE OF INVENTION: Yeast
 FILE REFERENCE: 98428
 CURRENT APPLICATION NUMBER: US/09/275,680
 CURRENT FILING DATE: 1999-03-24
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 9
 LENGTH: 17
 TYPE: DNA
 ORGANISM: Saccharomyces cerevisiae
 US-09-275-680-9

Query Match 0.9%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 92 GCGCACTCGGCCG 106
 Db 3 GCGCACTCGGCCG 17

RESULT 225

US-09-599-164-10/c
 Sequence 10, Application US/09599164
 Patent No. 6261784
 GENERAL INFORMATION:
 APPLICANT: Nadeau, James G.
 APPLICANT: Heieh, Helen V.
 APPLICANT: Pitner, James B.
 APPLICANT: Linn, Carl P.
 TITLE OF INVENTION: Detection of Nucleic Acids by

; TITLE OF INVENTION: Fluorescence Quenching
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company
 ; STREET: 1 Becton Drive
 ; CITY: Franklin Lakes
 ; STATE: NJ
 ; COUNTRY: US
 ; ZIP: 07417
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/599,164
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/933,749
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fugit, Donna R.
 ; REGISTRATION NUMBER: 32,135
 ; REFERENCE/DOCKET NUMBER: P-3749
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-09-599-164-10

Query Match 0.9%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GAGCGGCGGCGGAG 37
 DB 15 GAGCGGCGGCGGAG 2

RESULT 226
 US-09-412-289-3/c
 ; Sequence 3, Application US/09412289
 ; Patent No. 6271210
 ; GENERAL INFORMATION:
 ; APPLICANT: Sivaraman, Vimala S.
 ; APPLICANT: Malbon, Craig C.
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED
 ; TITLE OF INVENTION: PROTEIN KINASES AS THERAPY FOR CANCER
 ; FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)
 ; CURRENT APPLICATION NUMBER: US/09/412,289
 ; CURRENT FILING DATE: 1999-10-05
 ; EARLIER APPLICATION NUMBER: 08/909,742
 ; EARLIER FILING DATE: 1997-08-12
 ; EARLIER APPLICATION NUMBER: 08/831,994
 ; EARLIER FILING DATE: 1997-04-01
 ; EARLIER APPLICATION NUMBER: 08/827,520
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthesized
 ; OTHER INFORMATION: antisense oligonucleotide
 US-09-412-289-3

Query Match 0.9%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGCGGGCGGCG 1384
 DB 15 GCGCGGCGGGCGGCG 1

RESULT 227
 US-09-412-289-4/c
 ; Sequence 4, Application US/09412289
 ; Patent No. 6271210
 ; GENERAL INFORMATION:
 ; APPLICANT: Sivaraman, Vimala S.
 ; APPLICANT: Wang, Hsien-Yu
 ; APPLICANT: Malbon, Craig C.
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR MITOGEN-ACTIVATED
 ; TITLE OF INVENTION: PROTEIN KINASES AS THERAPY FOR CANCER
 ; FILE REFERENCE: Seq. 1-4 (178-225 CIP II/CON)
 ; CURRENT APPLICATION NUMBER: US/09/412,289
 ; CURRENT FILING DATE: 1999-10-05
 ; EARLIER APPLICATION NUMBER: 08/909,742
 ; EARLIER FILING DATE: 1997-08-12
 ; EARLIER APPLICATION NUMBER: 08/831,994
 ; EARLIER FILING DATE: 1997-04-01
 ; EARLIER APPLICATION NUMBER: 08/827,520
 ; EARLIER FILING DATE: 1997-03-28
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthesized
 ; OTHER INFORMATION: antisense oligonucleotide
 US-09-412-289-4

Query Match 0.9%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 1.7e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1370 GGGGGCGGGCGGCG 1384
 DB 15 GCGCGGCGGGCGGCG 1

RESULT 228
 US-09-474-432B-438
 ; Sequence 438, Application US/09474432B
 ; Patent No. 6528640
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Beigelman, Leo
 ; APPLICANT: Burgin, Alex
 ; APPLICANT: Beaudry, Amber
 ; APPLICANT: Karpeisky, Alex
 ; APPLICANT: Adamic, Jasenka
 ; APPLICANT: Sweedler, David
 ; APPLICANT: Zinnen, Shawn
 ; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
 ; FILE REFERENCE: MEH800-831-B (247/276)
 ; CURRENT APPLICATION NUMBER: US/09/474,432B
 ; CURRENT FILING DATE: 1999-12-19
 ; PRIOR APPLICATION NUMBER: US 60/064,866
 ; PRIOR FILING DATE: 1997-11-05
 ; PRIOR APPLICATION NUMBER: US 60/084,727
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: US 09/186,675
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: US 09/301,511
 ; PRIOR FILING DATE: 1999-04-28
 ; NUMBER OF SEQ ID NOS: 1526

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-438

Query Match 0.9%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 759 CCACGGTGACCTGG 773
Db 2 CCACGGUGACUGG 16

RESULT 229

US-09-205-921-12/c
; Sequence 12, Application US/09205921A
; Patent No. 6008048
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: ex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
; FILE REFERENCE: RTS-0028
; CURRENT APPLICATION NUMBER: US/09/205,921A
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-921-12

Query Match 0.9%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 GAGATGCTGCTGCTG 163
Db 15 GAGATGATGCTGCTG 1

RESULT 230

US-08-486-408-17
; Sequence 17, Application US/08486408
; Patent No. 5718846
; GENERAL INFORMATION:
; APPLICANT: Brown, Steven Joel
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Naidu, Yathi M.
; TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
; TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
; TITLE OF INVENTION: mRNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,408
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CBI009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-486-408-17

Query Match 0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 431 GCGGACAGGCTGATG 445
Db 1 GCGGACAGGCTAATG 15

RESULT 231

US-08-975-570-17
; Sequence 17, Application US/08975570
; Patent No. 5945336
; GENERAL INFORMATION:
; APPLICANT: Brown, Steven Joel
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Naidu, Yathi M.
; TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
; TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
; TITLE OF INVENTION: mRNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,570
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/486,408
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CBI009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-975-570-17

Query Match 0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 431 GCGGACAGCTGATG 445
DB 1 GCGGACAGCTGATG 15

RESULT 232

US-09-144-367-43
Sequence 43, Application US/09144367
Patent No. 6432639
GENERAL INFORMATION:
APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 43
LENGTH: 19
TYPE: DNA
ORGANISM: H. sapiens
US-09-144-367-43

Query Match 0.9%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 AAGCGCAAGAGAGAG 69
DB 3 AAGCGCAAGAGAG 17

RESULT 233

US-07-627-538-6
Sequence 6, Application US/07627538
Patent No. 5248600
GENERAL INFORMATION:
APPLICANT: Topal, Michael D.
APPLICANT: Conrad, Michael
TITLE OF INVENTION: Method of Cleaving DNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5248600th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/627,538
FILING DATE: 19901214
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5052-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175

TELEX: 575102
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
US-07-627-538-6

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 641 CTGGCGGTGGAGCGCGC 658
DB 1 CTGGGTGGGCGCGCGC 18

RESULT 234

US-08-128-369-6
Sequence 6, Application US/08128369
Patent No. 5418150
GENERAL INFORMATION:
APPLICANT: Topal, Michael D.
APPLICANT: Conrad, Michael J.
TITLE OF INVENTION: METHOD OF CLEAVING DNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
ADDRESSEE: Gibson
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5418150th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/128,369
FILING DATE: 21-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-128-369-6

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 641 CTGGCGGTGGAGCGCGC 658
DB 1 CTGGGTGGGCGCGCGC 18

RESULT 235

US-08-072-063-10
; Sequence 10, Application US/08072063
; Patent No. 5439807
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Grina, Lynn S
; APPLICANT: Horwitz, Arnold
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19930519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-072-063-10

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 GCGCTGCTGCTCACCGC 954
Db 1 GCACCTGCTACTGACCGC 18

RESULT 236
US-08-050-232-11
; Sequence 11, Application US/08050232
; Patent No. 5525492
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Amplifying Nucleic Acid
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marks & Murase
; STREET: 2001 L Street, N.W., Suite 750
; CITY: Washington
; STATE: D.C.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordstar
; CURRENT APPLICATION DATA:
; FILING DATE: 14-MAY-1993
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9024005.2
; FILING DATE: 05-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01935
; FILING DATE: 05-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michael D. Bednarek
; REGISTRATION NUMBER: 32,329
; REFERENCE/DOCKET NUMBER: SH-PCT-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-955-4900
; TELEFAX: 202-955-4932
; TELEX: 248749
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-050-232-11

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 673 CTACGAGTCCAGGCACA 690
Db 1 CTGCAAGGCCAAGGCACA 18

RESULT 237
US-08-145-704-42/c
; Sequence 42, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Pennwald, Susan
; APPLICANT: Zendegeul, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:

/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: /note= "Amine moiety attached to 3'
/ OTHER INFORMATION: end"
US-08-145-704-42

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e-02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGGCGGGGAGGGG 1562
|||||
DB 18 GGGGGGCGGGGAGGGG 1

RESULT 238
US-08-145-704-43/c
; Sequence 43, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanoxine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety attached to 3'
; OTHER INFORMATION: end and phosphorothioate backbone"
US-08-145-704-43

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e-02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGGCGGGGAGGGG 1562
|||||
DB 18 GGGGGGCGGGGAGGGG 1

RESULT 239
US-08-161-673A-5
; Sequence 5, Application US/08161673A
; Patent No. 5578716
; GENERAL INFORMATION:
; APPLICANT: Szylf, Moshe
; APPLICANT: von Hofe, Eric
; TITLE OF INVENTION: Antisense Oligonucleotides Having
; TITLE OF INVENTION: Tumorigenicity-Inhibiting Activity
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 S. Wacker
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/161,673A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,142
; REFERENCE/DOCKET NUMBER: 93,1027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..18
; OTHER INFORMATION: /note= "PRIMER 1-18"
US-08-161-673A-5

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e-02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 212 GGACTGGCTGGGACCG 229
|||||
DB 1 GGACTGGCTGGGACCG 18

RESULT 240
US-08-435-350-38
; Sequence 38, Application US/08435350
; Patent No. 5599704
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR

```

; TITLE OF INVENTION: TREATMENT OF BREAST CANCER
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,350
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936,531
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/245
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-350-38

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 2.2e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1503 CCTGCACCGCTGGGCA 1520
DB 1 CCUGCAAGGCGUGGCA 18

RESULT 241
US-08-064-693-10
; Sequence 10, Application US/08064693
; GENERAL INFORMATION:
; APPLICANT: Thecfan, Georgia
; APPLICANT: Grinna, Lynn S
; APPLICANT: Horwitz, Arnold
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Borun
; STREET: 6300 Sears Tower, 233 South Wacker
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,693
; FILING DATE: 19930519
; CLASSIFICATION: 424
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-064-693-10

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 GCGCTCTCTGCTACCGC 954
DB 1 GCACCTGCTACTGACGC 18

RESULT 242
US-08-483-122-7/c
; Sequence 7, Application US/08483122
; Patent No. 5750376
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo
; TITLE OF INVENTION: Proliferation and Use of Multipotent
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESS: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,122
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-2/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1389
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; US-08-483-122-7
```

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTGCTGCTGGC 165
Db 18 CGAGGTGATGCCGCTGGC 1

RESULT 243

US-08-483-122-8
; Sequence 8, Application US/08483122
; Patent No. 5750376
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baerge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo
; TITLE OF INVENTION: Proliferation and Use of Multipotent
; TITLE OF INVENTION: Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,122
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-2/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-483-122-8

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTGCTGCTGGC 165
Db 1 CGAGGTGATGCCGCTGGC 18

RESULT 244

US-08-661-767-11
; Sequence 11, Application US/08661767
; Patent No. 5824515
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton HILL
; TITLE OF INVENTION: Process for Amplifying Nucleic Acid
; NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,767
FILING DATE: June 11, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9024005.2
FILING DATE: 05-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB91/01935
FILING DATE: 05-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 263/KPVM1540US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-661-767-11

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 673 CTACGAGTCCAAAGGCACA 690
Db 1 CTGCAAGGCCAAGGCACA 18

RESULT 245

US-08-117-952-745/c
; Sequence 745, Application US/08117952
; Patent No. 5851760
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; APPLICANT: Smith, Michael W.
; TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
; TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,952
; FILING DATE: 07-SEP-1993

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,471
; FILING DATE: 15-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 745:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Oligonucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-117-952-745

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 CACGCGGGGAGAGCGCA 28
Db 18 CACGAGTCAGTGAGCGCA 1

RESULT 246
US-08-486-648-7/c
; Sequence 7, Application US/08486648
; Patent No. 5851832
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,648
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-1/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-486-648-8

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGGC 165
Db 1 CGAGGTGATGCCGCTGGC 18

RESULT 248
US-08-875-445-1
; Sequence 1, Application US/08875445
; Patent No. 5869642
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hamman, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,648
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-1/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; US-08-486-648-7
```

APPLICANT: Kanta SAKAMOTO
TITLE OF INVENTION: DETECTION OF THE GENUS PECTINATUS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,445
FILING DATE: July 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotides
US-08-875-445-1
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e-02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 436 CAGGCTGATGACTCAG 453
Db 1 CAGGCGGATGACTAAGC 18
RESULT 249
US-08-875-445-11/c
Sequence 11, Application US/08875445
Patent No. 5869642
GENERAL INFORMATION:
APPLICANT: Kanta SAKAMOTO
TITLE OF INVENTION: DETECTION OF THE GENUS PECTINATUS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,445
FILING DATE: July 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotides
US-08-875-445-11
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e-02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 436 CAGGCTGATGACTCAG 453
Db 18 CAGGCGGATGACTAAGC 1
RESULT 250
US-08-358-556A-24/c
Sequence 24, Application US/08358556A
Patent No. 5869643
GENERAL INFORMATION:
APPLICANT: Chatelain, Francois
APPLICANT: Kumarev, Viktor
TITLE OF INVENTION: Process for Preparing Polynucleotides on
TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
TITLE OF INVENTION: Implementation
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
NAME/KEY: CDS
LOCATION: 1..18
US-08-358-556A-24

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGGCGGGGAGGGG 1562
|||||
DB 18 GGGGGGGGGGGGGGGG 1

RESULT 251
US-08-611-280-15
Sequence 15, Application US/08611280
Patent No. 5891666
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Canada Inc.
STREET: 8733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6J8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olecki, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-611-280-15

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 502 GCCAGGAGTGAAGTGG 519
|||||
DB 1 CCTAGAGTGAAGTGG 18

RESULT 252
US-08-734-973-30
Sequence 30, Application US/08734973
Patent No. 5912147
GENERAL INFORMATION:
APPLICANT: Stoler, Daniel L.
APPLICANT: Basik, Mark
APPLICANT: Anderson, Garth R.
TITLE OF INVENTION: A Rapid Means For Quantitating
TITLE OF INVENTION: Genomic Instability
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
STREET: 1800 One Mt Plaza
CITY: Buffalo

STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows
SOFTWARE: WordPerfect for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,973
FILING DATE: October 1996
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCKET NUMBER: 03551.0021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: (716) 849-0349
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
US-08-734-973-30

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 72 CACAGGCACACCCGCC 89
|||||
DB 1 CACACACACACACACC 18

RESULT 253
US-08-481-876-5
Sequence 5, Application US/08481876
Patent No. 5919772
GENERAL INFORMATION:
APPLICANT: Szyf, Moshe
APPLICANT: von Hofe, Eric
TITLE OF INVENTION: Antisense Oligonucleotides Having
TITLE OF INVENTION: Tumorigenicity-Inhibiting Activity
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,876
FILING DATE: June 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,1027-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs


```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..18
; OTHER INFORMATION: /note="PRIMER 1-18"
US-08-481-876-5

Query Match
Best Local Similarity 0.8%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 212 GGACTGGCGTGGGACCG 229
DB 1 GGACTGGCGTGGGACCG 18

RESULT 254
US-08-885-126-12/c
; Sequence 12, Application US/08885126A
; Patent No. 5955597
; GENERAL INFORMATION:
; APPLICANT: Arnold, Lyle J.
; APPLICANT: Riley, Timothy A.
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE
; FILE REFERENCES: GENTA-020FW2
; CURRENT APPLICATION NUMBER: US/08/885,126A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/343,018
; EARLIER FILING DATE: 1994-11-21
; EARLIER APPLICATION NUMBER: 08/154,013
; EARLIER FILING DATE: 1993-11-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized oligomer
US-08-885-126-12

Query Match
Best Local Similarity 0.8%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 AGCGAGGAGAGAGCGAG 29
DB 18 AGAGAGAGAGAGAGAG 1

RESULT 255
US-08-486-307-7/c
; Sequence 7, Application US/08486307
; Patent No. 5940885
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo
; TITLE OF INVENTION: Proliferation and Use of Multipotent
; TITLE OF INVENTION: Neural Stem Cells and their
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSES: & Herbert

```

```

; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,307
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,061
; REFERENCE/DOCKET NUMBER: A-61105-3/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-486-307-7

Query Match
Best Local Similarity 0.8%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGCG 165
DB 18 CGAGGTGATGCTGCTGCG 1

RESULT 256
US-08-486-307-8
; Sequence 8, Application US/08486307
; Patent No. 5950885
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo
; TITLE OF INVENTION: Proliferation and Use of Multipotent
; TITLE OF INVENTION: Neural Stem Cells and their
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSES: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,307
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.

```

```
/
/   REGISTRATION NUMBER: 35,081
/   REFERENCE/DOCKET NUMBER: A-61105-3/DJB/JPB
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (415) 781-1989
/   TELEFAX: (415) 398-3249
/   TELEX: 910 277299
/   INFORMATION FOR SEQ ID NO: 8:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 18 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: unknown
/   TOPOLOGY: unknown
/   MOLECULE TYPE: cDNA
/   US-08-486-307-8
/
/   Query Match
/   Best Local Similarity 83.3%; Pred. No. 2.2e+02;
/   Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/   QY 148 CGAGATGCTGCTGCTGCGC 165
/   Db 1 CGAGGTGATGCCCTGCGC 18
/
/   RESULT 257
/   US-09-205-860-14
/   Sequence 14, Application US/09205860
/   Patent No. 5981732
/   GENERAL INFORMATION:
/   APPLICANT: Lex M. Cowsett
/   TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
/   FILE REFERENCE: RTS-0031
/   CURRENT APPLICATION NUMBER: US/09/205,860
/   CURRENT FILING DATE: 1998-12-04
/   NUMBER OF SEQ ID NOS: 87
/   SEQ ID NO 14
/   LENGTH: 18
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: Antisense Oligonucleotide
/   US-09-205-860-14
/
/   Query Match
/   Best Local Similarity 83.3%; Pred. No. 2.2e+02;
/   Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/   QY 603 CTGACCGCGACGCGCAGCA 620
/   Db 1 CGAGCCGCGACGCGCAGGA 18
/
/   RESULT 258
/   US-09-205-921-34/c
/   Sequence 34, Application US/09205921A
/   Patent No. 6008048
/   GENERAL INFORMATION:
/   APPLICANT: Brett P. Monia
/   APPLICANT: ex M. Cowsett
/   TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
/   FILE REFERENCE: RTS-0028
/   CURRENT APPLICATION NUMBER: US/09/205,921A
/   CURRENT FILING DATE: 1998-12-04
/   NUMBER OF SEQ ID NOS: 47
/   SEQ ID NO 34
/   LENGTH: 18
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: Antisense Oligonucleotide
/   US-09-205-921-34
/
/   Query Match
/   Best Local Similarity 83.3%; Pred. No. 2.2e+02;
/   Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/   QY 1194 TCACGGCCCGCAGGCACCA 1211
/   Db 18 TCCCGGGCCGAGTCAGCA 1
/
/   RESULT 259
/   US-09-289-376-9
/   Sequence 9, Application US/09289376
/   Patent No. 6013788
/   GENERAL INFORMATION:
/   APPLICANT: Brett P. Monia
/   APPLICANT: Lex M. Cowsett
/   TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD3 EXPRESSION
/   FILE REFERENCE: RTS-0043
/   CURRENT APPLICATION NUMBER: US/09/289,376
/   CURRENT FILING DATE: 1999-04-09
/   NUMBER OF SEQ ID NOS: 47
/   SEQ ID NO 9
/   LENGTH: 18
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: Antisense Oligonucleotide
/   US-09-289-376-9
/
/   Query Match
/   Best Local Similarity 83.3%; Pred. No. 2.2e+02;
/   Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/   QY 814 GGACCGCGTCTGCTGCGGC 831
/   Db 1 GGAGGCGTCTGCGCGCGC 18
/
/   RESULT 260
/   US-09-289-376-30/c
/   Sequence 30, Application US/09289376
/   Patent No. 6013788
/   GENERAL INFORMATION:
/   APPLICANT: Brett P. Monia
/   APPLICANT: Lex M. Cowsett
/   TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD3 EXPRESSION
/   FILE REFERENCE: RTS-0043
/   CURRENT APPLICATION NUMBER: US/09/289,376
/   CURRENT FILING DATE: 1999-04-09
/   NUMBER OF SEQ ID NOS: 47
/   SEQ ID NO 30
/   LENGTH: 18
/   TYPE: DNA
/   ORGANISM: Artificial Sequence
/   FEATURE:
/   OTHER INFORMATION: Antisense Oligonucleotide
/   US-09-289-376-30
/
/   Query Match
/   Best Local Similarity 83.3%; Pred. No. 2.2e+02;
/   Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/   QY 114 ACGGGGACAGCTCGGAAG 131
/   Db 18 ACGGAGACATCGGAAG 1
/
/   RESULT 261
/   US-09-185-437-5
/   Sequence 5, Application US/09185437
/   Patent No. 6054439
/   GENERAL INFORMATION:
/   APPLICANT: SZYE, Moshe
/   APPLICANT: von Hofe, Eric
```

;; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES HAVING
;; TITLE OF INVENTION: TUMORIGENICITY-INHIBITING ACTIVITY
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: HALE AND DORR LLP
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: United States of America
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/185,437
;; FILING DATE: 17-FEB-1998
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KEOWN, Wayne A.
;; REGISTRATION NUMBER: 33,923
;; REFERENCE/DOCKET NUMBER: 106.101.138
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617 526 6000
;; TELEFAX: 617 526 5000
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1..18
;; OTHER INFORMATION: /note= "PRIMER 1-18"
US-09-185-437-5

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 212 GGACTGGCGTGGGACCG 229
|||||
Db 1 GGACTGGCGTGGGACCG 18

RESULT 262

US-08-479-795-7/c
; Sequence 7, Application US/08479795
; Patent No. 6071889
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo
; TITLE OF INVENTION: Proliferation and Use of Multipotent
; TITLE OF INVENTION: Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/479,795
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Brunelle, Jan P.
;; REGISTRATION NUMBER: 35,081
;; REFERENCE/DOCKET NUMBER: A-61105-6/DJB/JPB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: CDNA
US-08-479-795-7

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGGC 165
|||||
Db 18 CGAGGTGATGCGCTGGC 1

RESULT 263

US-08-479-795-8
; Sequence 8, Application US/08479795
; Patent No. 6071889
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo
; TITLE OF INVENTION: Proliferation and Use of Multipotent
; TITLE OF INVENTION: Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,795
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-6/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid

```

; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
US-08-479-795-8

Query Match          0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 148 CGAGATGCTGCTGTGGC 165
Db 1 CGAGGTGATCGCGTGGC 18

RESULT 264
US-09-143-212-44
; Sequence 44, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Coweart
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RTS-0005
; CURRENT APPLICATION NUMBER: US/09/143.212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-44

Query Match          0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1368 GCGGGCGCGCGCGGCA 1385
Db 1 GCGGCGGCGCGGCTTCA 18

RESULT 265
US-08-987-574-42/c
; Sequence 42, Application US/08987574
; Patent No. 6150339
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; TITLE OF INVENTION: Anti-Vital Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04529

Query Match          0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1545 GGGGGCGGGGGAGGGG 1562
Db 18 GGGGGGGGGGGGGGGG 1

RESULT 266
US-08-987-574-43/c
; Sequence 43, Application US/08987574
; Patent No. 6150339
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; TITLE OF INVENTION: Anti-Vital Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/987,574
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04529
; FILING DATE: 28-OCT-1993
; APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end and phosphorothioate
OTHER INFORMATION: backbone"
US-08-987-574-43

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1545 GGGGGCGGGGGGAGGGG 1562
|||||
Db 18 GGGGGGGGGGGGGGGG 1

RESULT 267
US-08-652-425-3
Sequence 3, Application US/08652425
Patent No. 6184211
GENERAL INFORMATION:
APPLICANT: SVzf, Moshe
TITLE OF INVENTION: INHIBITION OF DNA METHYLTRANSFERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: United States of America
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,425
FILING DATE: 30-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Keown, Wayne A
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 106.101.161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-652-425-3

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 212 GGACTGGGTGGGACCG 229
|||||
Db 1 GGACTGGGTGGGACCG 18

RESULT 268
US-08-535-168-42/c
Sequence 42, Application US/08535168
Patent No. 6184369
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Pennewald, Susan
APPLICANT: Zendegeui, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,168
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end"
US-08-535-168-42

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1545 GGGGGCGGGGGGAGGGG 1562
|||||
Db 18 GGGGGGGGGGGGGGGG 1

RESULT 269
US-08-535-168-43/c
Sequence 43, Application US/08535168

Patent No. 6184369
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennewald, Susan
APPLICANT: Zendegeui, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,168
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04529
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: US 08/053,027
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D. 32,714
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5574-CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5151
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end and phosphorothioate
OTHER INFORMATION: backbone"
US-08-535-168-43

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGGGGGGGGGGGGG 1562
DB 18 GGGGGGGGGGGGGGGGG 1

RESULT 270
US-08-849-488-11/c
Sequence 11, Application US/08849488
Patent No. 6238670
GENERAL INFORMATION:
APPLICANT: Fearon, Douglas T.
APPLICANT: Dempsey, Paul W.
TITLE OF INVENTION: Modulating the Immune Response
FILE REFERENCE: A-64962/WH/D/DAV
CURRENT APPLICATION NUMBER: US/08/849,488

CURRENT FILING DATE: 1997-10-21
EARLIER APPLICATION NUMBER: PCT/GB95/02851
EARLIER FILING DATE: 1995-12-06
EARLIER APPLICATION NUMBER: GB 9424631.1
EARLIER FILING DATE: 1994-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligomer
US-08-849-488-11

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 124 CTCGGAAGTCATCAGTTC 141
DB 18 CTCAGAGTCTTCAGATC 1

RESULT 271
US-09-195-940-15
Sequence 15, Application US/09195940
Patent No. 6258935
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6J8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,940
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-195-940-15

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 502 GCCAGAGTGGAAGTCGC 519
DB 18 GCCAGAGTGGAAGTCGC 1

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 GCTAGAGTCAAACTGAG 18

RESULT 272

US-09-437-076-3
; Sequence 3, Application US/09437076
; Patent No. 6261779

GENERAL INFORMATION:

APPLICANT: Barber-Guillem, Emilio
APPLICANT: Nelson, M. Bud

APPLICANT: Castro, Stephanie

TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form

CURRENT APPLICATION NUMBER: US/09/437,076

CURRENT FILING DATE: 1999-11-09

EARLIER APPLICATION NUMBER:

EARLIER FILING DATE:

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Word for Windows

SEQ ID NO 3

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY:

LOCATION:

OTHER INFORMATION: synthesized

US-09-437-076-3

Query Match 0.8%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCCGGGGGAGGGG 1562

Db 1 GGGGGGGGGGGGGGGGG 18

RESULT 273

US-09-437-076-4/c

; Sequence 4, Application US/09437076

; Patent No. 6261779

GENERAL INFORMATION:

APPLICANT: Barber-Guillem, Emilio

APPLICANT: Nelson, M. Bud

APPLICANT: Castro, Stephanie

TITLE OF INVENTION: Nanocrystals having polynucleotide strands and their use to form

CURRENT APPLICATION NUMBER: US/09/437,076

CURRENT FILING DATE: 1999-11-09

EARLIER APPLICATION NUMBER:

EARLIER FILING DATE:

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Word for Windows

SEQ ID NO 4

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY:

LOCATION:

OTHER INFORMATION: synthesized

US-09-437-076-4

Query Match 0.8%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1546 GGGGGCCGGGGGAGGGG 1563

Db 18 GGGGGGGGGGGGGGGGG 1

RESULT 274

US-08-885-366-10

; Sequence 10, Application US/08885366

; Patent No. 6274348

GENERAL INFORMATION:

APPLICANT: Theofan, Georgia

APPLICANT: Grinna, Lynn S

APPLICANT: Horwitz, Arnold

TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 South Wacker

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/885,366

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/064,693

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Meyers Thomas C.

REGISTRATION NUMBER: 36,989

REFERENCE/DOCKET NUMBER: 30659

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-885-366-10

Query Match 0.8%; Score 13.2; DB 1; Length 18;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 GGCCTGCTGCTCACC GC 954

Db 1 GCACCTGCTACTGACGC 18

RESULT 275

US-09-017-974-42/c

; Sequence 42, Application US/09017974

; Patent No. 6288042

GENERAL INFORMATION:

APPLICANT: Rando, Robert F.

APPLICANT: Ojwang, Joshua O.

APPLICANT: Hogan, Michael E.

APPLICANT: Wallace, Thomas L.

APPLICANT: Cossum, Paul A.

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Tetrad Forming Oligonucleotides

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1800

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

```

;
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,974
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end"
; US-09-017-974-42

```

```

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1545 GGGGGCCGGGGAGGGG 1562
Db 18 GGGGGGGGGGGGGGGGG 1

```

```

RESULT 276
US-09-017-974-43/c
; Sequence 43, Application US/09017974
; Patent No. 6286042
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Wallace, Thomas L.
; APPLICANT: Cosum, Paul A.
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Tetrad Forming Oligonucleotides
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tavon, P.C.
; STREET: 600 Travis, Suite 1800
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,974
; FILING DATE:

```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/037,374
; FILING DATE: 04-FEB-97
; APPLICATION NUMBER:
; FILING DATE: 09-DEC-97
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, C. Steven
; REGISTRATION NUMBER: 33,962
; REFERENCE/DOCKET NUMBER: 1472-06223
; TELEPHONE: 713/238-8010
; TELEFAX: 713/238-8008
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: /note= "Amine moiety
; OTHER INFORMATION: attached to 3' end and phosphorothioate
; OTHER INFORMATION: backbone"
; US-09-017-974-43

```

```

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 1545 GGGGGCCGGGGAGGGG 1562
Db 18 GGGGGGGGGGGGGGGGG 1

```

```

RESULT 277
US-08-484-406-7/c
; Sequence 7, Application US/08484406
; Patent No. 6294346
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hamang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and
; TITLE OF INVENTION: Use of Multipotent Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fiehr, Hohbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/484,406
; APPLICATION NUMBER: US/08/484,406
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-5/DJB/JPB
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249

```



```
TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-484-406-7

Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGGC 165
Db 18 CGAGGTGATGCCGTGGC 1

RESULT 278
US-08-484-406-8
; Sequence 8, Application US/08484406
; Patent No. 6294346
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and
; TITLE OF INVENTION: Use of Multipotent Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,406
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-5/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
US-08-484-406-8

Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGGC 165
Db 1 CGAGGTGATGCCGTGGC 18
```

```
RESULT 279
US-08-700-530-4/c
; Sequence 4, Application US/08700530
; Patent No. 6316186
; GENERAL INFORMATION:
; APPLICANT: EKINS, Roger P
; TITLE OF INVENTION: Binding assay using binding agents with tail groups
; FILE REFERENCE: 0380-P01180US0
; CURRENT APPLICATION NUMBER: US/08/700,530
; CURRENT FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: PC7/G995/00521
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: GB 9404709.9
; PRIOR FILING DATE: 1994-03-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-08-700-530-4

Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 AGCGAGGAGAGAGCGGAG 29
Db 18 AGAGAGAGAGAGAGAGAG 1

RESULT 280
US-08-682-255A-42/c
; Sequence 42, Application US/08682255A
; Patent No. 6323185
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennewald, Susan
; APPLICANT: Zendequi, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pomnier, Eyles
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tavon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS Windows 95
; SOFTWARE: MS Word 97 (saved as .txt file)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/682,255A
; FILING DATE: 17-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/535,168
; FILING DATE: 23-OCT-95
; APPLICATION NUMBER: 60/001,505
; FILING DATE: 19-JULY-95
; APPLICATION NUMBER: 60/014,007
; FILING DATE: 25-MARCH-96
```

APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 23-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end"
US-08-682-255A-42

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGG 1562
Db 18 GGGGGCGGGGGGGGGG 1

RESULT 281

US-08-682-255A-43/c
Sequence 43, Application US/08682255A
Patent No. 6323185
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyles
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,255A
FILING DATE: 17-JULY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,168
FILING DATE: 23-OCT-95
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007

FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/015,714
FILING DATE: 17-APRIL-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 23-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end and phosphorothioate
US-08-682-255A-43

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGG 1562
Db 18 GGGGGCGGGGGGGGGG 1

RESULT 282

US-09-429-130-42/c
Sequence 42, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zendequi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Eyles
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96

```

17-APRIL-96
23-APRIL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
attached to 3' end"
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-429-130-42
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGG 1562
Db 18 GGGGGCGGGGGGGGGG 1

RESULT 283
US-09-429-130-43/c
Sequence 43, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennewald, Susan
Zendequi, Joseph G.
Ojwang, Joshua O.
Hogan, Michael E.
Pommier, Yves
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSER: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
17-APRIL-96
23-APRIL-96
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
attached to 3' end and phosphorothioate
backbone"
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-429-130-43
Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGG 1562
Db 18 GGGGGCGGGGGGGGGG 1

RESULT 284
US-09-562-466-15
Sequence 15, Application US/09562466
Patent No. 6369202
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
Grossman, Alex
Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6J8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/562,466
; FILING DATE: 01-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/195,940
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Oleski, Nancy A.
; REGISTRATION NUMBER: 34,688
; REFERENCE/DOCKET NUMBER: A-338A
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-562-466-15

Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 502 GCCAGGAGTGAAACTGCG 519
Db 1 GCTAGAGTGAAACTGAG 18

RESULT 285
US-08-484-203-7/c
; Sequence 7, Application US/08484203
; Patent No. 6393369
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and
; TITLE OF INVENTION: Use of Multipotent Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-10/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
US-08-484-203-8

Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGCG 165
Db 1 CGAGGTGATGCCGCTGCG 1

RESULT 286
US-08-484-203-8
; Sequence 8, Application US/08484203
; Patent No. 6399369
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
; APPLICANT: Reynolds, Brent A.
; APPLICANT: Hammang, Joseph P.
; APPLICANT: Baetge, Edward E.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and
; TITLE OF INVENTION: Use of Multipotent Neural Stem Cells and their Progeny
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton
; ADDRESSEE: & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brunelle, Jan P.
; REGISTRATION NUMBER: 35,081
; REFERENCE/DOCKET NUMBER: A-61105-10/DJB/JPB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
US-08-484-203-8

Query Match      0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 148 CGAGATGCTGCTGCTGCG 165
Db 1 CGAGGTGATGCCGCTGCG 18

RESULT 287
US-08-486-313-7/c
; Sequence 7, Application US/08486313
; Patent No. 6497872
; GENERAL INFORMATION:
; APPLICANT: Weiss, Samuel
```

```
/ APPLICANT: Reynolds, Brent A.
/ APPLICANT: Hamang, Joseph P.
/ APPLICANT: Baetge, Edward B.
/ TITLE OF INVENTION: In Vitro and In Vivo Proliferation
/ TITLE OF INVENTION: and Use of Multipotent Neural Stem Cells and their
/ TITLE OF INVENTION: Progeny
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hobbach, Test, Albritton
/ ADDRESSEE: & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION NUMBER: US/08/486,313
/ APPLICATION NUMBER: US/08/486,313
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brunelle, Jan P.
/ REGISTRATION NUMBER: 35,081
/ REFERENCE/DOCKET NUMBER: A-61105-11/DJB/JPB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/
/ QUERY MATCH
/ BEST LOCAL SIMILARITY 83.3%; Score 13.2; DB 1; Length 18;
/ MATCHES 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 148 CGAGATGCTGCTGCTGCC 165
/ DB 18 CGAGGTGATGCGCTGCC 1
/
/ RESULT 288
/ US-08-486-313-8
/ Sequence 8, Application US/08486313
/ Patent No. 6497872
/ GENERAL INFORMATION:
/ APPLICANT: Weiss, Samuel
/ APPLICANT: Reynolds, Brent A.
/ APPLICANT: Hamang, Joseph P.
/ APPLICANT: Baetge, Edward B.
/ TITLE OF INVENTION: In Vitro and In Vivo Proliferation
/ TITLE OF INVENTION: and Use of Multipotent Neural Stem Cells and their
/ TITLE OF INVENTION: Progeny
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hobbach, Test, Albritton
/ ADDRESSEE: & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94111-4187
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
```

```
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION NUMBER: US/08/486,313
/ APPLICATION NUMBER: US/08/486,313
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brunelle, Jan P.
/ REGISTRATION NUMBER: 35,081
/ REFERENCE/DOCKET NUMBER: A-61105-11/DJB/JPB
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 781-1989
/ TELEFAX: (415) 398-3249
/
/ QUERY MATCH
/ BEST LOCAL SIMILARITY 83.3%; Score 13.2; DB 1; Length 18;
/ MATCHES 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 148 CGAGATGCTGCTGCTGCC 165
/ DB 1 CGAGGTGATGCGCTGCC 18
/
/ RESULT 289
/ US-09-422-978-5274/c
/ Sequence 5274, Application US/09422978
/ Patent No. 6537751
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
/ FILE REFERENCE: GENSET.020CPI
/ CURRENT APPLICATION NUMBER: US/09/422,978
/ EARLIER FILING DATE: 1999-10-20
/ EARLIER APPLICATION NUMBER: US 09/298,850
/ EARLIER FILING DATE: 1999-04-21
/ EARLIER APPLICATION NUMBER: US 60/109,732
/ EARLIER FILING DATE: 1998-11-23
/ EARLIER APPLICATION NUMBER: US 60/082,614
/ EARLIER FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 11796
/ SEQ ID NO 5274
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: 1..18
/
/ OTHER INFORMATION: upstream amplification primer 99-23118 for SEQ 1340,
/ US-09-422-978-5274
/
/ QUERY MATCH
/ BEST LOCAL SIMILARITY 83.3%; Score 13.2; DB 1; Length 18;
/ MATCHES 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 433 GGACAGGCTGATGACTCA 450
/ DB 18 GGAGAGGCTTATCATCA 1
/
/ RESULT 290
/ US-09-422-978-9962/c
```

```
; Sequence 9962, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9962
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-8499 for SEQ 2097, in compleme
US-09-422-978-9962

Query Match          0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 416 GAAGAAACACCGGAGCG 433
DB 18 GAAGAAACACCGAGATCG 1

RESULT 291
US-09-679-298A-25/c
; Sequence 25, Application US/09679298A
; Patent No. 6566131
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHAD6 EXPRESSION
; FILE REFERENCE: R1S-0045
; CURRENT APPLICATION NUMBER: US/09/679,298A
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 25
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-679-298A-25

Query Match          0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1366 CCGCGGGGGCGGGCGGG 1383
DB 18 CAGCGGGCGGGCGGGTGG 1

RESULT 292
PCT-US93-04754-10
; Sequence 10, Application PC/TUS9304754
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Grinna, Lynn S
; APPLICANT: Horwicz, Arnold
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
```

```
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/04754
; FILING DATE: 19930519
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US93-04754-10

Query Match          0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 937 GCGCTGCTGCTCACC GC 954
DB 1 GCACCTGCTACTGACCGC 18

RESULT 293
PCT-US96-11786-42/c
; Sequence 42, Application PC/TUS9611786
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Fennwald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Ojwang, Joshua O.
; APPLICANT: Hogan, Michael E.
; APPLICANT: Pommier, Yves
; APPLICANT: Mazumder, Abhijit
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Conley, Rose & Tayon, P.C.
; STREET: 600 Travis, Suite 1850
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77002-2912
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/11786
; FILING DATE: 17-JULY-1996
```

CLASSIFICATION:
PRIOR APPLICATION DATA: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
APPLICATION NUMBER: 60/015,714; 60/016,271
FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
FILING DATE: APRIL-96; 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end"
PCT-US96-11786-42

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGG 1562
||||| ||||| ||||| ||||| |||||
Db 18 GGGGGCGGGGGAGGGG 1

RESULT 294
PCT-US96-11786-43/C
Sequence 43, Application PC/TUS9611786
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
APPLICANT: Fennwald, Susan
APPLICANT: Zengdegi, Joseph G.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Hogan, Michael E.
APPLICANT: Pommier, Yves
APPLICANT: Mazumder, Abhijit
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11786
FILING DATE: 17-JULY-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,168; 60/001,505; 60/014,007; 60/013,688;
APPLICATION NUMBER: 60/015,714; 60/016,271
FILING DATE: 23-OCT-95; 17-JULY-96; 25-MARCH-96; 19-MARCH-96; 23-
FILING DATE: APRIL-96; 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: /note= "Amine moiety
OTHER INFORMATION: attached to 3' end and phosphorothioate
OTHER INFORMATION: backbone"
PCT-US96-11786-43

Query Match 0.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1545 GGGGGCGGGGGAGGGG 1562
||||| ||||| ||||| ||||| |||||
Db 18 GGGGGCGGGGGAGGGG 1

RESULT 295
US-08-623-891-23
Sequence 23, Application US/08623891
Patent No. 5795778
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,891
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,200
FILING DATE:
APPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-623-891-23

Query Match 0.8%; Score 13; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1293 GCCTGGCGCAGC 1305
 |||:|||||

Db 1 GCCUGGCGCAGC 13

RESULT 296

US-09-340-861-23
 ; Sequence 23, Application US/09340861
 ; Patent No. 6432704

; GENERAL INFORMATION:

; APPLICANT: Kenneth G. Draper
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
 ; TITLE OF INVENTION: VIRUS REPLICATION
 ; NUMBER OF SEQUENCES: 115

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
 ; STREET: 611 West Sixth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/340,861
 ; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/987,133
 ; FILING DATE:

; APPLICATION DATA:

; APPLICATION NUMBER: 07/882,921
 ; FILING DATE: May 14, 1992
 ; APPLICATION NUMBER: 07/948,359
 ; FILING DATE: September 18, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 200/209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELETYPE: 67-3510

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; US-09-340-861-23

Query Match 0.8%; Score 13; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1293 GCCTGGCGCAGC 1305
 |||:|||||

Db 1 GCCUGGCGCAGC 13

RESULT 297

US-09-634-262-23
 ; Sequence 23, Application US/09634262
 ; Patent No. 6440719

; GENERAL INFORMATION:

; APPLICANT: Kenneth G. Draper
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
 ; TITLE OF INVENTION: VIRUS REPLICATION
 ; NUMBER OF SEQUENCES: 115

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon
 ; STREET: 611 West Sixth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90017

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/634,262
 ; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/987,133
 ; FILING DATE:

; APPLICATION DATA:

; APPLICATION NUMBER: 07/882,921
 ; FILING DATE: May 14, 1992
 ; APPLICATION NUMBER: 07/948,359
 ; FILING DATE: September 18, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 200/209

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELETYPE: 67-3510

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; US-09-634-262-23

Query Match 0.8%; Score 13; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1e+02;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1293 GCCTGGCGCAGC 1305
 |||:|||||

Db 1 GCCUGGCGCAGC 13

RESULT 298

US-08-554-612C-35/c
 ; Sequence 35, Application US/08554612C
 ; Patent No. 5747860

; GENERAL INFORMATION:

; APPLICANT: Orlicky, David
 ; TITLE OF INVENTION: PROTAGLANDIN F2' RECEPTOR REGULATORY
 ; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
 ; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 2200 Sand Hill Road, Suite 100
 ; CITY: Menlo Park
 ; STATE: California

COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 336
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-554-612C-35

Query Match 0.8%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 154 GCTGCTGCTGGCG 166
DB 15 GCTGCTGCTGGCG 3

RESULT 299

US-09-205-860-11/c
Sequence 11, Application US/09205860
Patent No. 5981732
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0031
CURRENT APPLICATION NUMBER: US/09/205,860
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 11
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-11

Query Match 0.8%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1373 GGCGGCGGCGGCA 1385
DB 18 GGCGGCGGCGGCA 6

RESULT 300

US-09-344-579-42
Sequence 42, Application US/09344579
Patent No. 6054316
GENERAL INFORMATION:
APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
FILE REFERENCE: RTS-0063

CURRENT APPLICATION NUMBER: US/09/344,579
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 42
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-579-42

Query Match 0.8%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 868 CACTTTCCTGGAC 880
DB 4 CACTTTCCTGGAC 16

RESULT 301

US-09-422-978-5498
Sequence 5498, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 5498
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-4681 for SEQ 1564,
US-09-422-978-5498

Query Match 0.8%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1246 GGTATCGAGGAG 1258
DB 6 GGTATCGAGGAG 18

RESULT 302

US-08-181-664-18/c
Sequence 18, Application US/08181664
Patent No. 6025127
GENERAL INFORMATION:
APPLICANT: Sidransky, David
TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN
TITLE OF INVENTION: HISTOLOGIC TISSUE
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA


```

; GENERAL INFORMATION:
; APPLICANT: Brown, Steven Joel
; APPLICANT: Dattagupta, Nambhushan
; APPLICANT: Naidu, Yathi M.
; TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
; TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
; TITLE OF INVENTION: mRNA
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,408
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CB1009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-486-408-4

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 574 CGAGGGCGCGCGAGTG 589
Db 17 CGAGGGGACTCGCAGTG 2

RESULT 309
US-08-758-306-795
; Sequence 795, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 574 CGAGGGCGCGCGAGTG 589
Db 17 CGAGGGGACTCGCAGTG 2

RESULT 310
US-08-710-134-15/c
; Sequence 15, Application US/08710134
; Patent No. 5834181
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,134
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-8.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 795:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-795

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1016 TCGGGCTCGGGCGCGC 1031
Db 2 UCGGUUCGAGCGCGC 17

RESULT 310
US-08-710-134-15/c
; Sequence 15, Application US/08710134
; Patent No. 5834181
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,134
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-8.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

```

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-710-134-15

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1514 CTGGCGCATGGCGGTCA 1529
DB 17 CTGCCCATGGCGGTCA 2

RESULT 311
US-08-710-134-32/c
; Sequence 32, Application US/08710134
; Patent No. 5849481
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,134
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-8.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotides"
US-08-710-134-32

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1514 CTGGCGCATGGCGGTCA 1529
DB 17 CTGCACATGGCGGTCA 2

RESULT 312
US-08-885-15/c
; Sequence 15, Application US/08485885
; Patent No. 5849483
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
```

```

; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,885
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-12.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
US-08-485-885-15

Query Match      0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1514 CTGGCGCATGGCGGTCA 1529
DB 17 CTGCCCATGGCGGTCA 2

RESULT 313
US-08-485-885-32/c
; Sequence 32, Application US/08485885
; Patent No. 5849483
; GENERAL INFORMATION:
; APPLICANT: SHUBER, ANTHONY P.
; TITLE OF INVENTION: HIGH THROUGHPUT SCREENING METHOD FOR
; TITLE OF INVENTION: SEQUENCES OR GENETIC ALTERATIONS IN NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genzyme Corporation
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,885
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
```

REFERENCE/DOCKET NUMBER: GEN4-12.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotides"
US-08-485-885-32

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1514 CTGGGCATGGGGTCA 1529
DB 17-CTGCACATGGGGTCA 2

RESULT 314
US-08-975-570-4/c
Sequence 4, Application US/08975570
Patent No. 5945336
GENERAL INFORMATION:
APPLICANT: Brown, Steven Joel
APPLICANT: Dattagupta, Nanihubhan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
TITLE OF INVENTION: PROLIFERATION USING ANTISENSE OLIGONUCLEOTIDES TO INTERLEUKIN-
TITLE OF INVENTION: mRNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,570
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,408
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A.
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CEI009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-975-570-4

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 574 CGAGGGCGCGCAGTG 589
DB 17 CGAGGGACTCGCAGTG 2

RESULT 315
US-08-665-259-42
Sequence 42, Application US/0865259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.
TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: One Mountain Road
CITY: Framingham
STATE: Massachusetts
COUNTRY: United States of America
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,259
FILING DATE: 17-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dugan, Deborah A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IGS-9.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide primer"
US-08-665-259-42

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 AAGCTGGTGAAGGACC 803
DB 2 ACGCTGGTGAAGGAGC 17

RESULT 316
US-08-665-259-55
Sequence 55, Application US/0865259
Patent No. 6028173
GENERAL INFORMATION:
APPLICANT: Landes, Gregory M.
APPLICANT: Burn, Timothy C.
APPLICANT: Connors, Timothy D.
APPLICANT: Dackowski, William R.
APPLICANT: Van Raay, Terence J.
APPLICANT: Klinger, Katherine W.

```

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-9.1
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide primer"
; US-08-665-259-55

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 788 AAGCTGGTGAAGGACC 803
Db 2 ACGCTGGTGAAGGACC 17

RESULT 317
US-08-762-500-42
; Sequence 42, Application US/08/762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315

```

```

; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-9.3
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide primer"
; US-08-762-500-42

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 788 AAGCTGGTGAAGGACC 803
Db 2 ACGCTGGTGAAGGACC 17

RESULT 318
US-08-762-500-55
; Sequence 55, Application US/08/762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315

```

REFERENCE/DOCKET NUMBER: IG5-9.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide primer"
US-08-762-500-55

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 788 AAGCTGGTGAAGGACC 803
|||
DB 2 ACGTGGTGAAGGAC 17

RESULT 319
US-08-998-099-32/c
Sequence 32, Application US/08998099A
Patent No. 6103890
GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MCSWIGEN, JAMES A.
APPLICANT: STINCHCOMB, DAN T.
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
FILE REFERENCE: 231/175
CURRENT APPLICATION NUMBER: US/08/998,099A
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 08/373,124
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 08/245,466
EARLIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-08-998-099-32

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 786 CCAAGCTGGTGAAGGA 801
|||
DB 17 CCAATGCTGGAGAAGGA 2

RESULT 320
US-08-998-099-49
Sequence 49, Application US/08998099A
Patent No. 6103890
GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: MCSWIGEN, JAMES A.
APPLICANT: STINCHCOMB, DAN T.
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
FILE REFERENCE: 231/175
CURRENT APPLICATION NUMBER: US/08/998,099A
CURRENT FILING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658

EARLIER FILING DATE: 1997-01-23
EARLIER APPLICATION NUMBER: 08/373,124
EARLIER FILING DATE: 1995-01-13
EARLIER APPLICATION NUMBER: 08/245,466
EARLIER FILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-08-998-099-49

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 56.2%; Pred. No. 2.3e+02;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 184 CCTCGTCTCCTCGCTG 199
|||
DB 1 CCUGGUCUCUCUG 16

RESULT 321
US-09-324-867-54
Sequence 54, Application US/09324867A
Patent No. 6251632
GENERAL INFORMATION:
APPLICANT: Lillcrap, David
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-059
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 54
LENGTH: 17
TYPE: DNA
ORGANISM: Synthetic oligonucleotide
US-09-324-867-54

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1287 CCTTCCGCGCTGGCGCA 1302
|||
DB 1 CCTTCCGCGCGCGCA 16

RESULT 322
US-07-974-409C-72/c
Sequence 72, Application US/07974409C
Patent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA

COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-974-409C-72

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 642 TGGCGGTGGAGCCGG 657
DB 16 TGGCGGTGGAGCCGAG 1

RESULT 323
US-09-364-707A-6
Sequence 6, Application US/09364707A
Patent No. 6310191
GENERAL INFORMATION:
APPLICANT: Collins, John
APPLICANT: Roettgen, Peter
TITLE OF INVENTION: Generation of Diversity in Combinatorial
TITLE OF INVENTION: Libraries
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,707A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP98/00533
FILING DATE: 02-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 97101539.1
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491

REFERENCE/DOCKET NUMBER: 29473/35824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA oligo"
US-09-364-707A-6

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 762 CGGTGCACCTGGAGCA 777
DB 2 CGGTGCACCTGGAGCA 17

RESULT 324
US-08-584-040-1462/c
Sequence 1462, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1462:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-584-040-1462

Query Match 0.8%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 805 GAGCCCCGGGACCGC 820
 Db 17 GAGCCCCGGGACCGC 2

RESULT 325

US-08-584-040-2129
 Sequence 2129, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: McSwiggen, James

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES OR

TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: GROWTH FACTOR

NUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,974

FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 2129:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-584-040-2129

Query Match

Best Local Similarity 0.8%; Score 12.8; DB 1; Length 17;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 942 TGCTGCTACCGCCG 957
 Db 2 UGCGUCGCCCGCCC 17

RESULT 326

US-08-584-040-3971

Sequence 3971, Application US/08584040
 Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: McSwiggen, James

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES OR

TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: GROWTH FACTOR

NUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/584,040

FILING DATE: January 11, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/005,974

FILING DATE: October 26, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3971:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-584-040-3971

Query Match 0.8%; Score 12.8; DB 1; Length 17;

Best Local Similarity 68.8%; Pred. No. 2.3e+02;

Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1447 CCACGTGCTACTCGCAG 1462

Db 1 CCACGUAUUGGCAG 16

RESULT 327

US-08-584-040-7869/c

Sequence 7869, Application US/08584040

Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela

APPLICANT: McSwiggen, James

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES OR

TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7869:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-7869

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 499 GTGGCCAGAGTGAGAA 514
Db 17 GAGGCCAGAGTGAGA 2

RESULT 328
US-09-220-510B-1
Sequence 1, Application US/09220510B
Patent No. 6440726
GENERAL INFORMATION:
APPLICANT: RESNICK, NITZAN
TITLE OF INVENTION: EXPRESSION VECTORS COMPRISING MULTIPLE SHEAR STRESS
RESPONSIVE ELEMENTS (SSRE) AND METHODS OF USE FOR
TITLE OF INVENTION: TREATING DISORDERS RELATED TO VASCULOGENESIS AND/OR
TITLE OF INVENTION: ANGIOGENESIS IN A SHEAR STRESS ENVIRONMENT
FILE REFERENCE: P-2771-US
CURRENT APPLICATION NUMBER: US/09/220,510B
CURRENT FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequence:
OTHER INFORMATION: A PDGF-A Shear Stress Response Element.
US-09-220-510B-1

Query Match 0.8%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1547 GGGGCGGGGGGGGG 1562
Db 1 GGGGCGGGGGGGGG 16

RESULT 329

US-09-343-698-2/c
Sequence 2, Application US/09343698
Patent No. 6475485
GENERAL INFORMATION:
APPLICANT: Seeman, Gerhard
Bosslet, Klaus
Czech, Joerg
Kolar, Cenek
Hoffman, Dieter
Sedlacek, Hans-Harald
TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process For
Preparation Thereof And The Use Thereof In Combination With
Functionalized Tumor-Specific Enzyme Conjugates
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,698
FILING DATE: 30-Jun-1999
CLASSIFICATION: <Unknown>
APPLICATION DATA:
APPLICATION NUMBER: 08/325,955
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ogden, Stasia L.
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: 05552.0981-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-343-698-2

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1368 GCGGGCGGGCGGGCGG 1383
Db 16 GCAGCGGGCGGGCGG 1

RESULT 330

US-09-474-432B-592/c
Sequence 592, Application US/09474432B
Patent No. 6528640

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBH00-831-B (247/276)
CURRENT APPLICATION NUMBER: US 09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 592
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-592

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1502 GCCTGACACCTCTGG 1517
Db 17 GCCTGACACCTCTGG 2

RESULT 331
US-09-474-432B-815
Sequence 815, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MBH00-831-B (247/276)
CURRENT APPLICATION NUMBER: US 09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 815
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-815

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1352 AGCGCGCGGGGACC 1367
Db 2 AGUGCGGUGGGGACC 17

RESULT 332
US-09-371-772B-7/c
Sequence 7, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Referred to as Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00.876-J (237/198)
CURRENT APPLICATION NUMBER: US 09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-7

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 805 GAGCCCCGGGACCGC 820
Db 17 GAGCCCCGGGACCGC 2

RESULT 333
US-09-371-772B-674
Sequence 674, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Referred to as Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00.876-J (237/198)
CURRENT APPLICATION NUMBER: US 09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 674
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-371-772B-674

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 88.8%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 942 TGCTGCTCAGCGCGC 957
:|||||:
Db 2 UGUGUCCCGCGCC 17

RESULT 334

US-09-371-772B-1738
; Sequence 1738, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1738
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1738

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1447 CCACGTGGTACTCGCAG 1462
:|||||:
Db 1 CCACUGGUUUGGCAG 16

RESULT 335

US-09-371-772B-3652/c
; Sequence 3652, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3652
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3652

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 499 GTGCCAGGAGTGAAA 514
:|||||:
Db 17 GAGGCCAGGAGTGAGA 2

RESULT 336

US-09-371-772B-4170/c
; Sequence 4170, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4170
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4170

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 805 GAGCCCCGGGACCGC 820
:|||||:
Db 16 GAGCCCCGGGACCGC 1

RESULT 337

US-09-371-772B-5005
; Sequence 5005, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5005
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5005

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 2.3e+02;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 938 CGCCTGCTGCTCACC 953

TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-72

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 642 TGGCGGTGGAGCGG 657
DB 16 TGGCGGTGGAGCGG 1

RESULT 342
PCT-US94-05617-15
Sequence 15, Application PC/TUS9405617
GENERAL INFORMATION:
APPLICANT: Antigen Express, Inc.
TITLE OF INVENTION: Regulation of Antigen Presentation
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05617
FILING DATE: 18-MAY-1994
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,400
FILING DATE: May 19, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9301 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-05617-15

Query Match 0.8%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1306 GCTCCTGGCTGCACTG 1321
DB 2 GCTCCTGGCTGATG 17

RESULT 343
US-07-910-867B-9
Sequence 9, Application US/07910867B
Patent No. 5597895
GENERAL INFORMATION:
APPLICANT: Gaynor, Richard B.

APPLICANT: Garcia, Joseph A.
APPLICANT: Harrich, David
TITLE OF INVENTION: Transdominant Tat Mutants and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/910,867B
FILING DATE: 02-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:263/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/414-7577
TELEX: N/A

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-07-910-867B-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1545 GGGGGGCGGGGAGG 1560
DB 2 GGGGAGCGCGGAGG 17

RESULT 344
US-08-346-613-9
Sequence 9, Application US/08346613
Patent No. 5686264
GENERAL INFORMATION:
APPLICANT: GAYNOR, RICHARD B.
APPLICANT: GARCIA, JOSEPH A.
APPLICANT: HARRICH, DAVID
TITLE OF INVENTION: TRANSDOMINANT TAT MUTANTS AND USES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,613

/ FILING DATE: 435
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/910,867
/ FILING DATE: 07/02/92
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MAYFIELD, DENISE L.
/ REGISTRATION NUMBER: 33,732
/ REFERENCE/DOCKET NUMBER: UTSD:263/MAY
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 512-320-7200
/ TELEFAX: 512-474-7577
/ TELEX: NOT APPLICABLE
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-346-613-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1545 GGGGGCGCGGGGAGG 1560
Db 2 GGGAGCGCGCGGAGG 17

RESULT 345
US-08-796-883-9/c
/ Sequence 9, Application US/08796883
/ Patent No. 5744353
/ GENERAL INFORMATION:
/ APPLICANT: Herman, Jean; Coulie, Pierre;
/ APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
/ APPLICANT: Luescher, Immanuel.
/ TITLE OF INVENTION: Tumor Rejection Antigens Presented By
/ TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
/ STATE: New York
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/796,883
/ FILING DATE: 06-FEB-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/602,506
/ FILING DATE: 20-FEBRUARY-1996
/ APPLICATION NUMBER: 08/531,864
/ FILING DATE: 21-SEPTEMBER-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373,636
/ FILING DATE: 17-JANUARY-1995
/ APPLICATION NUMBER: 08/253,503
/ FILING DATE: 3-JUNE-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 5744353man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5436
/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: nucleic acid
/ FEATURE:
/ NAME/KEY: PCR primer
/ US-08-796-883-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1013 TCCTCGGGCTCGGGC 1028
Db 17 TCCTCGGACTCGTGGC 2

RESULT 346
US-08-796-883-11/c
/ Sequence 11, Application US/08796883
/ Patent No. 5744353
/ GENERAL INFORMATION:
/ APPLICANT: Herman, Jean; Coulie, Pierre;
/ APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
/ APPLICANT: Luescher, Immanuel.
/ TITLE OF INVENTION: Tumor Rejection Antigens Presented By
/ TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
/ STATE: New York
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/796,883
/ FILING DATE: 06-FEB-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/602,506
/ FILING DATE: 20-FEBRUARY-1996
/ APPLICATION NUMBER: 08/531,864
/ FILING DATE: 21-SEPTEMBER-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373,636
/ FILING DATE: 17-JANUARY-1995
/ APPLICATION NUMBER: 08/253,503
/ FILING DATE: 3-JUNE-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 5744353man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5436
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: nucleic acid


```
/
/ FEATURE:
/ NAME/KEY: PCR primer
US-08-796-883-11
/
/ Query Match 0.8%; Score 12.8; DB 1; Length 18;
/ Best Local Similarity 87.5%; Pred. No. 2.6e+02;
/ Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
QY 1013 TCCTCGGGCTCGGGGC 1028
/
/ DB 17 TCCTCGGACTCGTGGC 2
/
/
/ RESULT 347
/ US-08-611-280-11
/ Sequence 11, Application US/08611280
/ Patent No. 5891666
/ GENERAL INFORMATION:
/ APPLICANT: Matsuyama, Toshifumi
/ APPLICANT: Grossman, Alex
/ APPLICANT: Richardson, Christopher D.
/ TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Angen Canada Inc.
/ STREET: 6733 Mississauga Road, Suite 303
/ CITY: Mississauga
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: L5N 6J8
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/611.280
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Oleski, Nancy A.
/ REGISTRATION NUMBER: 34,698
/ REFERENCE/DOCKET NUMBER: A-338A
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-611-280-11
/
/ Query Match 0.8%; Score 12.8; DB 1; Length 18;
/ Best Local Similarity 87.5%; Pred. No. 2.6e+02;
/ Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
QY 504 CAGGAGTGAACCTGG 519
/
/ DB 3 CAGGAGTGAACCTGAG 18
/
/
/ RESULT 348
/ US-08-448-561-23/c
/ Sequence 23, Application US/08448561
/ Patent No. 5908827
/ GENERAL INFORMATION:
/ APPLICANT: SIRNA, Antonio
/ TITLE OF INVENTION: NEW PROTEIN FROM URINE NAMED COMPONENT B
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/448.561
/ FILING DATE: 22-JAN-1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: IT RM 92 A/919
/ FILING DATE: 22-DEC-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: SIRNA-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-08-448-561-23
/
/ Query Match 0.8%; Score 12.8; DB 1; Length 18;
/ Best Local Similarity 87.5%; Pred. No. 2.6e+02;
/ Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
/
QY 785 ACCAAGCTGGTGAAGG 800
/
/ DB 17 ACCACGCTGGTGACGG 2
/
/
/ RESULT 349
/ US-08-531-864-9/c
/ Sequence 9, Application US/08531864
/ Patent No. 5977300
/ GENERAL INFORMATION:
/ APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry
/ TITLE OF INVENTION: Isolated No. 5977300a- and Decapeptides Which
/ TITLE OF INVENTION: Bind to HLA-B*44 Molecules And The Use Thereof
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felfe & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York City
/ STATE: New York
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: Wordperfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/531.864
/ FILING DATE: 21-September-1995
/ CLASSIFICATION: 436
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/373.636
/ FILING DATE: 17-JANUARY-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/253.503
/ FILING DATE: 3-JUNE-1994
/ ATTORNEY/AGENT INFORMATION:
```

NAME: Hanson, No. 5977300man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5378.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
FEATURE:
NAME/KEY: PCR primer
US-08-531-864-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGGCTCGGGC 1028
DB 17 TCCTCGGACTCGTGGC 2

RESULT 350
US-08-531-864-11/c
Sequence 11, Application US/08531864
Patent No. 5977300
GENERAL INFORMATION:
APPLICANT: Coulie, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated No. 5977300a- and Decapeptides Which
Bind to HLA-B44 Molecules And The Use Thereof
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531.864
FILING DATE: 21-September-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373.636
FILING DATE: 17-JANUARY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253.503
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5977300man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5378.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
FEATURE:
NAME/KEY: PCR primer
US-08-531-864-11

NAME: Hanson, No. 5977300man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5378.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
FEATURE:
NAME/KEY: PCR primer
US-08-373-636C-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGGCTCGGGC 1028
DB 17 TCCTCGGACTCGTGGC 2

RESULT 351
US-08-373-636C-9/c
Sequence 9, Application US/08373636C
Patent No. 5997870
GENERAL INFORMATION:
APPLICANT: Coulie, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Codes
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373.636C
FILING DATE: 17-JANUARY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253.503
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5997870man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5378.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
FEATURE:
NAME/KEY: PCR primer
US-08-373-636C-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGGCTCGGGC 1028
DB 17 TCCTCGGACTCGTGGC 2

RESULT 352
US-08-373-636C-11/c
Sequence 11, Application US/08373636C
Patent No. 5997870
GENERAL INFORMATION:
APPLICANT: Coulie, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Codes
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373.636C
FILING DATE: 17-JANUARY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253.503
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5957870man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5378.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
FEATURE:
NAME/KEY: PCR primer
US-08-373-636C-11

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGGCTCGGGC 1028
|||||
DB 17 TCCTCGGACTCGTGC 2

RESULT 353
US-09-205-921-13/c
Sequence 13, Application US/09205921A
Patent No. 6008048
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: ex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF EGR-1 EXPRESSION
FILE REFERENCE: RTS-0028
CURRENT APPLICATION NUMBER: US/09/205,921A
CURRENT FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 13
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-921-13

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGGGCGCGCGCG 1383
|||||
DB 18 GCGGTGAGGCGCGG 3

RESULT 354

US-09-344-520-18/c
Sequence 18, Application US/09344520
Patent No. 6037176
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF Integrin beta 3 EXPRESSION
FILE REFERENCE: RTS-0070
CURRENT APPLICATION NUMBER: US/09/344,520
CURRENT FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 18
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-520-18

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 439 GCTGATGACTCAGG 454
|||||
DB 18 GCTGATGACTGAGAG 3

RESULT 355
US-09-029-045-9/c
Sequence 9, Application US/09029045
Patent No. 6056952
GENERAL INFORMATION:
APPLICANT: Rosenberg, Amy Sonya
TITLE OF INVENTION: Selective Elimination of T Cells That
Recognize Specific Preslected Targets
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,045
FILING DATE: 02-JUN-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,964
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/13873
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-236100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear


```
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-46

Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e-02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1123 CGCGCGGCTCTGCCC 1138
Db 16 CGCGCGCACCTGCCC 1

RESULT 359
US-09-166-186-13
; Sequence 13, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanshan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF- $\alpha$  EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 13
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-166-186-13

Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e-02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 CGGTTGCGGAGAGGA 251
Db 1 CGGTTGCGAGAGATGA 16

RESULT 360
US-09-197-380-8/c
; Sequence 8, Application US/09197380
; Patent No. 6096543
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF MEK1 EXPRESSION
; FILE REFERENCE: KTS-0016
; CURRENT APPLICATION NUMBER: US/09/197,380
; CURRENT FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 8
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-197-380-8

Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e-02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 14 CGAGGAGAGAGCGAG 29
Db 17 CGAGGAGAGAGCGAG 2

RESULT 361
US-08-863-813A-62
; Sequence 62, Application US/08863813A
; Patent No. 6140466
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Gottesfeld, Joel M.
; APPLICANT: Wright, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES
; TITLE OF INVENTION: AND METHODS THEREFOR
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,813A
; FILING DATE: 27-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,318
; FILING DATE: 18-JUL-1996
; APPLICATION NUMBER: 08/183,119
; FILING DATE: 18-JAN-1996
; APPLICATION NUMBER: US95/00829
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A., Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08401/010001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-863-813A-62

Query Match      0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e-02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1368 GCGGCGCGCGCGCGG 1383
Db 1 GCGTGGCGCGGGCGG 16

RESULT 362
US-08-211-882-15
; Sequence 15, Application US/08211882
; Patent No. 6153737
; GENERAL INFORMATION:
; APPLICANT: Manoharan et al.
; TITLE OF INVENTION: Derivatized Oligonucleotides Having
; TITLE OF INVENTION: Improved Uptake And Other Properties
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 61537377ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,882
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/782,374
FILING DATE: 24-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-0649
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-211-882-15

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 GCGAGCGGAGCGAGG 48
| | | | | | | | | | | | | | | | | |
Db 2 GGGAGCGGTAGCGAGG 17

RESULT 363
US-09-487-444-11/c
; Sequence 11, Application US/09487444
; Patent No. 6159697
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD7 EXPRESSION
; FILE REFERENCE: R1S-0133
; CURRENT APPLICATION NUMBER: US/09/487,444
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-444-11

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGCGC 166
| | | | | | | | | | | | | | | | | |
Db 16 GCTGCTGCTGCTGCTG 1

RESULT 364
US-09-266-294-9/c

; Sequence 9, Application US/09266294
; Patent No. 6171806
; GENERAL INFORMATION:
; APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated No. 6171806a- and Decapeptides Which
; Bind to HLA-B44 Molecules And The Use Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/266,294
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,864
; FILING DATE: 21-September-1995
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6171806man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5378.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 688-3884
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; FEATURE:
; NAME/KEY: PCR primer
US-09-266-294-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1013 TCCTCGGCTCGGGC 1028
| | | | | | | | | | | | | | | | | |
Db 17 TCCTCGGCTCGGGC 2

RESULT 365
US-09-266-294-11/c
; Sequence 11, Application US/09266294
; Patent No. 6171806
; GENERAL INFORMATION:
; APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated No. 6171806a- and Decapeptides Which
; Bind to HLA-B44 Molecules And The Use Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/266,294

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/531,864

FILING DATE: 21-September-1995

APPLICATION NUMBER: 08/373,636

FILING DATE: 17-JANUARY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/253,503

FILING DATE: 3-JUNE-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6171806man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5378.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic acid

FEATURE:

NAME/KEY: PCR primer

US-09-266-294-11

Query Match 0.8%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1013 TCCTCGGGCTCGGGC 1028

Db 17 TCCTCGGACTCGTGGC 2

RESULT 366

US-09-313-932-13

Sequence 13, Application US/09313932A

Patent No. 6228642

GENERAL INFORMATION:

APPLICANT: Baker, Brenda

APPLICANT: Bennett, C. Frank

APPLICANT: Butler, Madeline M.

APPLICANT: Shanahan, William R.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-

FILE REFERENCE: ISPH-0356

CURRENT APPLICATION NUMBER: US/09/313,932A

NUMBER OF SEQ ID NOS: 501

SEQ ID NO 13

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-313-932-13

Query Match 0.8%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 236 GGCTTCGGAGAGGA 251

Db 1 GGCTTCGAGAGATGA 16

RESULT 367

US-09-179-281-9/c

Sequence 9, Application US/09179281

Patent No. 6245333

GENERAL INFORMATION:

APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Codes

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/179,281

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/373,636

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6245333man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5378.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: nucleic acid

FEATURE:

NAME/KEY: PCR primer

US-09-179-281-9

Query Match 0.8%; Score 12.8; DB 1; Length 18;

Best Local Similarity 87.5%; Pred. No. 2.6e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1013 TCCTCGGGCTCGGGC 1028

Db 17 TCCTCGGACTCGTGGC 2

RESULT 368

US-09-179-281-11/c

Sequence 11, Application US/09179281

Patent No. 6245333

GENERAL INFORMATION:

APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Codes

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

For A

For A


```
/ Sequence 30, Application US/09679298A
/ Patent No. 6566131
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ APPLICANT: Lex M. Cowert
/ TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD6 EXPRESSION
/ FILE REFERENCE: RTS-0045
/ CURRENT APPLICATION NUMBER: US/09/679,298A
/ CURRENT FILING DATE: 2001-03-05
/ NUMBER OF SEQ ID NOS: 47
/ SEQ ID NO 30
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-679-298A-30

Query Match          0.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 151 GATGCTGCTGCTGGCG 166
DB 17 GCTGCTGCTGCTGGAG 2

RESULT 379
US-09-083-123-5
/ Sequence 5, Application US/09083123
/ Patent No. 6326143
/ GENERAL INFORMATION:
/ APPLICANT: Orum, Hendrik
/ APPLICANT: Seeger, Corina
/ TITLE OF INVENTION: Method for Generating Multiple Double Stranded Nucleic
/ FILE OF INVENTION: Acids
/ FILE REFERENCE: sequence listing
/ CURRENT APPLICATION NUMBER: US/09/083,123
/ CURRENT FILING DATE: 1998-05-22
/ EARLIER APPLICATION NUMBER: EP 95118600.6
/ EARLIER FILING DATE: 1995-11-25
/ EARLIER APPLICATION NUMBER: PCT/EP96/05149
/ EARLIER FILING DATE: 1996-11-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: made by humans
US-09-083-123-5

Query Match          0.8%; Score 12.8; DB 1; Length 32;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 76 CCACACACCCCGCCGCGCACTCGCGCCGG 107
DB 1 CCCCCCCCCCCCCCCCCCCCCCCCCCGG 32

RESULT 380
US-08-985-162-1770
/ Sequence 1770, Application US/08985162
/ Patent No. 6057156
/ GENERAL INFORMATION:
/ APPLICANT: Akhtar, Saghir
/ APPLICANT: Fell, Patricia
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
/ TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
/ TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
```

```
/ TITLE OF INVENTION: FACTOR RECEPTORS
/ NUMBER OF SEQUENCES: 1877
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/985,162
/ FILING DATE: 04 December 1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/036,476
/ FILING DATE: 31 January 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 230/107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1770:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-985-162-1770

Query Match          0.8%; Score 12.4; DB 1; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1304 GCGCTCTGCTGC 1317
DB 1 GCGCGCGCGCGC 14

RESULT 381
US-07-997-455-4
/ Sequence 4, Application US/07997455
/ Patent No. 5429948
/ GENERAL INFORMATION:
/ APPLICANT: Crespi, Charles L.
/ APPLICANT: Penman, Bruce W.
/ APPLICANT: Davies, Robin L.
/ TITLE OF INVENTION: Human Cell Line Stably Expressing 5CDNAs
/ TITLE OF INVENTION: Encoding Procarcinogen-Activating Enzymes and Related
/ TITLE OF INVENTION: Mutagenicity
/ NUMBER OF SEQUENCES: 5
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
/ STREET: 600 Atlantic Avenue
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: United States of America
/ ZIP: 02210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/07/997,455
FILING DATE: 19921228
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/597,815
FILING DATE: 15-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/771,520
FILING DATE: 04-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/162,895
FILING DATE: 02-MAR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: G0307/7004
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-997-455-4

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. NO. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 165 CGAGATGTCGTG 178
Db 2 CGAGATGTCGCG 15

RESULT 382
US-08-153-051B-52/c
Sequence 52, Application US/08153051B
Patent No. 5645986
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/153,051B
FILING DATE: No. 5645986member 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 204/195
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-153-051B-52

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. NO. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 72 CACACGCACACAC 85
Db 15 CACACACACACAC 2

RESULT 383
US-08-291-932A-266/c
Sequence 266, Application US/08291932A
Patent No. 5658780
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: NF-KB
NUMBER OF SEQUENCES: 830
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/291,932A
FILING DATE: August 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/157
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 266:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-291-932A-266

Query Match 0.8%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 644 GCGGTGGAGGCCGG 657
 Db 14 GAGGTGGAGGCCGG 1

RESULT 384

US-08-060-952C-51/c
 ; Sequence 51, Application US/08060952C
 ; Patent No. 5695932

GENERAL INFORMATION:
 APPLICANT: Michael D. West
 APPLICANT: Jerry W. Shay
 APPLICANT: Woodring E. Wright
 APPLICANT: Elizabeth Blackburn
 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
 TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
 TITLE OF INVENTION: TELOMERASE ACTIVITY
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/060,952C
 FILING DATE: May 13, 1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/882,438
 FILING DATE: May 13, 1992
 APPLICATION NUMBER: 08/038,766
 FILING DATE: March 24, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 202/045
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-060-952C-51

Query Match 0.8%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 2e+02;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 72 CACACGCACACACC 85
 Db 15 CACACGCACACACC 2

RESULT 385

US-08-363-240A-139
 ; Sequence 139, Application US/08363240A
 ; Patent No. 5705388

GENERAL INFORMATION:
 APPLICANT: Couture, Larry
 APPLICANT: McSwiggen, James
 APPLICANT: Bisgaier, Charles
 APPLICANT: Pape, Michael
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 TITLE OF INVENTION: PREVENTION, INHIBITION OF
 TITLE OF INVENTION: PROGRESSION AND REGRESSION
 TITLE OF INVENTION: OF VASCULAR DISEASES
 NUMBER OF SEQUENCES: 1243
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/363,240A
 FILING DATE: December 23, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 210/096
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 139:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-363-240A-139

Query Match 0.8%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 675 ACAGTCCAGGCA 688
 Db 2 ACAGTCCAGGCA 15

RESULT 386

US-08-363-240A-140
 ; Sequence 140, Application US/08363240A
 ; Patent No. 5705388

GENERAL INFORMATION:
 APPLICANT: Couture, Larry

APPLICANT: McSwiggen, James
APPLICANT: Bisgaier, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PREVENTION, INHIBITION OF
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-140

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 675 ACAGTCCAGGCA 688
DB 1 ACAGUCCAAGCA 14

RESULT 387
US-08-311-486C-58/c
Sequence 58, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-311-486C-58

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 235 GGGGTTCCGGAAGA 248
DB 15 GGGGTTCCGGAAGA 2

RESULT 388
US-08-151-477A-52/c
Sequence 52, Application US/08151477A
Patent No. 5830644
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Jerry W. Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine Strahl
APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151.477A
FILING DATE: No. 5830644ember 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 202/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-151-477A-52

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGACACACC 85
DB 15 CACACACACACC 2

RESULT 389
US-08-585-684B-48
Sequence 48, Application US/08585584B
Patent No. 5877021
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-585-684B-48

Query Match 0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 2e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 898 GAAGGCTCTCTACG 911
DB 2 GAGGGUCUUCUACG 15

RESULT 390
US-08-819-867-79/c
Sequence 79, Application US/08819867
Patent No. 6007989
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
APPLICANT: Catherine M. Strahl
APPLICANT: Michael J. Meeachern
APPLICANT: Jerry Shay
APPLICANT: Woodring E. Wright
APPLICANT: Elizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO
TELOMERASE LENGTH AND/OR
TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: California
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/153,051
FILING DATE: No. 6007989ember 12, 1993
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:

```
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-819-867-79

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 72 CACACGCACACACC 85
Db 15 CACACACACACACC 2

RESULT 391
US-09-038-073-48
/ Sequence 48, Application US/09038073
/ Patent No. 6194150
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Daniel T.
/ APPLICANT: Jarvis, Thale
/ APPLICANT: McSwiggen, James
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
/ TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
/ NUMBER OF SEQUENCES: 2751
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb.
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/038,073
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/585,684
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/078
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-09-038-073-48

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 2e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 898 GAAGGCTCTTCTACG 911
Db 2 GAGGUCUUCUACG 15

RESULT 392
US-09-081-646-627/c
/ Sequence 627, Application US/09081646
/ Patent No. 6333152
/ GENERAL INFORMATION:
/ APPLICANT: Kinzler, Kenneth
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Zhang, Lin
/ APPLICANT: Zhou, Wei
/ TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
/ TITLE OF INVENTION: Cancer Cells
/ FILE REFERENCE: 01107.74664
/ CURRENT APPLICATION NUMBER: US/09/081,646
/ CURRENT FILING DATE: 1998-05-20
/ EARLIER APPLICATION NUMBER: 60/047,352
/ EARLIER FILING DATE: 1997-05-21
/ NUMBER OF SEQ ID NOS: 871
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 627
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-081-646-627

Query Match      0.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 TCATCAGTTCATG 145
Db 14 TCATCATTCCATG 1

RESULT 393
US-08-464-011B-51/c
/ Sequence 51, Application US/08464011B
/ Patent No. 6368789
/ GENERAL INFORMATION:
/ APPLICANT: Michael D. West
/ APPLICANT: Jerry W. Shay
/ APPLICANT: Woodring E. Wright
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
/ TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
/ TITLE OF INVENTION: TELOMERASE ACTIVITY
/ NUMBER OF SEQUENCES: 61
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/464,011B
/ FILING DATE: 05-Jun-1995
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/882,438
/ FILING DATE: May 13, 1992
/ APPLICATION NUMBER: 08/038,766
/ FILING DATE: March 24, 1993
/ APPLICATION NUMBER: 08/060,952
/ FILING DATE: May 13, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 202/045
```


; Gaps 0;

Db 16 TGTGACGAAGATGG 3

RESULT 396
US-08-311-760A-349/c
; Sequence 349, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-760A-349

Query Match 0.8%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1485 GGCTCTGGCAGC 1498
Db 16 GGCTCTGGCAGC 3

RESULT 397
US-07-789-738-1
; Sequence 1, Application US/07789738
; Patent No. 5824857
; GENERAL INFORMATION:
; APPLICANT: Beachy, Roger N.
; APPLICANT: Bhattacharyya, Maitrayee
; TITLE OF INVENTION: Plant Promoter
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774.310
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 5824857th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789.738
; FILING DATE: 19920330
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10540)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-07-789-738-1

Query Match 0.8%; Score 12.4; DB 1; Length 16;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 897 AGAAGTCTTCTAC 910
Db 1 AGAAGTCTTCTAC 14

RESULT 398
US-08-774-310-349/c
; Sequence 349, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774.310
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:

QY 1323 CGCCCGCGGCACG 1336
|||||
Db 14 CGCCCGCGCTCAG 1

RESULT 401

US-08-196-218-8/c
; Sequence 8, Application US/08196218
; Patent No. 5614619
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; TITLE OF INVENTION: Use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,218
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-196-218-8

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1277 GCCTTCGCGCCCTT 1290
|||||
Db 17 GCCTTCGCGCTCCTT 4

RESULT 402

US-08-196-218-9
; Sequence 9, Application US/08196218
; Patent No. 5614619
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen

; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; TITLE OF INVENTION: Use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,218
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-196-218-9

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1277 GCCTTCGCGCCCTT 1290
|||||
Db 1 GCCTTCGCGCTCCTT 14

RESULT 403

US-08-681-953-8/c
; Sequence 8, Application US/08681953
; Patent No. 5710032
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kampiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; TITLE OF INVENTION: Use.
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,953
; FILING DATE: 30-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/196,218
; FILING DATE: 25-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-681-953-8

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1277 GCCTTCGCGCCTT 1290
DB      17 GCCTTCGCGCCTT 4

RESULT 404
US-08-681-953-9
; Sequence 9, Application US/08681953
; Patent No. 5710032
; GENERAL INFORMATION:
; APPLICANT: Piepersberg, Wolfgang
; APPLICANT: Stockmann, Michael
; APPLICANT: Taleghani, Kamiz Mansouri
; APPLICANT: Distler, Jurgen
; APPLICANT: Grabley, Susanne
; APPLICANT: Sichel, Petra
; APPLICANT: Brau, Barbara
; TITLE OF INVENTION: Secondary-Metabolite Biosynthesis Genes
; TITLE OF INVENTION: From Actinomycetes, Method of Isolating Them, and Their
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,953
; FILING DATE: 30-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/196,218
; FILING DATE: 25-AUG-1994
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 02481.1372-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-681-953-9

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1277 GCCTTCGCGCCTT 1290
DB      1 GCCTTCGCGCCTT 14

RESULT 405
US-08-748-068-11
; Sequence 11, Application US/08748068
; Patent No. 5770410
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Chiral Synthesis
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,068
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,959
; FILING DATE: 05-OCT-1994
; APPLICATION NUMBER: GB 92 02033.8
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 04702.6
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 93/00204
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-748-068-11

Query Match      0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1173 CCGCGGCGCGCTAC 1186
DB      3 CCGCGGCGCGCAAC 16

RESULT 406
US-08-485-689-27/c
; Sequence 27, Application US/08485689
```



```
; Patent No. 5856188
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,689
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-C1X/JPW/KJP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-485-689-27

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 CGGGGACAGCGCG 1358
Db 15 CGGGGACAGCGCG 2

RESULT 407
US-08-476-021A-27/C
; Sequence 27, Application US/08476021A
; Patent No. 5858785
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,021A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-DZ/JPW/KJP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-476-021A-27

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 CGGGGACAGCGCG 1358
Db 15 CGGGGACAGCGCG 2

RESULT 408
US-08-478-608B-27/C
; Sequence 27, Application US/08478608B
; Patent No. 5863339
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,608B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-C1Z/JPW/KJP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
; US-08-478-608B-27

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 CGGGGACAGCGCG 1358
Db 15 CGGGGACAGCGCG 2
```

RESULT 409
US-08-849-021-16
; Sequence 16, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-849-021-16

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 71 GCACACGACACACAC 84
Db 3 GCACACACACAC 16

RESULT 410
US-08-460-890A-8/c
; Sequence 8, Application US/08460890A
; Patent No. 5994109
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,890A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725
; FILING DATE: March 19, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; FEATURE:
; OTHER INFORMATION: "C" stands for 5-methylcytosine
US-08-460-890A-8

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 AGGAGAGAGCGAG 29
Db 17 AGGAGAGAGAGAG 4

RESULT 411
US-08-157-641C-8/c
; Sequence 8, Application US/08167641C
; Patent No. 6033884
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage


```
/
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq for Windows 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/167,641C
/ FILING DATE: December 14, 1993
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/855,389
/ FILING DATE: March 20, 1992
/ APPLICATION NUMBER: PCT/US93/02725
/ FILING DATE: March 19, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 205/012
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Other nucleic acid
/ FEATURE:
/ OTHER INFORMATION: "C" stands for 5-methylcytosine
/ US-08-167-641C-8

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 AGGAGAGAGCGAG 29
Db 17 AGGAGAGAGAGAG 4

RESULT 412
US-08-985-162-220/c
; Sequence 220, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; APPLICATION NUMBER: 60/036,476
```

```
/
/ FILING DATE: 31 January 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 230/107
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 220:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-985-162-220

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 348 TCTCCAGAACTCC 361
Db 17 TCTCCAGAACTCC 4

RESULT 413
US-08-985-162-221/c
; Sequence 221, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; APPLICATION NUMBER: 60/036,476
```

TOPOLOGY: linear
US-08-985-162-221

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 348 TCTCCAGAACTCC 361
DB 16 TCTCCACAACTCC 3

RESULT 414
US-08-779-916A-77/c
; Sequence 77, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,942
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 1 of human RB1 gene
US-08-779-916A-77

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1323 CGCCCGCGGCTCAG 1336
DB |||||

DB 14 CGCCCGCGGCTCAG 1

RESULT 415
US-08-998-099-10/c
; Sequence 10, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-10

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1550 GCGCGGCGGAGGCG 1563
DB 16 GCGCGGCGGAGGCG 3

RESULT 416
US-08-998-099-47
; Sequence 47, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-47

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 2.7e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 182 GTCTCTGCTCTCTC 195
DB 4 GCCCUGGUCUCCUC 17

RESULT 417

US-08-998-099-48
; Sequence 48, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-48

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 2.7e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 182 GTCTGCTGCTCCTC 195
Db 1 GCCCUGGCUCCUC 14

RESULT 418

US-08-998-099-75/c
; Sequence 75, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-75

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 476 TTGGCCATCTCGGT 489
Db 14 TTGGCAATCTCGGT 1

RESULT 419

US-08-998-099-120
; Sequence 120, Application US/08998099A
; Patent No. 6103890
; GENERAL INFORMATION:
; APPLICANT: JARVIS, THALE
; APPLICANT: MCSWIGGEN, JAMES A.
; APPLICANT: STINCHCOMB, DAN T.
; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
; FILE REFERENCE: 231/175
; CURRENT APPLICATION NUMBER: US/08/998,099A
; CURRENT FILING DATE: 1997-12-24
; EARLIER APPLICATION NUMBER: 60/037,658
; EARLIER FILING DATE: 1997-01-23
; EARLIER APPLICATION NUMBER: 08/373,124
; EARLIER FILING DATE: 1995-01-13
; EARLIER APPLICATION NUMBER: 08/245,466
; EARLIER FILING DATE: 1994-05-18
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-08-998-099-120

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1453 GTACTGCGAGCTGC 1466
Db 4 GUACUCCAGCUGC 17

RESULT 420

US-08-460-971A-8/c
; Sequence 8, Application US/08460971A
; Patent No. 6150168
; GENERAL INFORMATION:
; APPLICANT: Woo, Savio L.C.
; APPLICANT: Smith, Louis C.
; APPLICANT: Cristiano, Richard J.
; APPLICANT: Gottchalk, Stephen
; TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,971A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,641
; FILING DATE: December 14, 1993
; APPLICATION NUMBER: 07/855,389
; FILING DATE: March 20, 1992
; APPLICATION NUMBER: PCT/US93/02725

FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
FEATURE:
OTHER INFORMATION: "C" stands for 5-methylcytosine
US-08-460-971A-8

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 AGGAGAGAGCGAG 29
DB 17 AGGAGAGAGAGAG 4

RESULT 421
US-08-462-040-8/c
Sequence 8, Application US/08462040
Patent No. 6177554
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
FEATURE:
OTHER INFORMATION: "C" stands for 5-methylcytosine
US-08-462-040-8

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 AGGAGAGAGCGAG 29
DB 17 AGGAGAGAGAGAG 4

RESULT 422
US-08-476-423A-27/c
Sequence 27, Application US/08476423A
Patent No. 6221661
GENERAL INFORMATION:
APPLICANT: Hampel, Arnold E.
APPLICANT: Tritz, Richard H.
TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States Of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,423A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 43863-C2/JFW/KJP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-278-0526
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-476-423A-27

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1345 CGGGGACAGCGCG 1358
DB 15 CGGGGACAGCGCG 2

RESULT 423
US-08-584-040-5410/c

; Sequence 5410, Application US/08584040
; Patent No. 6346398

GENERAL INFORMATION:

; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 5410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-5410

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 483 TCTCGGTGATGAAC 496

Db 16 TCTCGGTGATGTAC 3

RESULT 424

US-09-474-432B-599
; Sequence 599, Application US/09474432B
; Patent No. 6528640

GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleos

; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 599
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-474-432B-599

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGAGGCGAGCCAGC 14

Db 4 GCGAGGCGAGCCAGC 17

RESULT 425

US-09-474-432B-697/c
; Sequence 697, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot

; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 697
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-474-432B-697

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1301 CACGCGCTCCTGGC 1314

Db 15 CACGCGCTCCTGGC 2

RESULT 426

US-09-474-432B-758
; Sequence 758, Application US/09474432B

; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US 09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 758
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-758

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 2.7e+02;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 759 CCACGGTGCACCTG 772
|||||:|:|:
DB 4 CCACGGUGACGUG 17

RESULT 427
US-09-474-432B-818
; Sequence 818, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US 09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 818
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-818

Query Match 0.8%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 245 AAGAGGAGGACCC 258
|||||:|:|:
DB 1 AAGAGGAGGACCC 14

RESULT 428
US-09-371-772B-2309/c
; Sequence 2309, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-J (237/198)
; CURRENT APPLICATION NUMBER: US 09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2309
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2309

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 483 TCTCGGTGATGAAC 496
|||||:|:|:
DB 16 TCTCGGTGATGTAC 3

RESULT 429
US-09-371-772B-4193
; Sequence 4193, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-J (237/198)
; CURRENT APPLICATION NUMBER: US 09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4193
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4193

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1164 GCAGGAGCGCGG 1177
| | | | | | | | | |
Db 3 GCAGGAGCGCGG 16

RESULT 430

US-09-371-772B-4965/c
; Sequence 4965, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4965
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4965

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1530 AGTCAGCTGAAGC 1543
| | | | | | | | | |
Db 17 AGTCAGCTGAAGC 4

RESULT 431

US-09-371-772B-4966/c
; Sequence 4966, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4966
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4966

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1530 AGTCAGCTGAAGC 1543
| | | | | | | | | |
Db 15 AGTCAGCTGAAGC 2

RESULT 432

US-09-371-772B-4967/c
; Sequence 4967, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4967
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4967

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1530 AGTCAGCTGAAGC 1543
| | | | | | | | | |
Db 14 AGTCAGCTGAAGC 1

RESULT 433

US-09-371-772B-6383
; Sequence 6383, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6383
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6383

Query Match 0.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 2.7e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

[illegible]


```
/ APPLICATION NUMBER: US/08/127,954
/ FILING DATE:
/ CLASSIFICATION: 436
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Petry, Douglas A.
/ REGISTRATION NUMBER: 35,321
/ REFERENCE/DOCKET NUMBER: 8873
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (510) 814-2974
/ TELEFAX: (510) 814-2977
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-127-954-8

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 33 GCGAGCCGCGAGGAGGA 49
Db 17 GCGAGCCGCGAGGATGA 1

RESULT 437
US-08-196-538-15/c
; Sequence 15, Application US/08196538
; Patent No. 5639608
; GENERAL INFORMATION:
; APPLICANT: Stanley Tabor
; APPLICANT: Charles C. Richardson
; TITLE OF INVENTION: USE OF SHORT OLIGONUCLEOTIDES AS PRIMERS
; TITLE OF INVENTION: FOR DNA SEQUENCING
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,538
; FILING DATE: February 14, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/985,468
; FILING DATE: December 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-196-538-15
```

```
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 44 CGAGGAGGGAAGGCC 60
Db 17 CGAGGAGGGAAGGACTC 1

RESULT 438
US-08-233-030-48
; Sequence 48, Application US/082333030
; Patent No. 5639855
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF PROMYELOCYTIC
; TITLE OF INVENTION: LEUKEMIA
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,030
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,910
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/240
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-233-030-48

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1556 GGAGGGCGCGGAGGG 1572
Db 1 GGUGGGCGCGGACGG 17

RESULT 439
US-08-373-124A-1477
; Sequence 1477, Application US/08373124A
; Patent No. 5646042
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
```

```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,124A
; FILING DATE: January 13, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-373-124A-1477

```

```

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1205 GGCACCACTTCATCAA 1221
Db 1 GGCACCAUUCUGGACAA 17

```

```

RESULT 440
US-08-530-492-57
; Sequence 57, Application US/08530492
; Patent No. 5689052
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; TITLE OF INVENTION: Expression in Monocytoidous Plants and Method For
; TITLE OF INVENTION: Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Parkway No. 5689052th
; CITY: St. Louis
; STATE: Missouri

```

```

; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,492
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,333
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10605)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-530-492-57

```

```

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1225 GGTGCTGGCTCGTCT 1241
Db 1 GGCCTGCTCGTCTCT 17

```

```

RESULT 441
US-08-623-891-30/C
; Sequence 30, Application US/08623891
; Patent No. 5795778
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/623,891
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,200
; FILING DATE:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359

```

```
/ FILING DATE: September 18, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 200/209
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-623-891-30

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1549 GCGCGGGGAGGGGCGC 1565
Db 17 GCGCGGGGAGGGGCGC 1

RESULT 442
US-08-758-306-11
/ Sequence 11, Application US/08758306
/ Patent No. 5807743
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: McSwiggen, James A.
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES
/ TITLE OF INVENTION: ASSOCIATED WITH
/ TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
/ TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
/ NUMBER OF SEQUENCES: 1379
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/758,306
/ FILING DATE: December 3, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 212/132
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-758-306-457/c

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 15 GAGGCGAGAGGAGGCGC 31
Db 17 GAGGCGAGAGGAGGCGG 1

RESULT 444
US-08-758-306-457/c

/ FILING DATE: September 18, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 200/209
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-758-306-11

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 128 GAAGTCATCATGTTCCAT 144
Db 1 GAAGCCCAUUAUCCAU 17

RESULT 443
US-08-758-306-455/c
/ Sequence 455, Application US/08758306
/ Patent No. 5807743
/ GENERAL INFORMATION:
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: McSwiggen, James A.
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES
/ TITLE OF INVENTION: ASSOCIATED WITH
/ TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
/ TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
/ NUMBER OF SEQUENCES: 1379
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/758,306
/ FILING DATE: December 3, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 212/132
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 455:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-758-306-455

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 15 GAGGCGAGAGGAGGCGC 31
Db 17 GAGGCGAGAGGAGGCGG 1

RESULT 444
US-08-758-306-457/c
```

; Sequence 457, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 457:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-457

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e-02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GCGAGGAGAGAGCGAG 29
DB 17 GCGAGGAGAGAGCGAG 1

RESULT 445
US-08-758-306-459/c
; Sequence 459, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 459:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-459

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e-02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 AGCGAGGAGAGAGCGGA 28
DB 17 AGCGAGGAGAGAGCGGA 1

RESULT 446
US-08-758-306-463/c
; Sequence 463, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996

```
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 463:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-463

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 41 GAGCGAGGAGGGAAG 57
Db 17 GAGGAGGAGGGAAG 1

RESULT 447
US-08-758-306-811/c
; Sequence 811, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 811:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-811
```

```
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-758-306-811

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 426 CCGGAGCGGACAGGCTG 442
Db 17 CCCGAGTGGACAGGCTG 1

RESULT 448
US-08-435-628-1477
; Sequence 1477, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1477:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-628-1477
```

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1205 GGCACCAATTCATCAAA 1221
DB 1 GGCACCAUUCUGGACAA 17

RESULT 449

US-08-173-489C-96/C
; Sequence 96, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 bases
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from superoxide
; DESCRIPTION: dismutase sequence region in Seq ID No. 586124495
; HYPOTHETICAL: yes
; ANTI-SENSE: no
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 96 :FROM 1 TO 17

US-08-173-489C-96
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1558 AGGGGCGCGGAGGGG 1574
DB 17 AGGGGCGCGGAGGGG 1

RESULT 450

US-08-849-021-3
; Sequence 3, Application US/08849021
; Patent No. 5955276

GENERAL INFORMATION:
; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENT IN-RELEASE #1.0, VERSION 1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,021
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/346,456
; FILING DATE: 28 NOVEMBER 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: BB-1064-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-992-7949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-849-021-3

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 AGGAGGAGAGAGCGCA 28
DB 1 AGAGAGAGAGAGAGAGA 17

RESULT 451

US-08-849-021-4
; Sequence 4, Application US/08849021
; Patent No. 5955276
; GENERAL INFORMATION:

; APPLICANT: MORGANTE, MICHELE
; APPLICANT: VOGEL, JULIE M.
; TITLE OF INVENTION: COMPOUND MICROSATELLITE
; TITLE OF INVENTION: PRIMERS FOR THE
; TITLE OF INVENTION: DETECTION OF GENETIC
; TITLE OF INVENTION: POLYMORPHISMS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND
; ADDRESSEE: COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-849-021-4

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GCGAGGGAGAGAGCGAG 29
DB 1 GAGAGAGAGAGAGAG 17

RESULT 452
US-08-849-021-5/c
Sequence 5, Application US/08849021
Patent No. 5955276
GENERAL INFORMATION:
APPLICANT: MORGANTE, MICHELE
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064-A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-849-021-5

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 AGCGAGGGAGAGCGGA 28
DB 17 AGAGAGAGAGAGAGAGA 1

RESULT 453
US-08-849-021-6/c
Sequence 6, Application US/08849021
Patent No. 5955276
GENERAL INFORMATION:

APPLICANT: MORGANTE, MICHELE
APPLICANT: VOGEL, JULIE M.
TITLE OF INVENTION: COMPOUND MICROSATELLITE
TITLE OF INVENTION: PRIMERS FOR THE
TITLE OF INVENTION: DETECTION OF GENETIC
TITLE OF INVENTION: POLYMORPHISMS
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND
COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT IN RELEASE #1.0, VERSION 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/849,021
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/346,456
FILING DATE: 28 NOVEMBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1064-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFAX: 302-992-7949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-849-021-6

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 GCGAGGAGAGAGCGAG 29
 Db 17 GAGAGAGAGAGAGAG 1

RESULT 454

US-08-985-162-553/c
 ; Sequence 553, Application US/08985162
 ; Patent No. 6057156

GENERAL INFORMATION:

APPLICANT: Akhtar, Saghir
 APPLICANT: Fell, Patricia
 APPLICANT: McSwiggen, James
 TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
 TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
 TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
 TITLE OF INVENTION: FACTOR RECEPTORS
 NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,162
 FILING DATE: 04 December 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/036,476
 FILING DATE: 31 January 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 230/107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 553:

SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-985-162-553

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 891 GCGCCCAAGAGGCTTC 907
 Db 17 GCGCCCATGAGGCCTTC 1

RESULT 455

US-08-985-162-554/c
 ; Sequence 554, Application US/08985162
 ; Patent No. 6057156

GENERAL INFORMATION:

APPLICANT: Akhtar, Saghir
 APPLICANT: Fell, Patricia
 APPLICANT: McSwiggen, James
 TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT

; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
 ; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
 ; TITLE OF INVENTION: FACTOR RECEPTORS
 ; NUMBER OF SEQUENCES: 1877

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,162
 FILING DATE: 04 December 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/036,476
 FILING DATE: 31 January 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 230/107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 554:

SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-985-162-554

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 890 GCGCCCAAGAGGCTTC 906
 Db 17 GCGCCCATGAGGCCTTC 1

RESULT 456

US-08-388-029A-4
 ; Sequence 4, Application US/08388029A
 ; Patent No. 6110665

GENERAL INFORMATION:

APPLICANT: FENGER, CLARA K.
 APPLICANT: GRANSTROM, DAVID R.
 APPLICANT: GAYADHAR, ALVIN A.
 TITLE OF INVENTION: SARCOCYSTIS NEURONA DIAGNOSTIC PRIMER
 NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
 STREET: 99 CANAL CENTER PLAZA, SUITE 300
 CITY: ALEXANDRIA
 STATE: VIRGINIA
 COUNTRY: US
 ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:


```
; APPLICATION NUMBER: US/08/388,029A
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PRICE, ROBERT L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 434-046
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; TELEX: AMERPAT
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-388-029A-4

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 503 CCAGGAGTGAACCTGCG 519
Db 1 CCAGGCGTGGAGCTGCG 17

RESULT 457
US-08-974-549A-478/c
; Sequence 478, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 478:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..17
; OTHER INFORMATION: /note= "Naml primer"
; US-08-974-549A-478

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1362 GGGACCGCGGGGGCGGC 1378
Db 17 GGCATCGCGGGGGTGGC 1

RESULT 458
US-08-906-517-57
; Sequence 57, Application US/08906517
; Patent No. 6180774
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; TITLE OF INVENTION: Expression in Monocotyledonous Plants and Method For
; TITLE OF INVENTION: Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
```

APPLICATION NUMBER: US/08/906,517
FILING DATE: Concurrently Herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: MOST:170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-906-517-57

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1225 GGTGCTGGCTCGTCT 1241
DB 1 GCGCTGGCTTCTCT 17

RESULT 459

US-09-040-774-4/c
Sequence 4, Application US/09040774
Patent No. 6207811
GENERAL INFORMATION:
APPLICANT: Tryggyvason, Karl
APPLICANT: Kestila, Marjo
APPLICANT: Lenkari, Ulla
APPLICANT: Mannikko, Minna
TITLE OF INVENTION: Nephlin Gene and Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff
STREET: 300 S. Wacker Drive, Suite 3200
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,774
FILING DATE: 18 MAR 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 97,842
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)913-0001
TELEFAX: (312)913-0002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer intron 2"

US-09-040-774-4
Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 319 AGGCGCCAGCGGAGGT 335
DB 17 AGCCACCAGCGGAGCT 1

RESULT 460

US-09-324-867-61
Sequence 61, Application US/09324867A
Patent No. 6251632
GENERAL INFORMATION:
APPLICANT: Lillcrap, David
APPLICANT: Cameron, Cherie
APPLICANT: No. 6251632ley, Colleen
APPLICANT: Horrocks, L. Suzanne Hoyle
APPLICANT: Hough, Christine
TITLE OF INVENTION: Canine Factor VIII Gene, Protein and Methods of Use
FILE REFERENCE: 1669.0010002/JAG/BJD
CURRENT APPLICATION NUMBER: US/09/324,867A
CURRENT FILING DATE: 1999-06-03
EARLIER APPLICATION NUMBER: 09/035,141
EARLIER FILING DATE: 1998-03-059
EARLIER APPLICATION NUMBER: 60/039,953
EARLIER FILING DATE: 1997-03-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
LENGTH: 17
TYPE: DNA
ORGANISM: Synthetic oligonucleotide
US-09-324-867-61

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 714 AGAAGCTCGGTGGCGCC 730
DB 1 AGACCTGCTGTGCGCC 17

RESULT 461

US-08-881-450A-6
Sequence 6, Application US/08881450A
Patent No. 6274310
GENERAL INFORMATION:
APPLICANT: Habener, J.F. and Stoffers, D.A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: PANCREATIC DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Inc.
STREET: One Financial Center
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,450A
FILING DATE: June 24, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 11275/7823

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-345-9100

TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

FEATURE:

NAME/KEY: primer S17b

US-08-881-450A-6

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 24 AGCGAGCGGGCGAGCCG 40

Db 1 AGCGAGCGGGCGAGCCG 17

RESULT 462

US-09-017-974-79/c

Sequence 79, Application US/09017974

Patent No. 6288042

GENERAL INFORMATION:

APPLICANT: Rando, Robert P.

APPLICANT: Ojwang, Joshua O.

APPLICANT: Hogan, Michael E.

APPLICANT: Wallace, Thomas L.

APPLICANT: Cossum, Paul A.

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Tetrad Forming Oligonucleotides

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1800

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/017,974

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/037,374

FILING DATE: 04-FEB-97

APPLICATION NUMBER:

FILING DATE: 09-DEC-97

NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962

REFERENCE/DOCKET NUMBER: 1472-06223

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/238-8010

TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-017-974-79

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 75 AGCGACACACCGCGCG 91

Db 17 ACCGACCCCGCGGCAC 1

RESULT 463

US-08-682-255A-79/c

Sequence 79, Application US/08682255A

Patent No. 6323185

GENERAL INFORMATION:

APPLICANT: Rando, Robert P.

APPLICANT: Fennewald, Susan

APPLICANT: Zendequi, Joseph G.

APPLICANT: Ojwang, Joshua O.

APPLICANT: Hogan, Michael E.

APPLICANT: Pommier, Yves

APPLICANT: Mazunder, Abhijit

TITLE OF INVENTION: Anti-Viral Guanosine-Rich

TITLE OF INVENTION: Oligonucleotides

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Conley, Rose & Tayon, P.C.

STREET: 600 Travis, Suite 1850

CITY: Houston

STATE: Texas

COUNTRY: U.S.A.

ZIP: 77002-2912

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS Windows 95

SOFTWARE: MS Word 97 (saved as .txt file)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/682,255A

FILING DATE: 17-JULY-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/535,168

FILING DATE: 23-OCT-95

APPLICATION NUMBER: 60/001,505

FILING DATE: 19-JULY-95

APPLICATION NUMBER: 60/014,007

FILING DATE: 25-MARCH-96

APPLICATION NUMBER: 60/013,688

FILING DATE: 19-MARCH-96

APPLICATION NUMBER: 60/015,714

FILING DATE: 17-APRIL-96

APPLICATION NUMBER: 60/016,271

FILING DATE: 23-APRIL-96

ATTORNEY/AGENT INFORMATION:

NAME: McDaniel, C. Steven

REGISTRATION NUMBER: 33,962

REFERENCE/DOCKET NUMBER: 1472-06214

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713/238-8010

TELEFAX: 713/238-8008

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-682-255A-79

```

QY      75  ACGCACACCGCGGC 91
Db      17  ACCACCCACCGCGC 1

RESULT 464
US-08-584-040-1471/c
; Sequence 1471, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1471:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-1471

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      978  CGCACACGACTCGGC 994
Db      17  CGGCCAACGACCGGC 1

RESULT 465
US-08-584-040-3972
; Sequence 3972, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela

```

```

; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3972:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-3972

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1449  ACTGGTACTCGCAGCTG 1465
Db      1  ACUGGUAUUGGCAGUUG 17

RESULT 466
US-08-584-040-3997/c
; Sequence 3997, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

```

```
/
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 3997:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-3997

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 260 AAAAAGCTGACCCCTTT 276
Db 17 ACAAGCTGACACATTT 1

RESULT 467
US-08-584-040-4075
Sequence 4075, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4075:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4075
```

```
/
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 4075:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-4075

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 2.9e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 400 CATCATATTTTACGATG 416
Db 1 CAUGUAUUGAAGGAUG 17

RESULT 468
US-08-584-040-7232
Sequence 7232, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4075:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-4075
```

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7232:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7232

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   734 TCGGAGGTGGTTCCTCC 750
Db    1 UCGGGUGUCGUUUC 17

RESULT 469
US-08-679-645-70
; Sequence 70, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-70

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.8%; Pred. No. 2.9e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7232:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7232

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   734 TCGGAGGTGGTTCCTCC 750
Db    1 UCGGGUGUCGUUUC 17

RESULT 469
US-08-679-645-70
; Sequence 70, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-679-645-70

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.8%; Pred. No. 2.9e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

QY 1015 CTCGGGCTCGGGCGGC 1031
 Db 1 CUCAGCCTCGGGGCGC 17

RESULT 471
 US-08-679-645-220
 ; Sequence 220, Application US/08679645
 ; Patent No. 6350934
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwick, Michael G.
 ; APPLICANT: Edington, Brent E.
 ; APPLICANT: McSwiggen, James A.
 ; APPLICANT: Merlo, Patricia Ann Owens
 ; APPLICANT: Guo, Lining
 ; APPLICANT: Skokut, Thomas A.
 ; APPLICANT: Young, Scott A.
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Merlo, Donald J.
 ; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
 ; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1263
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/679,645
 ; FILING DATE: July 12, 1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/001,135
 ; FILING DATE: July 13, 1995
 ; APPLICATION NUMBER: 08/300,726
 ; FILING DATE: September 2, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 219/247
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 220:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-679-645-220

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1367 CGCGGGGCGCGGCGG 1383
 Db 1 CUCGGGCGCGGCGG 17

RESULT 472
 US-08-679-645-220/c

; Sequence 220, Application US/08679645
 ; Patent No. 6350934
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwick, Michael G.
 ; APPLICANT: Edington, Brent E.
 ; APPLICANT: McSwiggen, James A.
 ; APPLICANT: Merlo, Patricia Ann Owens
 ; APPLICANT: Guo, Lining
 ; APPLICANT: Skokut, Thomas A.
 ; APPLICANT: Young, Scott A.
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Merlo, Donald J.
 ; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
 ; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
 ; NUMBER OF SEQUENCES: 1263
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/679,645
 ; FILING DATE: July 12, 1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/001,135
 ; FILING DATE: July 13, 1995
 ; APPLICATION NUMBER: 08/300,726
 ; FILING DATE: September 2, 1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 219/247
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 220:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-679-645-220

Query Match 0.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 2.9e+02;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 993 CCACCGGGGAGCCCGAG 1009
 Db 17 CCGCGGCGACCCCGAG 1

RESULT 473
 US-08-679-645-692
 ; Sequence 692, Application US/08679645
 ; Patent No. 6350934
 ; GENERAL INFORMATION:
 ; APPLICANT: Zwick, Michael G.
 ; APPLICANT: Edington, Brent E.
 ; APPLICANT: McSwiggen, James A.
 ; APPLICANT: Merlo, Patricia Ann Owens

APPLICANT: Guo, Lining
APPLICANT: Skokut, Thomas A.
APPLICANT: Young, Scott A.
APPLICANT: Folkerts, Otto
APPLICANT: Merlo, Donald J.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR
TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 692:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-692

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 941 CTGCTGCTCAGCGCGC 957
Db 1 CUGCTUCUCCGCGCGC 17

RESULT 474
US-09-429-130-79/c
Sequence 79, Application US/09429130
Patent No. 6355785
GENERAL INFORMATION:
APPLICANT: Rando, Robert F.
Fennwald, Susan
Zendequi, Joseph G.
Ojwang, Joshua O.
Hogan, Michael E.
Pommier, Yves
Mazumder, Abhijit
60/015,714
TITLE OF INVENTION: Anti-Viral Guanosine-Rich
Oligonucleotides
NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:
ADDRESSEE: Conley, Rose & Tayon, P.C.
STREET: 600 Travis, Suite 1850
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77002-2912
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Windows 95
SOFTWARE: MS Word 97 (saved as .txt file)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/429,130
FILING DATE: 28-Oct-1999
CLASSIFICATION: <Unknown>
19-JULY-95
25-MARCH-96
19-MARCH-96
17-APRIL-96
23-APRIL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/682,255
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/001,505
FILING DATE: 19-JULY-95
APPLICATION NUMBER: 60/014,007
FILING DATE: 25-MARCH-96
APPLICATION NUMBER: 60/013,688
FILING DATE: 19-MARCH-96
APPLICATION NUMBER: 60/016,271
FILING DATE: 17-APRIL-96
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
REGISTRATION NUMBER: 33,962
REFERENCE/DOCKET NUMBER: 1472-06214
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/238-8010
TELEFAX: 713/238-8008
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-429-130-79

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 75 AGCACACACCCGCGC 91
Db 17 ACCACCCACCGCGC 1

RESULT 475
US-09-340-861-30/c
Sequence 30, Application US/09340861
Patent No. 6432704
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California


```

; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,861
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-340-861-30

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1549 GGCGGGGGAGGGGGCGC 1565
Db 17 GGCGGGGGAGGGGGCGC 1

RESULT 476
US-09-634-262-30/c
; Sequence 30, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921

```

```

; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-634-262-30

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1549 GGCGGGGGAGGGGGCGC 1565
Db 17 GGCGGGGGAGGGGGCGC 1

RESULT 477
US-09-343-698-1
; Sequence 1, Application US/09343698
; Patent No. 6475486
; GENERAL INFORMATION:
; APPLICANT: Seeman, Gerhard
; Bosslet, Klaus
; Czech, Joerg
; Kolar, Cenek
; Hoffman, Dieter
; Sedlacek, Hans-Harald
; TITLE OF INVENTION: Glycosyl-Etoposide Prodrugs, A Process For
; Preparation Thereof And The Use Thereof In Combination With
; Functionalized Tumor-Specific Enzyme Conjugates
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/343,698
; FILING DATE: 30-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/325,955
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ogden, Stasia L.
; REGISTRATION NUMBER: 36,228
; REFERENCE/DOCKET NUMBER: 05552.0981-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs

```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-343-698-1

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1374 GCGCGCGCGCGACATA 1390
DB 1 GCGCGCGCGCGGTGCA 17

RESULT 478

US-08-912-951-245/c
Sequence 245, Application US/08912951
Patent No. 6475789

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-912-951-245

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1362 GGCACCGCGCGCGCGC 1378
DB 17 GGCATCGCGCGGTGCG 1

RESULT 479

US-09-474-432B-319/c
Sequence 319, Application US/09474432B
Patent No. 6528640

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpelsky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
FILE REFERENCE: MHB00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 319
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-319

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1548 GGCACCGCGCGCGCGC 1564
DB 17 GGCACCGCGCGCGCGC 1

RESULT 480

US-09-474-432B-377
Sequence 377, Application US/09474432B
Patent No. 6528640

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpelsky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David

APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
; FILE REFERENCE: MHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 377
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-377

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 184 CCTGCTCTCTCGTGC 200
Db 1 CCUCGUCGCCCCCUGC 17

RESULT 481
US-09-474-432B-672
; Sequence 672, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
; FILE REFERENCE: MHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 672
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-672

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1505 CTGACCCGCTGGGCAT 1521
Db 1 CUGCAAGGCGCGGCAU 17

RESULT 482

US-09-474-432B-689/c
; Sequence 689, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
; FILE REFERENCE: MHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 689
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-689

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1256 GAGCACAGCTGGCGCA 1272
Db 17 GCGCACAGCTGGTGCA 1

RESULT 483
US-09-371-772B-16/c
; Sequence 16, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Favco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-16

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 978 CGCACACGACTCGGCC 994

Db
17 CGGCCAACGACCCGGCC 1

RESIT.T 484

```

US-09-371-772B-1739
/ Sequence 1739, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McGisgen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for
/ TITLE OF INVENTION: Levels of Vascular En
/ FILE REFERENCE: MEHB00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ CURRENT FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/594,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 1739
/ LENGTH: 17
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-09-371-772B-1739

```

```

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e-02;
Matches 10; Conservative 4; Mismatches 3; Indels

QY 1449 ACTGGTACTCGCAGCTG 1465
      ||::||::||::||
Db 1 ACUGGAUUGGCAGUUG 17

```

RESULT 485

```

US-09-371-772B-1764/c
; Sequence 1764, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: StincComb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for
; TITLE OF INVENTION: Levels of Vascular En
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1764
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1764

```

Query Match	0.8%	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	82.4%;	Pred. No. 2.9e+02;		
Matches 14;	Conservative 0;	Mismatches 3;	Indels	
Qy	260	AAAAGCTGACCCCTTT	276	

Db 17 ACAAGCTGACACATTT 1

RESULT 486

```

US-09-371-772B-1842
; Sequence 1842, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for
; DETECTION OF HIV INFECTION
; FILE OF INVENTION: Levels of Vascular En
; FILE REFERENCE: MEH800.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIORITY APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIORITY APPLICATION NUMBER: US 08/594,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1842
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1842

```

```

Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. NO. 2.9e+02;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 400 CATCATATTTAAGGATG 416
   ||:|:|:|:|:|:|
Db 1 CAUGUAUUGAAGGAUG 17

```

RESULT 487

```

US-09-371-772B-3046
; Sequence 3046, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for
; TITLE OF INVENTION: Levels of Vascular Endothelial
; FILE REFERENCE: WEH000,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 6/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3046
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
; US-09-371-772B-3046

```

```
Query Match      0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 2.9e+00;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

RESULT 488

US-09-371-772B-4189/c
; Sequence 4189, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4189
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4189

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 983 AACGACTCGGCCACCGG 999
DB 17 AACGACCCCGGCCAG 1

RESULT 489

US-09-371-772B-4192
; Sequence 4192, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4192
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4192

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 922 GCGGGAGCGCGCGAGC 938
DB 1 GCGGGACCGCGCGAGC 17

RESULT 490

US-09-371-772B-4560
; Sequence 4560, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4560
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4560

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 540 AAGATGCCACCACTCA 556
DB 1 AAAUGGCCAUCACUA 17

RESULT 491

US-09-371-772B-4561
; Sequence 4561, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4561
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4561

Query Match 0.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 2.9e+02;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 541 AGATGCCACCACTCAG 557
DB 1 AAAUGGCCAUCACUA 17

RESULT 493
 US-08-136-811-23/c
 ; Sequence 23, Application US/08136811
 ; Patent No. 5510239
 ; GENERAL INFORMATION:
 ; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
 ; APPLICANT: Clarence Frank
 ; TITLE OF INVENTION: Oligonucleotide Interference with
 ; TITLE OF INVENTION: Multidrug Resistance
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Jane Massey Licata
 ; STREET: 210 Lake Drive East, Suite 201
 ; CITY: Cherry Hill
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08002
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/136,811
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: ISPH-
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (609) 779-2400
 ; TELEFAX: (609) 779-8488
 ; INFORMATION FOR SEQ ID NO: 23:

```

Query Match      0.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. NO. 4.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      927 AGCCGCGCGAGCCCTG 943
      ||| ||||| |||||
Db      19 AGCAGGCGGTGAGCCTG 3

```

RESULT 495
US-08-628-731-23/c
; Sequence 23, Application US/08628731
; Patent No. 5807838
; GENERAL INFORMATION:
; APPLICANT: Baracchini, Jr., Edgardo and Bennett,
; APPLICANT: Clarence Frank
; TITLE OF INVENTION: Oligonucleotide Interference with
; TITLE OF INVENTION: Multidrug Resistance
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,731
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/136,811
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-628-731-23

Query Match 0.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 927 AGCGCGCGGCGCGCTG 943
Db 19 AGCAGCGCGTGAGCCTG 3

RESULT 496
US-09-484-617-41/c
; Sequence 41, Application US/09484617
; Patent No. 630374
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION
; FILE REFERENCE: RTS-0103
; CURRENT APPLICATION NUMBER: US/09/484,617
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-484-617-41
Query Match 0.8%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 645 CGGTGGAGGCGCGCTTC 661
Db 17 CAGTGGATGCGGACTTC 1
RESULT 497
US-07-910-867B-13/c
; Sequence 13, Application US/07910867B
; Patent No. 5597895
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B.
; APPLICANT: Garcia, Joseph A.
; APPLICANT: Harrich, David
; TITLE OF INVENTION: Transdominant Tat Mutants and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: US
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,867B
; FILING DATE: 02-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSD:263/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-07-910-867B-13

Query Match 0.8%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1122 ACCGCGCGCTCC 1133
Db 12 ACCGCGCGCTCC 1
RESULT 498
US-08-346-613-13/c
; Sequence 13, Application US/08346613
; Patent No. 5686264
; GENERAL INFORMATION:
; APPLICANT: GAYNOR, RICHARD B.
; APPLICANT: GARCIA, JOSEPH A.
; APPLICANT: HARRICH, DAVID

```
/
/ TITLE OF INVENTION: TRANSDOMINANT Tat MUTANTS AND USES
/ TITLE OF INVENTION: THEREOF
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ARNOLD, WHITE & DURKEE
/ STREET: P.O. BOX 4433
/ CITY: HOUSTON
/ STATE: TEXAS
/ COUNTRY: USA
/ ZIP: 77210
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/346,613
/
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/910,867
/ FILING DATE: 07/02/92
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MAYFIELD, DENISE L.
/ REGISTRATION NUMBER: 33,732
/ REFERENCE/DOCKET NUMBER: UTSD:263/MAY
/ TELEPHONE: 512-320-7200
/ TELEFAX: 512-474-7577
/ TELEX: NOT APPLICABLE
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-346-613-13
/
/ Query Match 0.8%; Score 12; DB 1; Length 12;
/ Best Local Similarity 100.0%; Pred.No.1.3e+02;
/ Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1122 ACCGCCGCTCC 1133
/ Db 12 ACCGCCGCTCC 1
/
/ RESULT 499
/ US-08-457-273B-38/c
/ Sequence 38, Application US/08457273B
/ Patent No. 5849995
/ GENERAL INFORMATION:
/ APPLICANT: Hayden, Michael
/ APPLICANT: Lin, Biayang
/ APPLICANT: Nasir, Jamal
/ TITLE OF INVENTION: Mouse Model for Huntington's Disease and
/ TITLE OF INVENTION: Related DNA Sequences
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Virginia Bennett
/ STREET: PO Box 37428
/ CITY: Raleigh
/ STATE: No. 5849995th Carolina
/ COUNTRY: US
/ ZIP: 27627
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/457,273B
/
```

```
/
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bennett, Virginia C.
/ REGISTRATION NUMBER: 37,092
/ REFERENCE/DOCKET NUMBER: 3477-85A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-854-1400
/ TELEFAX: 919-854-1401
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/
/ US-08-457-273B-38
/
/ Query Match 0.8%; Score 12; DB 1; Length 12;
/ Best Local Similarity 100.0%; Pred.No.1.3e+02;
/ Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1373 GCGCGCGCGGC 1384
/ Db 12 GCGCGCGCGGC 1
/
/ RESULT 500
/ US-09-475-947A-346
/ Sequence 346, Application US/09475947A
/ Patent No. 6472154
/ GENERAL INFORMATION:
/ APPLICANT: Garner, Harold R.
/ APPLICANT: Wren, Jonathan D.
/ APPLICANT: Minna, John D.
/ TITLE OF INVENTION: Polymorphic Repeats in Human Genes
/ FILE REFERENCE: UTSD0667
/ CURRENT APPLICATION NUMBER: US/09/475,947A
/ CURRENT FILING DATE: 1999-12-31
/ NUMBER OF SEQ ID NOS: 346
/ SOFTWARE: Patent in Ver. 2.1
/ SEQ ID NO 346
/ LENGTH: 12
/ TYPE: DNA
/ ORGANISM: human
/
/ US-09-475-947A-346
/
/ Query Match 0.8%; Score 12; DB 1; Length 12;
/ Best Local Similarity 100.0%; Pred.No.1.3e+02;
/ Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1374 GCGCGCGCGGCA 1385
/ Db 1 GCGCGCGCGGCA 12
/
/ RESULT 501
/ US-08-623-891-42
/ Sequence 42, Application US/08623891
/ Patent No. 5795778
/ GENERAL INFORMATION:
/ APPLICANT: Kenneth G. Draper
/ TITLE OF INVENTION: METHOD AND REAGENT FOR
/ TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
/ TITLE OF INVENTION: VIRUS REPLICATION
/ NUMBER OF SEQUENCES: 115
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 611 West Sixth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90017
/
```



```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-42
Query Match 0.8%; Score 12; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 1.9e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 532 CTGGGACGAGA 543
Db 1 CUGGGACGAGA 12

RESULT 504
US-08-985-162-1759/c
; Sequence 1759, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; TITLE OF INVENTION: ENZYMOLOGICAL NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1759:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-1759
Query Match 0.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1373 GCGGGCGGCGC 1384
Db 14 GCGGGCGGCGC 3

RESULT 505
US-08-985-162-1760/c
; Sequence 1760, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; TITLE OF INVENTION: ENZYMOLOGICAL NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1760:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-1760
Query Match 0.8%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1372 GCGGGCGGCGC 1383
Db 12 GCGGGCGGCGC 1

RESULT 506
US-08-319-492B-57/c
; Sequence 57, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; FILING DATE: December 7, 1992
; NAME: Warburg, Richard
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-319-492B-57

```

```

Query Match 0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 457 TAAGGACAAAGTT 468
DB 15 TAAGGACAAAGTT 4

```

```

RESULT 507
US-08-319-492B-58/c
; Sequence 58, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OF IL-5
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

```

```

; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; FILING DATE: December 7, 1992
; NAME: Warburg, Richard
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-319-492B-58

```

```

Query Match 0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 457 TAAGGACAAAGTT 468
DB 12 TAAGGACAAAGTT 1

```

```

RESULT 508
US-08-929-856-57
; Sequence 57, Application US/08929856
; Patent No. 6136568
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Rose, Floyd
; TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING
; TITLE OF INVENTION: ROLLING TEMPLATES
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ &
; ADDRESSEE: MENTLIK
; STREET: 600 South, Avenue West
; CITY: Westfield
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,856
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Foley, Shawn P.
; REGISTRATION NUMBER: 33,071
; REFERENCE/DOCKET NUMBER: ROSE 3.0-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-654-5000
; TELEFAX: 908-654-7866
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs

```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-929-856-57

Query Match      0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      244 GAAGAGGAGGCA 255
Db      4 GAAGAGGAGGCA 15

RESULT 509
US-09-275-850-25/c
; Sequence 25, Application US/09275850A
; Patent No. 626174
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Gold, Larry
; APPLICANT: Shtatland, Timur
; APPLICANT: Javornik, Brenda
; TITLE OF INVENTION: Truncation SELEX Method
; FILE REFERENCE: NEX 79
; CURRENT APPLICATION NUMBER: US/09/275,850A
; CURRENT FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: RNA
; ORGANISM: E. coli
US-09-275-850-25

Query Match      0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      154 GCTGCTGCTGGC 165
Db      12 GCTGCTGCTGGC 1

RESULT 510
US-09-081-646-571/c
; Sequence 571, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 0107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-571

Query Match      0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      592 CATCACCAAGTC 603
Db      15 CATCACCAAGTC 4

RESULT 511
US-09-344-667-9/c
; Sequence 9, Application US/09344667A
; Patent No. 6361944
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Strohoff, James J.
; APPLICANT: Elghariani, Robert
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 4149-1-1-1
; CURRENT APPLICATION NUMBER: US/09/344,667A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: random
; OTHER INFORMATION: synthetic sequence
US-09-344-667-9

Query Match      0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 GAGAGAGGAAA 56
Db      14 GAGAGAGGAAA 3

RESULT 512
US-09-693-352-9/c
; Sequence 9, Application US/09693352
; Patent No. 6417340
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Strohoff, James J.
; APPLICANT: Elghariani, Robert
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 4149-1-1-1
; CURRENT APPLICATION NUMBER: US/09/693,352
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-693-352-9

Query Match 0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAAGGGGAAA 56
|||
Db 14 GAGGAAGGGGAAA 3

RESULT 513

US-09-565-063-6/c
; Sequence 6, Application US/09565063
; Patent No. 6489156
; GENERAL INFORMATION:
; APPLICANT: DISPIRITO, ALAN A.
; APPLICANT: DO, YOUNG S.
; APPLICANT: PHILLIPS, GREGORY J.
; APPLICANT: ZAHN, JAMES A.
; TITLE OF INVENTION: A RHODOBACTER STRAIN FOR ODOOR REMEDIATION OF ANAEROBIC
; TITLE OF INVENTION: LIVESTOCK WASTE LAGOONS AND BIOMASS PRODUCTION
; FILE REFERENCE: 19000.0044/P044
; CURRENT APPLICATION NUMBER: US/09/565,063
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133,087
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide probe
US-09-565-063-6

Query Match 0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 85.7%; Pred.No. 2.3e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 77 GCACACACCCGCCG 90
|||
Db 15 GCACACACCCGCCG 2

RESULT 514

US-09-693-005A-9/c
; Sequence 9, Application US/09693005A
; Patent No. 6495324
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 00-713-L
; CURRENT APPLICATION NUMBER: US/09/693,005A
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29

; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-693-005A-9

Query Match 0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAAGGGGAAA 56
|||
Db 14 GAGGAAGGGGAAA 3

RESULT 515

US-09-603-830-9/c
; Sequence 9, Application US/09603930
; Patent No. 6506364
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.
; APPLICANT: Mucic, Robert C.
; APPLICANT: Storhoff, James J.
; APPLICANT: Elghanian, Robert
; APPLICANT: Taton, Thomas A.
; TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 4149-1-1-1
; CURRENT APPLICATION NUMBER: US/09/603,830
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/031,809
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: PCT/US97/12783
; PRIOR FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 09/240,755
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 09/344,667
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/200,161
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:random
; OTHER INFORMATION: synthetic sequence
US-09-603-830-9

Query Match 0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAAGGGGAAA 56
|||
Db 14 GAGGAAGGGGAAA 3

RESULT 516

US-09-976-978A-9/c
; Sequence 9, Application US/09976978A
; Patent No. 6532097
; GENERAL INFORMATION:
; APPLICANT: Mirkin, Chad A.
; APPLICANT: Letsinger, Robert L.

```
/ APPLICANT: Mucic, Robert C.
/ APPLICANT: Storhoff, James J.
/ APPLICANT: Elghanian, Robert
/ APPLICANT: Taton, Thomas A.
/ TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
/ FILE REFERENCE: 00-713-117
/ CURRENT APPLICATION NUMBER: US/09/976,978A
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: 09/603,830
/ PRIOR FILING DATE: 2000-06-26
/ PRIOR APPLICATION NUMBER: 09/344,667
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/240,755
/ PRIOR FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: PCT/US97/12783
/ PRIOR FILING DATE: 1997-07-21
/ PRIOR APPLICATION NUMBER: 60/031,809
/ PRIOR FILING DATE: 1996-07-29
/ PRIOR APPLICATION NUMBER: 60/200,161
/ PRIOR FILING DATE: 2000-04-26
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Microsoft Word 2000
/ SEQ ID NO 9
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:random
/ OTHER INFORMATION: synthetic sequence
US-09-976-978A-9

Query Match          0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 GAGGAAGGGAAA 56
        |||||
Db      14 GAGGAAGGGAAA 3

RESULT 517
US-09-961-949A-9/c
/ Sequence 9, Application US/09961949A
/ Patent No. 6582921
/ GENERAL INFORMATION:
/ APPLICANT: Mirkin, Chad A.
/ APPLICANT: Letsinger, Robert L.
/ APPLICANT: Mucic, Robert C.
/ APPLICANT: Storhoff, James J.
/ APPLICANT: Elghanian, Robert
/ APPLICANT: Taton, Thomas A.
/ TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
/ FILE REFERENCE: 00-713-11
/ CURRENT APPLICATION NUMBER: US/09/961,949A
/ CURRENT FILING DATE: 2001-09-20
/ PRIOR APPLICATION NUMBER: 09/603,830
/ PRIOR FILING DATE: 2000-06-26
/ PRIOR APPLICATION NUMBER: 09/344,667
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/240,755
/ PRIOR FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: PCT/US97/12783
/ PRIOR FILING DATE: 1997-07-21
/ PRIOR APPLICATION NUMBER: 60/031,809
/ PRIOR FILING DATE: 1996-07-29
/ PRIOR APPLICATION NUMBER: 60/200,161
/ PRIOR FILING DATE: 2000-04-26
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Microsoft Word 2000
/ SEQ ID NO 9
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:random
/ OTHER INFORMATION: synthetic sequence
US-09-976-978A-9

Query Match          0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 GAGGAAGGGAAA 56
        |||||
Db      14 GAGGAAGGGAAA 3

RESULT 517
US-09-961-949A-9/c
/ Sequence 9, Application US/09961949A
/ Patent No. 6582921
/ GENERAL INFORMATION:
/ APPLICANT: Mirkin, Chad A.
/ APPLICANT: Letsinger, Robert L.
/ APPLICANT: Mucic, Robert C.
/ APPLICANT: Storhoff, James J.
/ APPLICANT: Elghanian, Robert
/ APPLICANT: Taton, Thomas A.
/ TITLE OF INVENTION: NANOPARTICLES HAVING OLIGONUCLEOTIDES ATTACHED THERETO
/ FILE REFERENCE: 00-713-11
/ CURRENT APPLICATION NUMBER: US/09/961,949A
/ CURRENT FILING DATE: 2001-09-20
/ PRIOR APPLICATION NUMBER: 09/603,830
/ PRIOR FILING DATE: 2000-06-26
/ PRIOR APPLICATION NUMBER: 09/344,667
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/240,755
/ PRIOR FILING DATE: 1999-01-29
/ PRIOR APPLICATION NUMBER: PCT/US97/12783
/ PRIOR FILING DATE: 1997-07-21
/ PRIOR APPLICATION NUMBER: 60/031,809
/ PRIOR FILING DATE: 1996-07-29
/ PRIOR APPLICATION NUMBER: 60/200,161
/ PRIOR FILING DATE: 2000-04-26
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: Microsoft Word 2000
/ SEQ ID NO 9
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:random
/ OTHER INFORMATION: synthetic sequence
US-09-976-978A-9
```

```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:random
/ OTHER INFORMATION: synthetic sequence
US-09-961-949A-9

Query Match          0.8%; Score 12; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      45 GAGGAAGGGAAA 56
        |||||
Db      14 GAGGAAGGGAAA 3

RESULT 518
US-08-981-321-5/c
/ Sequence 5, Application US/08981321A
/ Patent No. 6146871
/ GENERAL INFORMATION:
/ APPLICANT: GARCIA LOPEZ, et al, Jose Luis
/ TITLE OF INVENTION: PROCESS FOR MODIFYING THE ENZYME
/ TITLE OF INVENTION: 7B-(4-CARBOXYBUTANAMIDE) CE PHALOS PORI NACYLAS E AND
/ TITLE OF INVENTION: PURIFYING SAID ENZYME IN A SINGLE CHROMATOGRAPHIC STEP
/ FILE REFERENCE: U-011559-6
/ CURRENT APPLICATION NUMBER: US/08/981,321A
/ CURRENT FILING DATE: 1998-08-13
/ EARLIER APPLICATION NUMBER: PCT/ES97/00098
/ EARLIER FILING DATE: 1997-04-19
/ EARLIER APPLICATION NUMBER: P9600890
/ EARLIER FILING DATE: 1996-04-19
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 16
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic oligonucleotide for site-directed
/ OTHER INFORMATION: mutagenesis of gla gene
US-08-981-321-5

Query Match          0.8%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      748 CCGGGGCTCGGC 759
        |||||
Db      12 CCGGGGCTCGGC 1

RESULT 519
US-08-152-313-20
/ Sequence 20, Application US/08152313
/ Patent No. 5561041
/ GENERAL INFORMATION:
/ APPLICANT: Sidransky, David
/ TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
/ TITLE OF INVENTION: ANALYSIS OF SPUTUM
/ NUMBER OF SEQUENCES: 128
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Spensley Horn Jubas & Lubitz
/ STREET: 1880 Century Park East, Suite 500
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: USA
/ ZIP: 90067
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,313
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; US-08-152-313-20

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 CACACACCCGCC 89
Db 4 CACACACCCGCC 15

RESULT 520
US-08-579-223-20
; Sequence 20, Application US/08579223
; Patent No. 5728019
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; METHOD OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,223
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/152,313
; FILING DATE: 12-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; US-08-579-223-20

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 CACACACCCGCC 89
Db 4 CACACACCCGCC 15

RESULT 521
US-08-584-040-3970
; Sequence 3970, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Favco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
; CONDITIONS RELATED TO LEVELS
; OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3970:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-3970

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1444 CATCCACTGGTA 1455
||:||||:|

```

Db 6 CAUCCACUGUA 17

RESULT 522

US-08-584-040-7583/c
; Sequence 7583, Application US/08584040
; Patent No. 6346398

; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; NAME: Warburg, Richard J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 7583:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-7583

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 TCCGAGCGATT 370
Db 16 TCCGAGCGATT 5

RESULT 523

US-08-584-040-7584/c
; Sequence 7584, Application US/08584040
; Patent No. 6346398

; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; NAME: Warburg, Richard J.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 7584:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-584-040-7584

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 TCCGAGCGATT 370
Db 12 TCCGAGCGATT 1

RESULT 524

US-08-679-645-829/c
; Sequence 829, Application US/08679645
; Patent No. 6350934

; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merio, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merio, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,645
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 829:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-679-645-829

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 620 AAGTACGGCATG 631
DB 12 AAGTACGGCATG 1

RESULT 525
US-09-474-432B-587/c
Sequence 587, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MBH00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patent in version 3.0
SEQ ID NO 587

LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-587

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 CTCGGGACTGGC 219
DB 16 CTCGGGACTGGC 5

RESULT 526
US-09-474-432B-878/c
Sequence 878, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MBH00-831-B (247/276)
CURRENT APPLICATION NUMBER: US/09/474,432B
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: Patent in version 3.0
SEQ ID NO 878
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-474-432B-878

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1442 GGCATCCACTGG 1453
DB 17 GGCATCCACTGG 6

RESULT 527
US-09-371-772B-1737
Sequence 1737, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
FILE REFERENCE: MBH00-876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1737
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-1737

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1444 CATCCACTGGTA 1455
||:||||:|
Db 6 CAUCCACUGGUA 17

RESULT 528
US-09-371-772B-3379/c
; Sequence 3379, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3379
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3379

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 TCCGAGCGATT 370
|||||||
Db 16 TCCGAGCGATT 5

RESULT 529
US-09-371-772B-3380/c
; Sequence 3380, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040

; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3380
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3380

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 TCCGAGCGATT 370
|||||||
Db 12 TCCGAGCGATT 1

RESULT 530
US-09-371-772B-6382
; Sequence 6382, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6382
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6382

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1444 CATCCACTGGTA 1455
||:||||:|
Db 5 CAUCCACUGGUA 16

RESULT 531
PCT-US94-12947A-20
; Sequence 20, Application PC/TUS9412947A
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12947A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
PCT-US94-12947A-20

Query Match 0.8%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 CACACACCGGCC 89
DB 4 CACACACCGGCC 15

RESULT 532
US-09-475-947A-332/c
; Sequence 332, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 30
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-332

Query Match 0.8%; Score 12; DB 1; Length 30;
Best Local Similarity 64.3%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1413 CCGACGCTCGGTGCGGGCGGCCCGC 1440
DB 29 CCGCGCGCGCGCGCGCGCGCGCGCGC 2

RESULT 533
US-08-182-968A-375
; Sequence 375, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,847
```

```

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-375

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 382 CCCCAATTACACCC 396
DB 1 CCGGAUUAACACCC 15

RESULT 534
US-08-334-847-117/c
; Sequence 117, Application US/08334847
; Patent No. 5693532
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Draper, Kenneth
; APPLICANT: Pavco, Pam
; APPLICANT: Woolf, Tod
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING RESPIRATORY
; TITLE OF INVENTION: SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 909
; CORRESPONDENCE ADDRESS:
; ADDRESS: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,847
```

; FILING DATE: No. 5693532ember 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-334-847-117

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e-02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 406 ATTATGAGTGAAGA 420
DB 15 ATTATGAGTGAAGA 1

RESULT 535
US-08-363-240A-9
; Sequence 9, Application US/08363240A
; Patent No. 5705388

; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: December 23, 1994
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e-02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1453 GTACTCGAGCTGCT 1467
DB 15 GGACTCGAGCTGCT 1

; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-9

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e-02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1302 ACGGCTCTGGCTG 1316
DB 1 ACGGCTCTGGCTG 15

RESULT 536
US-08-363-240A-199/c
; Sequence 199, Application US/08363240A
; Patent No. 5705388

; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: December 23, 1994
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 199:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-199

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e-02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1453 GTACTCGAGCTGCT 1467
DB 15 GGACTCGAGCTGCT 1

RESULT 537
US-08-363-240A-647
; Sequence 647, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 647:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-647

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1274 CGGGCCTTCGGCC 1288
DB 1 CGCGCCUCCGCC 15

RESULT 538
US-08-363-240A-648
; Sequence 648, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES

NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 648:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-648
Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1274 CGGGCCTTCGGCC 1288
DB 1 CGCGCCUCCGCC 15
RESULT 539
US-08-363-240A-659
; Sequence 659, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0

```

; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; INFORMATION FOR SEQ ID NO: 659:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-659

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1027 GCGCCTTCGGGGG 1041
DB 1 GCGGCGUCCAGGAG 15

RESULT 540
US-08-363-240A-660
; Sequence 660, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwigen, James
; APPLICANT: Bisgaler, Charles
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440

```

```

; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 660:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-660

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1027 GCGCCTTCGGGGG 1041
DB 1 GCGGCGUCCAGGAG 15

RESULT 541
US-08-311-486C-57/c
; Sequence 57, Application US/08311486C
; Patent No. 5811300
; GENERAL INFORMATION:
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth Draper
; APPLICANT: Kevin Kisich
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwigen
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: TNF-
; NUMBER OF SEQUENCES: 1157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,486C
; FILING DATE: September 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-486C-57

```

Query Match 0.7%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 237 GGTCGGAGAGGA 251
 DB 15 GGTCGAGAGATGA 1

RESULT 542
 US-08-311-486C-165/c
 ; Sequence 165, Application US/08311486C
 ; Patent No. 5811300
 ; GENERAL INFORMATION:
 ; APPLICANT: Sean Sullivan
 ; APPLICANT: Kenneth Draper
 ; APPLICANT: Kevin Kisich
 ; APPLICANT: Dan T. Stinchcomb
 ; APPLICANT: James McSwiggen
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; DISEASES OR CONDITIONS
 ; TITLE OF INVENTION: RELATED TO LEVELS OF
 ; TITLE OF INVENTION: TNF- α
 ; NUMBER OF SEQUENCES: 1157
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/311,486C
 ; FILING DATE: September 23, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below:
 ; APPLICATION NUMBER: 08/008,895
 ; FILING DATE: January 19, 1993
 ; APPLICATION NUMBER: 07/989,849
 ; FILING DATE: December 7, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 209/166
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 165:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-311-486C-165

Query Match 0.7%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 38 CCGAGGAGGAGG 52
 DB 15 CTGAGAGGAGG 1

RESULT 543
 US-08-311-486C-675/c
 ; Sequence 675, Application US/08311486C
 ; Patent No. 5811300
 ; GENERAL INFORMATION:
 ; APPLICANT: Sean Sullivan
 ; APPLICANT: Kenneth Draper
 ; APPLICANT: Kevin Kisich
 ; APPLICANT: Dan T. Stinchcomb
 ; APPLICANT: James McSwiggen
 ; TITLE OF INVENTION: RIBOZYME TREATMENT OF
 ; DISEASES OR CONDITIONS
 ; TITLE OF INVENTION: RELATED TO LEVELS OF
 ; TITLE OF INVENTION: TNF- α
 ; NUMBER OF SEQUENCES: 1157
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/311,486C
 ; FILING DATE: September 23, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below:
 ; APPLICATION NUMBER: 08/008,895
 ; FILING DATE: January 19, 1993
 ; APPLICATION NUMBER: 07/989,849
 ; FILING DATE: December 7, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 209/166
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 675:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-311-486C-675

Query Match 0.7%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 328 CCGAGGATGAGG 342
 DB 15 CTGAAGGTAGGAGG 1

RESULT 544
 US-08-292-620A-200/c
 ; Sequence 200, Application US/08292620A
 ; Patent No. 5837542
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm

Query Match 0.7%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 328 CCGAGGATGAGG 342
 DB 15 CTGAAGGTAGGAGG 1

RESULT 544
 US-08-292-620A-200/c
 ; Sequence 200, Application US/08292620A
 ; Patent No. 5837542
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm

Query Match 0.7%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 328 CCGAGGATGAGG 342
 DB 15 CTGAAGGTAGGAGG 1

RESULT 544
 US-08-292-620A-200/c
 ; Sequence 200, Application US/08292620A
 ; Patent No. 5837542
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm

Query Match 0.7%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 2.5e+02;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 328 CCGAGGATGAGG 342
 DB 15 CTGAAGGTAGGAGG 1

RESULT 544
 US-08-292-620A-200/c
 ; Sequence 200, Application US/08292620A
 ; Patent No. 5837542
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-200

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1469 TACCAATAGGCACC 1483
DB 15 TACCAATAGGCAGC 1

RESULT 545
US-08-173-489C-329
Sequence 329, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 16S rRNA gene from Mycoplasma
DESCRIPTION: pneumoniae (Accession # M29061) nucleotides
DESCRIPTION: 1150 to 1164
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Mycoplasma pneumoniae
PUBLICATION INFORMATION:
AUTHORS: Weisburg, W G, Tully, J G, Rose, D L,
AUTHORS: Petzel, J P, Oyaizu, H, Yang, D, Mandelco,
AUTHORS: L, Sechrest, J, Lawrence, T G, Van Etten, J,
AUTHORS: Maniloff, J, Woese, C R.
TITLE: A phylogenetic analysis of
TITLE: the mycoplasmas: Basis for their classification
JOURNAL: Journal of Bacteriology
VOLUME: 171
PAGES: 6455-6467
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 329 :FROM 1 TO 15
US-08-173-489C-329

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 40 GGAGCGGAGGAGGGA 54
DB 1 GGAGGAGGAGGAGGGA 15

RESULT 546
US-08-774-306A-375
Sequence 375, Application US/08774306A
Patent No. 5869253
GENERAL INFORMATION:
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HEPATITIS C
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street

STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774,306A
FILING DATE: December 26, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/227
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 375:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-306A-375

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 382 CCCCAATTACACCC 396
Db 1 CCGGAUUACACCC 15

RESULT 547
US-08-232-081B-16/c
Sequence 16, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIJDNES, JOHN
APPLICANT: NOGUCHI, HIROSHI
TITLE OF INVENTION: HUMANIZED B-B10
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R

REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 20-3484
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-232-081B-16

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 782 GGCACCAAGCTGGTG 796
Db 15 GGCACCAAGCTGGAG 1

RESULT 548
US-08-856-141-19
Sequence 19, Application US/08856141
Patent No. 5948616
GENERAL INFORMATION:
APPLICANT: CHAO, LEE
APPLICANT: CHAO, JULIE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
CORRELATING TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH
TITLE OF INVENTION: ESSENTIAL HYPERTENSION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street, NE
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,141
FILING DATE: 14-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Mary L
REGISTRATION NUMBER: 39,303
REFERENCE/DOCKET NUMBER: 19070.0045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
TELEFAX: 404/688-9880
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-856-141-19

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	Db	Sequence	Score	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415	DB 416	DB 417
----	----	----------	-------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------

```

; APPLICATION NUMBER: US/08/629,039
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/140,138
; FILING DATE: 03-NOV-1993
; APPLICATION NUMBER: SE 9101433-2
; FILING DATE: 13-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 003300-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-629-039-11

Query Match      0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1548 GGGCGGGGGGAGGGG 1562
Db 1 GGGGGGGGGSMGGGS 15

RESULT 552
US-08-550-120-3/c
; Sequence 3, Application US/08550120
; Patent No. 5985554
; GENERAL INFORMATION:
; APPLICANT: Hitoshi TANIMURA et al.
; TITLE OF INVENTION: METHOD FOR PROBING THE FUNCTION OF A PROTEIN
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/550,120
; FILING DATE: October 30, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-269417
; FILING DATE: No. 5985554ember 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 bases
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
; US-08-550-120-3

Query Match      0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1359 GCGGGGACCGCGGG 1373
Db 15 GCGGGGCGCGGGGG 1

RESULT 553
US-08-667-939A-11/c
; Sequence 11, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,939A
; FILING DATE: 24-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,123
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: LUO=2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-667-939A-11

Query Match      0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 CTGCTGCTAGTCTC 187
Db 15 CTGCTGCTAGTCTC 1

RESULT 554
US-08-667-939A-22
; Sequence 22, Application US/08667939A
; Patent No. 5998166
; GENERAL INFORMATION:
; APPLICANT: LUO, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,939A
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: L00-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-667-939A-22

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 173 CTGCTGCTAGTCTCTC 187
Db 1 CTGCTGCTAGTCTC 15

RESULT 555
US-08-994-946A-10/c
Sequence 10, Application US/08994946A
Patent No. 6046317
GENERAL INFORMATION:
APPLICANT: Koulou, Markku
APPLICANT: Karvonen, Matti
APPLICANT: Pesonen, Ullamari
APPLICANT: Uusitupa, Matti
TITLE OF INVENTION: A DNA Molecule Encoding a Mutant
TITLE OF INVENTION: Prepro-Neuropeptide Y, a Mutant Signal Peptide, and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rotwell, Pigg, Ernst & Kurz, P.C.
STREET: 555 13th Street NW, Suite 701-E
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,946A
FILING DATE: 19-DEC-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2328-110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-08-994-946A-10

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1362 GGGACCGCGGGCGG 1376
Db 15 GGGACCGCGGGACCG 1

RESULT 556
US-09-284-782-8/c
Sequence 8, Application US/09284782
Patent No. 6057111
GENERAL INFORMATION:
APPLICANT: ENTERPRISES, LTD., QBI
APPLICANT: Deiss, Louis P.
APPLICANT: Yehiely, Pruma
APPLICANT: Efimova, Elena
APPLICANT: Vasquez-Islaop, No. 6057111a C.
APPLICANT: Einat, Paz
TITLE OF INVENTION: GENE IDENTIFICATION METHOD
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6057111thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/284,782
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Irene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 0168-00022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer"
US-09-284-782-8

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 227 CCGGGCAGGGGCTTC 241
Db 15 CCGGGCAGGTGGATC 1

RESULT 557

US-08-827-036A-14/c
; Sequence 14, Application US/08827036A
; Patent No. 6080727
; GENERAL INFORMATION:
; APPLICANT: Gabriella Zupi
; TITLE OF INVENTION: Oligonucleotide Treatments and
; TITLE OF INVENTION: Compositions for Human Melanoma
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James A. Bradburne, Ph.D.
; STREET: 5 Palo Alto Square,
; STREET: 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 3.1/DOS 5.0
; SOFTWARE: Microsoft Word for Windows, vers. 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,036A
; FILING DATE: 03/25/97
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/014,089
; FILING DATE: 26-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: James A. Bradburne, Ph.D.
; REGISTRATION NUMBER: 38,389
; REFERENCE/DOCKET NUMBER: LYNK-031/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 843-5095
; TELEFAX: (650) 857-0663
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-827-036A-14

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 935 GAGCCCTGCTGCTC 949
Db 15 GAGCCCTGCTGCTC 1

RESULT 558

US-09-064-156A-375
; Sequence 375, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,156A
FILING DATE: April 21, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/774,306
FILING DATE: December 26, 1996
APPLICATION NUMBER: 08/182,968
FILING DATE: January 13, 1994
APPLICATION NUMBER: 07/882,888
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/083
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 375:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-064-156A-375

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 2.5e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 382 CCCCAATTACACCC 396
Db 1 CCCGAUUACACCC 15

RESULT 559

US-09-071-845-200/c
; Sequence 200, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

```
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,845
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/292,620
/ FILING DATE: August 17, 1994
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 208/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 200:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-071-845-200

Query Match          0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1469 TACCAATAAGGCACC 1483
DB 15 TACCAATAAGGCAGC 1

RESULT 560
US-08-787-321-24
/ Sequence 24, Application US/08787321A
/ Patent No. 6180777
/ GENERAL INFORMATION:
/ APPLICANT: Horn, Thomas
/ TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
/ FILE REFERENCE: (1300)-1199,002
/ CURRENT APPLICATION NUMBER: US/08/787,321A
/ FILING DATE: 1997-01-03
/ EARLIER FILING DATE: 1996-01-12
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: oligonucleotide
/ US-08-787-321-24

Query Match          0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 70 CGCACACGCACACAC 84
DB 1 CACACACACACACAC 15

RESULT 561
US-09-043-303-15/c
/ Sequence 15, Application US/09043303

/ Patent No. 6251589
/ GENERAL INFORMATION:
/ APPLICANT: TSUII, Shoji
/ APPLICANT: SANPEI, Kazujiro
/ TITLE OF INVENTION: Method for Diagnosing Spinocerebellar Ataxia Type 2 and
/ TITLE OF INVENTION: Primers Therefor
/ FILE REFERENCE: 0760-0241P
/ CURRENT APPLICATION NUMBER: US/09/043,303
/ CURRENT FILING DATE: 1998-05-18
/ EARLIER APPLICATION NUMBER: PCT/JP96/01999
/ EARLIER FILING DATE: 1996-07-18
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-043-303-15

Query Match          0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1369 CGGGGGCGGGCGGG 1383
DB 15 CGGGGGCGGGCGGTG 1

RESULT 562
US-09-081-646-344
/ Sequence 344, Application US/09081646
/ Patent No. 6333152
/ GENERAL INFORMATION:
/ APPLICANT: Kinzler, Kenneth
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Zhang, Lin
/ APPLICANT: Zhou, Wei
/ TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
/ TITLE OF INVENTION: Cancer Cells
/ FILE REFERENCE: 01107.74664
/ CURRENT APPLICATION NUMBER: US/09/081,646
/ CURRENT FILING DATE: 1998-05-20
/ EARLIER APPLICATION NUMBER: 60/047,352
/ EARLIER FILING DATE: 1997-05-21
/ NUMBER OF SEQ ID NOS: 871
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 344
/ LENGTH: 15
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-081-646-344

Query Match          0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1195 CACGGCCCGAGGCAC 1209
DB 1 CATGGCCCGAGGTAC 15

RESULT 563
US-09-081-646-424
/ Sequence 424, Application US/09081646
/ Patent No. 6333152
/ GENERAL INFORMATION:
/ APPLICANT: Kinzler, Kenneth
/ APPLICANT: Vogelstein, Bert
/ APPLICANT: Zhang, Lin
/ APPLICANT: Zhou, Wei
/ TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
/ TITLE OF INVENTION: Cancer Cells
/ FILE REFERENCE: 01107.74664
```

; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 424
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-424

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1195 CACGGCCAGGGCAC 1209
||| ||||| |||||
Db 1 CATGGCCAGGGCCC 15

RESULT 564

US-09-081-646-484
; Sequence 484, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 484
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-484

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 787 CAAGCTGGTGAAGGA 801
||| ||||| |||||
Db 1 CATGTTGGTGAAGGA 15

RESULT 565

US-09-081-646-730
; Sequence 730, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; TITLE OF INVENTION: Cancer Cells
; FILE REFERENCE: 01107.74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 730

; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-730

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 787 CAAGCTGGTGAAGGA 801
||| ||||| |||||
Db 1 CATGTTGGTGAAGGA 15

RESULT 566

US-09-495-140-19
; Sequence 19, Application US/09495140
; Patent No. 6376182
; GENERAL INFORMATION:
; APPLICANT: CHAO, LEE
; APPLICANT: CHAO, JULIE
; APPLICANT: SONG, QING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING
; TITLE OF INVENTION: TISSUE KALLIKREIN GENE PROMOTER POLYMORPHISMS WITH TREATMENT
; TITLE OF INVENTION: OF ESSENTIAL HYPERTENSION
; FILE REFERENCE: 19113.0081
; CURRENT APPLICATION NUMBER: US/09/495,140
; CURRENT FILING DATE: 2000-01-31
; EARLIER APPLICATION NUMBER: 09/389,566
; EARLIER FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 08/856,141
; EARLIER FILING DATE: 1997-05-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. 6376182e =
; OTHER INFORMATION: synthetic construct
US-09-495-140-19

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1561 GGCGCGGAGGGGC 1575
||| ||||| |||||
Db 1 GGAGCGGGGGGGGC 15

RESULT 567

US-08-433-123-11/c
; Sequence 11, Application US/08433123
; Patent No. 6444789
; GENERAL INFORMATION:
; APPLICANT: LUC, Shun
; TITLE OF INVENTION: CD16-II VARIANTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-433-123-11

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 CTGCTGCTAGTCTC 187
DB 15 CTGCTGCTAGTCTC 1

RESULT 568

US-08-433-123-22
Sequence 22, Application US/08433123
Patent No. 6444789

GENERAL INFORMATION:

APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-11 VARIANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,123
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-433-123-22

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 173 CTGCTGCTAGTCTC 187
DB 1 CTGCTGCTAGTCTC 15

RESULT 569

US-09-586-376-9
Sequence 9, Application US/09586376
Patent No. 6492115

GENERAL INFORMATION:

APPLICANT: Guida, Marco
TITLE OF INVENTION: GENETIC TYPING OF THE HUMAN CYTOCHROME P450 2A6 GENE
TITLE OF INVENTION: AND RELATED MATERIALS AND METHODS
FILE REFERENCE: 4389-20
CURRENT APPLICATION NUMBER: US/09/586,376
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 15
TYPE: DNA
ORGANISM: Homo sapiens
US-09-586-376-9

Query Match 0.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 GCACCCGCTGGCAT 1521
DB 1 GAACCCGCTGGCTT 15

RESULT 570

US-08-086-915-6
Sequence 6, Application US/08086915
Patent No. 544167

GENERAL INFORMATION:

APPLICANT: Pettersson, Kim SI
TITLE OF INVENTION: Variant Luteinizing Hormone Encoding DNA
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Adduci, Mastriani, Schaumberg & Schill
STREET: 1140 Connecticut Avenue, N.W., Suite 250
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,915
FILING DATE: 07-JUL-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kubovcik, Ronald J.
REGISTRATION NUMBER: 25,401
REFERENCE/DOCKET NUMBER: 15873005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-6300
TELEFAX: 202-466-2006
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-086-915-6

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1293 GCCTGGCGGCGGC 1307
Db 1 GCCTGGCGGCGGC 15

RESULT 571
US-07-977-284A-150
; Sequence 150, Application US/07977284A
; Patent No. 5558988
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvaniemi, Peritti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofer Nina
; TITLE OF INVENTION: METHODS OF DETECTING A GENETIC
; TITLE OF INVENTION: PREDISPOSITION FOR OSTEOARTHRITIS
; NUMBER OF SEQUENCES: 261
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988aris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,284A
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-0697
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-07-977-284A-150

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 561 AGTCTCTGCACTACG 575
Db 2 AGTCTCTGCACTAAG 16

RESULT 572
US-08-222-177A-439
; Sequence 439, Application US/08222177A
; Patent No. 5582979

; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (GC-CA)n (GG-GT)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865.601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 439:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-222-177A-439

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 70 CGCACGCGCACAC 84
Db 1 CACACACACACAC 15

RESULT 573
US-08-166-664-10/C
; Sequence 10, Application US/08166664
; Patent No. 5646020
; GENERAL INFORMATION:
; APPLICANT: James A. McSwiggen
; APPLICANT: J. Anthony Mamone
; TITLE OF INVENTION: HAMMERHEAD RIBOZYMES FOR
; TITLE OF INVENTION: PREFERRED TARGETS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/166,664
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/884,074
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/062
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-166-664-10

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 830 GCGGACGACGAGGC 844
Db 15 GCGGACGACGAGGC 1

RESULT 574

US-08-137-117D-97/c
Sequence 97, Application US/08137117D
Patent No. 5795965
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, Jose
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/A00K

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-137-117D-97

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1229 CTGGCCTCGTGCTAC 1243
Db 15 CTGGCCTCGTTTAC 1

RESULT 575

US-08-367-069-10/c
Sequence 10, Application US/08367069
Patent No. 5811538
GENERAL INFORMATION:
APPLICANT: Timothy A. Riley
APPLICANT: Mark A. Reynolds
APPLICANT: Lloyd R. Snyder
APPLICANT: Robert E. Klem
TITLE OF INVENTION: IMPROVED PROCESS FOR THE
TITLE OF INVENTION: PURIFICATION OF OLIGOMERS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,069
FILING DATE: December 30, 1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/176,851
FILING DATE: 30 December 1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-367-069-10

```
Query Match      0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      15 GAGGAGAGAGCGGAG 29
DB      15 GAGGAGAGAGAGAG 1

RESULT 576
US-08-436-717-97/c
; Sequence 97, Application US/08436717
; Patent No. 5817790
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,717
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-436-717-97

Query Match      0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1229 CTGGCCTCGTGCTAC 1243
DB      15 CTGGCCTCGTTTAC 1
```

```
RESULT 577
US-08-574-586-3
; Sequence 3, Application US/08574586
; Patent No. 5837512
; GENERAL INFORMATION:
; APPLICANT: Rabson, ArnoldRichard B.
; APPLICANT: Lin, Hsin-Ching
; APPLICANT: Bodkin, Marion
; APPLICANT: Strair, Roger
; TITLE OF INVENTION: Selective Biological Destruction of
; TITLE OF INVENTION: Tumor Cells
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices
; STREET: 758 Springfield avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: US
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/574,586
; FILING DATE: 14-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD1-026cip
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-273-4988
; TELEFAX: 908-273-4679
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-574-586-3

Query Match      0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      89 CGCGCGCACTCGCGC 103
DB      2 CGCGCGCGCGCGCGC 16

RESULT 578
US-08-574-586-3/c
; Sequence 3, Application US/08574586
; Patent No. 5837512
; GENERAL INFORMATION:
; APPLICANT: Rabson, ArnoldRichard B.
; APPLICANT: Lin, Hsin-Ching
; APPLICANT: Bodkin, Marion
; APPLICANT: Strair, Roger
; TITLE OF INVENTION: Selective Biological Destruction of
; TITLE OF INVENTION: Tumor Cells
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices
; STREET: 758 Springfield avenue
; CITY: Summit
; STATE: NJ
```

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-256-568B-42

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 478 GGCCATCTCGTGAT 492
Db 16 GGTCACTCGCGCAT 2

RESULT 580
US-08-520-385-1
Sequence 1, Application US/08520385
Patent No. 5855911
GENERAL INFORMATION:
APPLICANT: Lopez-Berestein, Gabriel
APPLICANT: Tari, Ana M.
TITLE OF INVENTION: LIPOSOMAL PHOSPHODIESTER,
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 750 Bering Dr., Ste. 400
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77057-2198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,385
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Kenneth D.
REGISTRATION NUMBER: 30,460
REFERENCE/DOCKET NUMBER: UTSC433
TELEPHONE: 713/787-1460
TELEFAX: 713/789-2879
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-520-385-1

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 89 CGCGCGCATCTCGGC 103
Db 15 CGCGCGCGCGCGC 1

RESULT 579
US-08-256-568B-42/c
Sequence 42, Application US/08256568B
Patent No. 5846704
GENERAL INFORMATION:
APPLICANT: MAERTENS, GERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 898 GAAGGCTTCTACGT 912
|||||
Db 1 GAAGGGCTTCTGGGT 15

RESULT 581

US-08-432-871C-52/c
; Sequence 52, Application US/08432871C
; Patent No. 5877010
; GENERAL INFORMATION:
; APPLICANT: Loeb, Lawrence A.
; APPLICANT: Black, Margaret E.
; TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,871C
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 240052.409C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-432-871C-52

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 639 GCCTGGCGGTGGAGG 653
|||||
Db 16 GCCTGGAGGTGGGG 2

RESULT 582

US-08-256-426B-150
; Sequence 150, Application US/08256426B
; Patent No. 5948611
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Ala-Kokko, Leena
; APPLICANT: Williams, Charlene J.
; APPLICANT: Ritvanieni, Pertti
; APPLICANT: Baldwin, Clinton
; APPLICANT: Hopkinson, Ian
; APPLICANT: Ahmad, Nilofar Nina
; TITLE OF INVENTION: Methods of Detecting A Genetic
; NUMBER OF SEQUENCES: 293
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris

STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,426B
; FILING DATE: 03-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/10964
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,284
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
US-08-256-426B-150

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 561 AGTCTCTGCCTACG 575
|||||
Db 2 AGTCTCTGGACTAG 16

RESULT 583

US-08-885-126-7/c
; Sequence 7, Application US/08885126A
; Patent No. 5955397
; GENERAL INFORMATION:
; APPLICANT: Arnold, Lyle J.
; APPLICANT: Riley, Timothy A.
; APPLICANT: Reynolds, Mark A.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE
; TITLE OF INVENTION: OLIGOMERS
; FILE REFERENCE: GENTA.020FW2
; CURRENT APPLICATION NUMBER: US/08/885,126A
; CURRENT FILING DATE: 1997-06-30
; EARLIER APPLICATION NUMBER: 08/343,018
; EARLIER FILING DATE: 1994-11-21
; EARLIER APPLICATION NUMBER: 08/154,013
; EARLIER FILING DATE: 1993-11-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized oligomer
US-08-885-126-7

PRIOR APPLICATION DATA:

Query Match 0.7%; Score 11.8; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. NO. 3e+02; 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GAGGAGAGAGCGGAG 29
 Db 2 GAGAGAGAGAGAG 16

RESULT 587
 US-08-611-587-16/c
 ; Sequence 16, Application US/08611587
 ; Patent No. 6150091
 ; GENERAL INFORMATION:
 ; APPLICANT: PANDOLFO, MASSIMO
 ; APPLICANT: MONTERMINI, LAURA
 ; APPLICANT: MOLTO, MARIA D.
 ; APPLICANT: KOENIG, MICHAEL
 ; APPLICANT: CAMPUZANO, VICTORIA
 ; APPLICANT: COSESE, MIREILLE
 ; TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSES: Fulbright & Jaworski L.L.P. Patent Dept.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.
 ; ZIP: 77010

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/611,587
 ; FILING DATE: 03-MAR-1996

CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brashears-Macatee, Sarah J.
 ; REGISTRATION NUMBER: 38,087
 ; REFERENCE/DOCKET NUMBER: D-5901
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-651-5620
 ; TELEFAX: 713-651-5246
 ; TELEX: 76-2829

INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; POSITION IN GENOME:
 ; UNITS: bp
 ; US-08-611-587-16

Query Match 0.7%; Score 11.8; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. NO. 3e+02; 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1345 CGGAGACAGCGCGG 1359
 Db 15 CGGAAACAGCGCGG 1

RESULT 588
 US-08-814-412-9/c
 ; Sequence 9, Application US/08814412
 ; Patent No. 6150141

GENERAL INFORMATION:
 ; APPLICANT: Jarrell Ph.D., Kevin A.
 ; TITLE OF INVENTION: Intron-Mediated Techniques and Reagents
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Choate, Hall & Stewart
 ; STREET: 53 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/814,412
 ; FILING DATE: 11-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jarrell Ph.D., Brenda H.
 ; REGISTRATION NUMBER: 39,223
 ; REFERENCE/DOCKET NUMBER: 0079571-0040
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617 248 5000
 ; TELEFAX: 617 248 4000
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 16 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "Ribozyme"
 ; IMMEDIATE SOURCE:
 ; CLONE: last 16 nt of K2 in Y7
 ; US-08-814-412-9

Query Match 0.7%; Score 11.8; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. NO. 3e+02; 2; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 772 GGAGCAGGCGGCAC 786
 Db 16 GGAGCAGGCGGCAC 2

RESULT 589
 US-08-814-412-45/c
 ; Sequence 45, Application US/08814412
 ; Patent No. 6150141
 ; GENERAL INFORMATION:
 ; APPLICANT: Jarrell Ph.D., Kevin A.
 ; TITLE OF INVENTION: Intron-Mediated Techniques and Reagents
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Choate, Hall & Stewart
 ; STREET: 53 State Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/814,412
 ; FILING DATE: 11-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:

NAME: Jarrell Ph.D., Brenda H.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 0079571-0040
TELEPHONE: 617 248 5000
TELEFAX: 617 248 4000
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "RNA"
IMMEDIATE SOURCE:
CLONE: PY7 exon sequence
US-08-814-412-45

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2;

QY 772 GGAGCAGCGCGGCAC 786
DB 16 GGAGCAGCTCGGCAC 2

RESULT 590

US-09-038-369B-42/c
Sequence 42, Application US/09038369B
Patent No. 6171784
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSELIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSELIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-038-369B-42

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2;

QY 478 GGCCATCTCGGTGAT 492
DB 16 GGTCACTCGGCAT 2

RESULT 591

US-09-109-663-69
Sequence 69, Application US/09109663
Patent No. 6277981
GENERAL INFORMATION:
APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 9855-3UI
CURRENT APPLICATION NUMBER: US/09/109,663
CURRENT FILING DATE: 1998-07-03
EARLIER APPLICATION NUMBER: 60/051,705
EARLIER FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 69
LENGTH: 16
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Known
OTHER INFORMATION: Effective ASO
US-09-109-663-69

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02; 2; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 2;

QY 805 GAGCCCGGGGACCG 819
DB 1 GATCCCGGGTACCG 15

RESULT 592

US-09-411-862A-21/c
Sequence 21, Application US/09411862A
Patent No. 6348583
GENERAL INFORMATION:
APPLICANT: David Segev
TITLE OF INVENTION: POLY(ETHER-THIOETHER), POLY(ETHER-SULFOXIDE) AND POLY(ETHER-SULFONE) NUCLEIC ACIDS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sol Sheinbein c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,

TELEPHONE: 972-3-6127676

```
; COMPUTER: IBM  
; OPERATING SYSTEM:
```

; OPERATING SYSTEM

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMaisters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.409C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-270-956-52

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 639 GCGTGGCGGTGGAGG 653
Db 16 GCGTGGAGGTGGGGG 2

RESULT 596
US-09-378-900A-42/c
Sequence 42, Application US/09378900A
Patent No. 6495670
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-378-900A-42
Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 478 GGCCATCTCGGTGAT 492
Db 16 GGTCATCTCGCGAT 2
RESULT 597
US-09-899-044-42/c
Sequence 42, Application US/09899044
Patent No. 6548244
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,044
FILING DATE: 06-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 42:

US-09-899-044-42

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 478 GGCCATCTCGGTGAT 492
DB 16 GGTCACTCTGGCGAT 2

RESULT 598

US-09-371-772B-5646
; Sequence 5646, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5646
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5646

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 922 GCGGAGCCCGCGGA 936
DB 2 GCUAGAGCCCGGAGA 16

RESULT 599

US-09-371-772B-5650
; Sequence 5650, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5650
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5650

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 CGCGCGCGGGACCG 1368
DB 1 CGCGCGCGGGACG 15

RESULT 600

US-09-371-772B-5656/c
; Sequence 5656, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5656
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5656

Query Match 0.7%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 3e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 911 GTGATCGAGCGCG 925
DB 16 GTGAGCGCGCGCG 2

RESULT 601

US-09-371-772B-5917
; Sequence 5917, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5917
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5917